

Protein signatures of spontaneous lipolysis and lipoprotein lipase activity in cow's milk

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1	Protein signatures of spontaneous lipolysis and lipoprotein lipase
2	activity in cow's milk
3	
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36 Animal welfare statement

- 37 The experiment was conducted in accordance with the French legislation on animal
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- 39 Consideration of Ethics in Animal Experimentation (Authorization: APAFiS #17944-
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42 **Conflict of interest statement**

- 43 The authors declare that they have no conflict of interest.
- 44

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- 57 curation, Formal analysis, Visualization, Writing original draft.
- 58 L. Bernard: Conceptualization and management of the Lipomec project, Resources,
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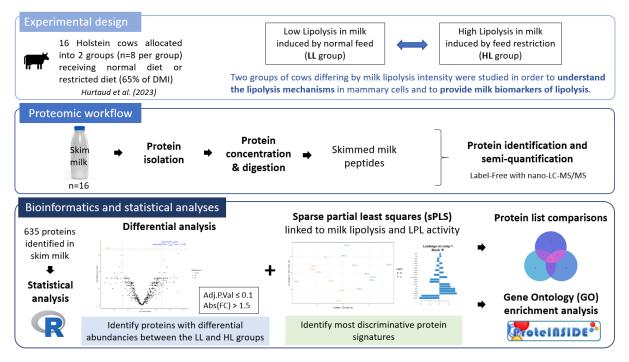
- A. Rau: Methodology, Software, Data curation, Validation, Formal analysis,
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- 67 M. Bonnet: Conceptualization of the proteome methodology, conceptualization of the
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- 69 C. Cebo: Conceptualization and management of the Lipomec project, Funding
- acquisition, Supervision, Data curation, Visualization, Writing original draft.
- All authors agree to be accountable for the content of the work.

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Highlights

- A specific protein signature is associated with high lipolysis levels in cow milk
- CD5L and GP2 in skim milk are putative biomarkers of lipolysis
- CUL9, SURF4 and HID1 are associated with low levels of lipolysis in skim milk
- LPL inhibitors contribute to explaining low lipolysis levels observed in cow milk

Graphical abstract



1

2 Abstract

- 3 Spontaneous milk lipolysis refers to the breakdown of triacylglycerols in milk.
- 4 Lipolysis impacts the organoleptic value of milk by causing off-flavours and reduces
- 5 the technological properties of milk. Lipolysis is caused by lipoprotein lipase (LPL), a
- 6 tightly regulated enzyme in milk. Our objective was to identify robust biomarkers of
- 7 lipolysis and putative regulators of LPL enzyme in bovine milk. To achieve this goal,
- 8 we used feed restriction as a lever to generate highly contrasted samples with regard
- 9 to milk lipolysis. We combined statistical methods on proteomics data, milk lipolysis
- 10 and LPL activity values. Following this strategy, we identified CD5L and GP2 as
- 11 robust biomarkers of high lipolysis in cow milk. We also identified HID1, SURF4 and
- 12 CUL9 as putative inhibitors of the lipolytic process in the milk. We thus proposed 5
- 13 putative biomarkers to be considered in future tools to manage milk lipolysis.
- 14

15 Keywords

- 16 Dairy cows, lipolysis, lipoprotein lipase, milk fat, milk proteins, biomarkers
- 17

18 Introduction

19 Fat is present in milk as fat globules, a supra-molecular structure made of a

triglyceride core surrounded by a complex membrane called the Milk Fat Globule

21 Membrane (MFGM). In freshly secreted milk, the MFGM is intact and forms an

22 effective barrier that protects fat from the action of milk lipases, with an efficiency that

- can vary according to the molecular composition of the membrane [1]. In addition, in
- some cases such as agitation, pumping or homogenization of milk, this membrane is
- damaged and lipases are able to reach the triglyceride core causing lipolysis [2].
- 26 Milk lipolysis, that is, enzymatic degradation of milk triglycerides into free fatty acids
- by the lipoprotein lipase (LPL; EC:3.1.1.34), severely impairs milk quality from both
- the organoleptic and the technological points of view. Off-flavours originating from
- 29 free fatty acids and their oxidation products in milk are not appreciated by
- 30 consumers. Moreover, the presence of partial triglycerides in milk impairs its
- technological properties, like foaming and creaming abilities [3]. Controlling milk
- 32 lipolysis is therefore an economic issue for dairy producers.
- 33 Spontaneous lipolysis of milk results from a complex interplay between farming
- 34 practices, animal physiology and animal genetics [4,5], but underlying mechanisms

are still poorly understood. At the molecular level, the lipolytic system is constituted 35 by the lipoprotein lipase, cofactors (activators and inhibitors) and substrate (milk 36 triglycerides), and the resulting products are free fatty acids and partial glycerides. In 37 the native bovine milk, the skim fraction is the richest source of LPL mainly 38 associated with the casein micelle through electrostatic interactions [3] and upon 39 cooling the proportion of LPL linked to the MFGM increases [6,7]. Inactive LPL can 40 refold into active LPL dimers in the presence of calcium ions and this phenomenon is 41 potentiated by the presence of activators, namely serum albumin, lipoproteins, 42 heparin or glycerol [8], which are mainly located in skim milk. The presence of LPL 43 inhibitors has also been documented in milk. A component of the milk proteose-44 peptone fraction PP3, also known as lactophorin, has been identified as a potential 45 LPL inhibitor [9]. The skim milk proteose-peptone component 5 (PP5, residues 1–105 46 47 and 1–107 of β -casein) has been identified in some studies as an activator of LPL [10] and in other studies, as an inhibitor of LPL [9]. However, most of these studies 48 49 dealing with the identification of milk and skim milk lipase activity regulators were conducted in the 1980s [9,11–13] and need to be reassessed in view of the major 50 advances in proteomics that have occurred over the past decade, especially with 51 regard to the analysis of milk protein fractions [14,15]. 52

The aim of the present study is to discover biomarkers of lipolysis in skim milk by 53 using a model of feed restriction as a lever to produce milk samples with contrasted 54 lipolysis rates [16]. To achieve this outcome, we combined statistical methods on our 55 proteomics data with milk lipolysis values and LPL enzyme activities to identify 56 robustly discriminant proteins of lipolysis in milk. Following this strategy, we further 57 describe the protein signatures of spontaneous lipolysis or LPL activity in skim milk. 58 We acknowledge some limitations in our approach. In order to perform satisfactory 59 proteomic analysis of skim milk, milk fat was removed with skimming, but part of the 60 LPL is located in the fat phase. However, our results help to better understand the 61 62 biological mechanisms of milk fat degradation through the identification of putative regulators of lipase activity in milk, which is a prerequisite to design a test to detect 63 lipolysis in milk samples. 64

65

66 1. Material and methods

67 **1.1 Animals and experimental design**

The experiment was conducted at the Installation Expérimentale Production Laitière, 68 INRAE, Dairy nutrition and physiology (IE PL, 35650 Le Rheu, France; 69 https://doi.org/10.15454/yk9g-pf68) with agreement for animal housing number C-35-70 275-23. This study was realized on samples from sixteen primiparous and 71 72 multiparous Holstein cows at 156 ± 20 days in milk fed with diet treatments based on corn silage and differing by the level of feeding. These cows are a subsample of the 73 74 44 cows included in a reverse design on feeding level during 4 weeks split into 2 twoweek periods in March 2019 [16]. Two feeding levels were considered: "non-75 restricted", with cows fed a corn silage-based diet at 100% of ad libitum dry matter 76 77 intake (DMI), and "restricted", corresponding to a corn silage-based diet at 65% of ad libitum DMI. For omics studies, 8 cows in each two-week period were used. During 78 79 period 1, each group of cows first received the non-restricted diet, followed by the restricted diet. During period 2, the order of feeding levels was reversed. Further 80 81 details about the feed offered in the two diets can be found in [16]. The animals had access to fresh water ad libitum. 82

83

1.2 Milk processing and lipolysis determination

The milk yields of individual animals were recorded over 6 milkings at 8:00 and 16:30 85 each week. Milk samples were collected individually on morning milking on the last 86 day of each experimental period, with one part immediately treated with bronopol-B2 87 preservative (LIAL, Aurillac, France) to measure fat, protein and lactose content 88 (MyLab, Chateaugiron, France). The other part of milk (unpreserved) was used to 89 determine the milk lipolysis level using the copper soap method (mEq/100g fat) [5,17] 90 as described in detail in [16]. The morning lipolysis levels of milk collected on the last 91 day of the period were used to define groups of low and high lipolysis cows based on 92 a threshold of 0.5 mEq/100 g fat: Low Lipolysis (LL group with mean of 0.32 ± 0.12 93 94 mEq/100 g fat) vs High Lipolysis (HL group, 0.84 ± 0.33 mEq/100 g fat). Unpreserved milk was also stored at -80°C for protein extraction and identification analyses and 95 LPL activity determination (nmol/mn/ml) measured in vitro using a radiolabelled 96 substrate [18]. 97

98 1.3 Major protein identification using LC-ESI-MS

99 Major milk proteins, namely the four caseins (α s1-caseins, α s2 caseins, β -caseins

and κ -caseins), α -lactalbumin, and β -lactoglobulin and all their isoforms were

identified and quantified using our improved method combining reverse-phase high 101 performance liquid chromatography (Ultimate LC 3 000 system, Thermo Fisher 102 Scientific, Waltham, MA) with an ESI-TOF mass spectrometer micrOTOF II focus 103 (Bruker Daltonics, Wissembourg, France) [19]. Briefly, milk samples were placed on 104 dry ice immediately after milking and stored at -80°C for further analyses. Milk 105 samples were rapidly thawed at 37°C then skimmed by centrifugation at 2 000 g and 106 4°C for 10 min. The cream was removed by means of a spatula and the skimmed 107 milk was aliquoted into fractions of 20 and 100 µL, frozen at -20°C and kept under 108 109 these conditions until analysis by Liquid Chromatography-Electro Spray Ionization-Mass Spectrometry (LC-ESI-MS). Identification of the main milk protein isoforms was 110 performed using our in-house mass database of bovine milk proteins containing 111 nearly 3 000 theoretical masses, corresponding to the multiple isoforms of milk 112 proteins including genetic and splicing variants, post-translationally modified proteins 113 (phosphorylated and glycosylated) and main known plasmin hydrolysis products. 114 115

116 **1.4 Minor protein identification using nano-LC-MS/MS**

117 **1.4.1 Skim milk protein isolation, concentration and digestion**

All reagents were purchased from Sigma-Aldrich (Saint Louis (MO)) except when 118 otherwise specified. The raw milk was slightly defrosted during one night at 4°C and 119 milk components equilibrated by incubation during 1 h at 37°C. The equilibrated raw 120 milk was centrifuged at 3 500 g for 15 min at 4°C to separate the cream from the 121 skimmed milk (SM). Acetic acid was added to the SM reaching pH 4.6 to precipitate 122 the caseins. The homogenate was centrifuged at 10 000 g for 10 min at 4°C to 123 discard caseins and supernatant recovered until protein concentration determination. 124 Enrichment of minor or low-abundance SM proteins was performed using the 125 ProteoMiner Small-Capacity columns (#163-3006, Bio-Rad Laboratories, Hercule 126 (CA)) according to the manufacturer's instructions. Column was washed twice, and 127 128 10 mg of proteins from SM were deposited on column and incubated 2 h at room temperature (RT) under agitation. Then, spin columns were washed with buffer twice 129 and with purified milli-Q water once (1 min at RT) followed by a 1 000 g centrifugation 130 in order to eliminate unbound proteins. Proteins enriched from medium- and low-131 132 abundance were incubated for two runs of 15 min in 20 µL of elution buffer (RT) and centrifuged at 1 000 g. Supernatant was recovered until protein concentration 133

- determination using Pierce[™] BCA protein assay kit (Fisher Scientific, Hampton (NH)).
- 136 Twenty µg of proteins were mixed with reducing sodium dodecylsulfate buffer (4%)
- 137 with dithiothreitol (20 mM) and incubated 10 min boiling in order to reduce disulphide
- bonds. Then proteins were alkylated in iodoacetamide (50 mM) during 45 min
- 139 protected from light. After acidification with phosphoric acid (1.2%), S-Trap® buffer
- 140 (triethylammonium bicarbonate 100 mM; in ethanol 90%) was added and proteins
- 141 were deposit on S-Trap® column (Protifi, Fairport, NY). Columns containing proteins
- were centrifuged at 4 000 g during 10 min, washed with S-Trap® buffer and this step
 was repeated 3 times.
- 144 SM protein digestion was performed with sequencing grade trypsin (Promega,
- 145 Madison (WI)) 1:50 [w/w] enzyme/protein ratio in triethylammonium bicarbonate (50
- 146 mM) with overnight incubation at 37°C. Tryptic peptides were extracted by adding 60
- ¹⁴⁷ μL of 0.2% formic acid in acetonitrile (50%) followed by centrifugation at 4 000 g
- during 10 min repeated twice. Supernatants containing peptides were dried by
- 149 SpeedVac vacuum concentrator (ThermoScientific, Illkirch (FR)). Peptides were
- recovered in 100 µL of 5% acetonitrile and 0.05% trifluoroacetic acid (TFA) solution
- 151 with sonication during 5 min and transferred into glass vials (Interchim, Montluçon
- 152 (FR)) prior to nano-LC-MS/MS analysis.
- 153 **1.4.2 Peptide analysis on nano-LC-MS/MS**
- Peptide mixtures were analysed by nano-LC-MS/MS using an Ultimate 3 000 system 154 coupled to a QExactive HF-X mass spectrometer (MS) (Thermo Fisher Scientific). A 155 volume of 6 µl of peptide extract was first concentrated and desalted at a flow rate of 156 30 µl/min on a C18 pre-column 5 cm length x 100 µm (Acclaim PepMap 100 C18, 5 157 µm, 100A nanoViper) equilibrated with Trifluoroacetic Acid 0.05% in water. Then this 158 preconcentration column was switched online with a nanoflow analytical C18 column 159 (Acclaim PepMap 100 - 75 µm inner diameter x 25 cm length; C18 - 3 µm -100Å - SN 160 161 10719167) equilibrated at a flow rate of 300 nL/min with a 95% solvent A (99.9% H2O, 0.1% formic acid). The peptides were separated according to their 162 hydrophobicity using a gradient of solvent B (99.9% acetonitrile, 0.1% formic acid) 163 from 5 to 32% during 50 min. For MS analysis, eluted peptides were electrosprayed 164 165 in positive-ion mode at 1.6 kV through a nanoelectrospray ion source heated to 250°C. The MS operated in data dependent mode: the parent ion was selected in the 166

orbitrap cell (FTMS) at a resolution of 120 000 and each MS analysis was followed by
 18 MS/MS with analysis of the MS/MS fragments at a resolution of 15 000.

At the end of the LC-MS/MS analysis, the raw data processing of peptide MS/MS 169 spectra was carried out with Progenesis QI software (version 4.2, Nonlinear 170 Dynamics, Newcastle upon Tyne, UK). The software defined a reference run used to 171 perform an automatic alignment of all other runs considering a maximum allowable 172 ion charged set to 5. The detected ions were grouped in a file (mgf) directly exported 173 to the Mascot v2.5 (http://www.matrixscience.com) interrogation engine and searched 174 against a Bos taurus decoy database (i.e. ref_bos_taurus, 37 513 sequences) with 175 the following parameters during the request: precursor mass tolerance of 10 ppm and 176 fragment mass tolerance of 0.05 Da, a maximum of two missed cleavage sites of 177 trypsin, carbamidomethylation (C), oxidation (M) and deamidation (NQ) set as 178 variable modifications. Protein identification was validated when at least two peptides 179 from one protein showed statistically significant identity above Mascot scores with a 180 false discovery rate (FDR) of 1%. For label-free protein quantification analysis, the 181 identified peptides from the database search were imported back to Progenesis QI 182 183 software. All unique validated peptides of an identified protein were included and the total cumulative abundance was calculated by summing the abundances of all 184 185 peptides allocated to the respective protein. Consequently, proteins were quantified based on the intensities of the specific validated peptides. 186

187

188 **1.5 Statistical analysis**

Statistical analyses were performed using R (version 4.2.1). All data came from 2 189 190 groups of 8 animals forming a part of the reverse design experiment (full details in Hurtaud et al., 2023). As cited earlier, the milk lipolysis level was used to constitute 191 the Low Lipolysis (LL) group with a mean of 0.32 ± 0.12 mEq/100 g fat and the High 192 Lipolysis (HL) group with a mean of 0.84 ± 0.33 mEq/100 g fat. Thus, the 193 experimental design consists of the following fixed effects: period (P1 vs P2, differing 194 by 15 d of lactation), sequence (order of feed restriction treatment), and lipolysis level 195 (LL vs HL). We note that as both diets (restricted and unrestricted) were fed in 196 succession to each cow, repeated measurements were available for each cow in this 197 design. 198

- Animal parameters (such as DMI, milk production and composition) and major
- 200 proteins from milk containing 0.3% missing variables were imputed by the k-nearest
- neighbour method (k=5) using the impute package (version 1.70.0).
- A linear mixed model with fixed effects (period, sequence and lipolysis) and a random
- animal effect was fit for animal parameters using the lme4 package (version 1.1.31),
- and statistical significance was evaluated using Type II sums of squares in the Anova
- function from the car package (version 3.1.1; p < 0.05). The sequence effect was not significant and was thus removed from the model.
- 207 Raw minor protein abundances from SM containing 0.4% missing variables were
- imputed by the k-nearest neighbour method (k=5) using the impute package.
- Abundances were then log-transformed. We applied two complementary statistical
- analyses to identify a proteomic signature that discriminates the LL and HL groups: i)
- a parametric univariate differential analysis (Diff-A) to identify significant proteins one
- by one based on their abundances; and to go further ii) a sparse multi-level
- 213 multivariate analysis to identify a concise signature of proteins strongly linked to
- either lipolysis (sPLS-lipolysis) or LPL activity (sPLS-LPL-activity). The parametric
- univariate differential analysis (Diff-A) was performed by fitting to each protein an
- 216 empirical Bayes linear model including lipolysis, sequence and period fixed effects
- and a random animal effect using the limma package (version 3.52.2). As no
- significant effect was observed across proteins for period and sequence, these were
- removed from the model. P-values were adjusted to control the FDR (adj.P.Val) using
- the Benjamini-Hochberg approach. Statistical significance was considered at
- adj.P.Val < 0.1 and an absolute fold change threshold of 1.5.
- 222 Sparse multi-level partial least square analyses (sPLS) were performed in regression
- mode with paired observations on cows using the mixOmics package (version 6.20.0,
- Rohart et al., 2017). Predictor variables (X) corresponded to the log protein
- abundances, and the response variable (Y) to either the milk lipolysis (sPLS-lipolysis)
- or the milk LPL activity (sPLS-LPL-activity). For each sPLS model, we retained 2
- components, both including a total of 30 proteins with non-zero loadings. A posteriori,
- the first sPLS component for each model was found to be highly discriminative
- 229 between the LL and HL groups. The proteins with non-zero loadings in the first
- 230 component were compiled into lists of milk lipolysis related proteins and LPL activity
- related proteins with their respective contributions. Contributions correspond to the

- weight assigned to each protein to define each component; larger absolute values 232
- mean that a given protein has a greater importance for a given component. 233
- Lists of proteins were mined for biological meaning by a gene ontology (GO) 234
- enrichment analysis, performed using the ProteINSIDE webservice online tool 235
- version 2.0 (available at https://umrh-236
- bioinfo.clermont.inrae.fr/ProteINSIDE 2/index.php?page=upload.php, [20]) based on 237
- Bos taurus and a search of biological reactions on Reactome based on Homo 238 239 sapiens.
- 240

2. Results 241

242 2.1 Highly contrasted milk samples with regard to spontaneous lipolysis levels

We used feed restriction of the cows as a lever to generate two groups of 8 cows with 243 244 contrasted milk in terms of lipolysis levels for use in omics studies. The performance data of these 8 dairy cows were comparable with those on the full set of 44 cows in 245 246 the original study [16].

- The parameters relative to the ingestion of the 8 dairy cows from the LL group (fed an 247
- unrestricted diet) and the HL group (fed a restricted diet) are reported in 248
- Supplementary Table S1. As expected, the milk yield and composition are 249
- dramatically divergent between LL and HL groups (Table 1). The milk production 250
- decreased by 9.7% in the HL compared with LL group (P<0.05). The total milk 251
- protein content was reduced by 16.7% in the HL group compared to the LL group 252
- (583.4 g and 486.1 g secreted in morning milk, respectively). Both the casein and 253
- soluble protein content were divergent between LL and HL groups (-6.5% and -9.6%, 254
- 255 respectively). At the same time, milk lipolysis increased by a factor of 2.6 in the HL
- group compared with the LL group (P<0.05). Interestingly, the milk LPL activity 256
- increased by a factor of only 1.4 in the HL group (P<0.05). Although the correlation 257
- between LPL activity and lipolysis in milk is high (r=0.69; P = 0.003; Figure 1), the 258
- 259 increase in the milk LPL activity (+44.5%) cannot solely explain the dramatic increase
- in lipolysis levels we observed in the HL group (+162.5%), thus suggesting that 260
- 261 regulators may amplify the lipolytic response in milk.
- 262

263 2.2 Spontaneous lipolysis modulates the abundances of skimmed milk proteins

- 635 proteins were identified in our study and raw abundances for each protein are 264 265
 - reported in Supplementary Table S3. Among these 635 proteins, the spontaneous

- lipolysis significantly impacts the milk abundances of eight proteins. The volcano plot
- 267 (Figure 2), resulting from the parametric univariate analysis, displays the seven
- proteins with higher abundance (A0A3Q1M3L6, CD5L, A0A3Q1LRW4, KRT10, GP2,
- APOA4, LBP) and the one with lower abundance (CUL9) in the HL compared with LL
- group (Table 2). Interestingly, the LPL protein (P11151) was 1.9 times more
- abundant in HL compared with LL group, but this increase was not statistically
- 272 significant.
- 273

274 **2.3 Milk protein signature of lipolysis in milk**

- 275 The sPLS multivariate analysis of milk lipolysis (Y) and log protein abundances (X)
- 276 reveals a component that is highly discriminative between the HL and LL groups
- 277 (Supplementary Figure S1). The corresponding milk proteins implicated in lipolysis
- are reported in Table 3. Among the 15 proteins associated with the HL group, the ten
- with the largest weights corresponded to two caseins (CSN1S2, CSN1S1), 3
- apolipoproteins (APOE, APOA4, APOA1), CD5L, LBP, A0A3Q1LRW4, CNTFR and
- GP2. Among the 15 proteins associated with the LL group, the ten with the largest
- weights are ALOX15, SDHA, FASN, GNG12, SURF4, STK38, HID1, ABCG2, MYO6and UQCRC2 (Table 3).
- The 15 proteins associated with HL are annotated by terms within the biological
 process (BP) ontology related to the "positive regulation of cholesterol esterification",
 the "steroid esterification" and the "very-low-density lipoprotein particle remodelling"
- for APOA1, APOA4 and APOE (Supplementary Table S3). Similarly, the 15 proteins
- associated with the LL group were annotated by terms within the BP ontology
- highlighting the "positive regulation of protein lipidation" and "lipoprotein metabolic
- 290 process" and the "establishment of protein localization at the membrane of reticulum
- endoplasmic" for both RAB3GAP1 and RAB3GAP2 (Supplementary Table S3).
- 292

293 2.4 Milk protein signature of LPL activity

- The first component of the sPLS multivariate analysis of milk LPL activity (Y) and log protein abundances (X) similarly discriminated between the HL and LL groups (Supplementary Figure S2). SM proteins related to the level of milk LPL activity are
- listed in Table 4. Seventeen proteins were strongly associated with the HL group (i.e.,
- positive loadings for component 1 of the sPLS) with GP2, BSPRY, KRT10, ANXA7,
- 299 MARCKS, CD5L, SLC5A9, SLC6A8, A0A3Q1M3L6 and IDH1 in the top 10. Among

- the 13 proteins associated with the LL group, HID1, SQLE, CUL9, VAT1, PHB2,
- ACSL3, NDRG4, ATP13A3, FASN and ANKRD13A were in the top 10 (Table 4).
- The 17 proteins associated with HL were significantly annotated by terms within the
- BP category that emphasized "localization" for CD5L, GP2, NAPA, SH3GLB1,
- 304 SLC5A9, SLC6A8, the "negative regulation of cholesterol metabolic process" for
- 305 ERLIN2 the "isocitrate metabolic process", the "glyoxylate cycle" and "tricarboxylic
- acid metabolic process" for IDH1. Moreover, 13 proteins among the 17 were
- annotated by the "membrane" term within the CC category (Supplementary TableS3).
- The 13 proteins associated with the LL group were annotated by terms within the BP
- category that highlight the "regulation of phospholipid metabolic process", particularly
- phosphatidylcholine, for ACSL3 and PHB2 and "negative regulation of protein
- 312 localization to endosome" for ANKRD13A (Supplementary Table S3).
- 313

314 **2.5 Putative milk biomarkers of milk lipolysis**

- 315 Crossing the protein lists resulting from the univariate and multivariate statistical
- analyses highlights the CD5 molecule like (CD5L) and the Glycoprotein 2 (GP2).
- These are therefore putative biomarkers of high lipolysis in milk (Figure 3). CD5L and
- 318 GP2 skim milk abundances correlated positively with milk lipolysis (r = 0.69; P =
- 319 0.003 and r = 0.5; P = 0.04) and milk LPL activity (r = 0.68; P = 0.003 and r = 0.6; P =
- 320 0.01) (Supplementary Table S4).
- Focusing on protein lists associated with the LL group, the Surfeit locus protein 4
- 322 (SURF4) and Chromosome 17 open reading frame 28 ortholog (HID1) are common
- proteins linked to milk lipolysis (sPLS-lipolysis) and milk LPL activity (sPLS-LPL
- activity) (Figure 4). SURF4, HID1 and CUL9 are negatively correlated with both
- lipolysis (r = -0.63, P = 0.008; r = -0.4, P = 0.1 and r = -0.48, P = 0.06) and LPL
- activity in milk (r = -0.74, P = 0.0009; r = -0.6, P = 0.01 and r = -0.59, P = 0.01)
- 327 (Supplementary Table S4). These proteins are therefore good candidates that may
- be indicative of low lipolysis in the milk of dairy cows.
- 329

330 3. Discussion

- As expected, the feed restriction of dairy cows dramatically induced lipolysis in milk
- (+162.5%; HL group) compared with cows fed with normal diet (LL group) [16,21].

Noticeably, while lipolysis increased 2.6 times in the HL compared to LL group, the 333 activity of the LPL enzyme only increased 1.4 times, thus suggesting that molecules 334 may act as regulators of the enzyme in skim milk (Table 1). However, the LPL activity 335 measured in vitro in optimal conditions represents the potential LPL activity and not 336 the in vivo activity. Furthermore, previous studies in cows showed that milk lipolysis 337 was poorly correlated to LPL activity [22], which is probably due at least in part to the 338 major cellular location of the LPL in the casein micelle fraction of milk in cows. These 339 340 considerations support giving more weight to the molecules identified as a signature of lipolysis within the skim milk. 341

The feed restriction necessarily impacts the milk proteome [21,23]. Our aim was to 342 343 identify robust biomarkers of milk lipolysis and a list of putative regulators of lipolysis in skim milk to better understand the lipolytic processes. To achieve this goal, we first 344 345 performed a classical univariate statistical analysis on our proteomics data to identify differentially abundant proteins between lipolysis treatments while accounting for 346 347 other experimental factors. We then performed two multivariate statistical analyses on the proteomics abundance data to identify proteins forming signatures of lipolysis 348 and milk LPL enzyme activity. sPLS is a powerful tool that seeks to maximize the 349 covariance between the proteomic abundances and response variable of interest 350 (lipolysis, LPL activity) using a set of latent components, where a lasso penalization 351 is used to focus interest on a concise set of predictive biomarkers. Finally, we 352 compared differential proteins and those forming signatures of lipolysis and LPL 353 activity to identify proteins involved in the regulation of the lipolytic process in milk. 354 Following this 3-step strategy, we identified CD5L and GP2 as robust biomarkers and 355 putative regulators of lipolysis in milk (Figure 3). These proteins were consistently 356 identified in the differential analysis, as well as sPLS-lipolysis and sPLS-LPL activity 357 analyses, highlighting them as key molecules involved in the lipolytic pathway in 358 bovine milk. CD5L, also called Apoptosis inhibitor of macrophage (AIM) or apoptosis 359 360 inhibitor 6 (Api6), is a soluble member of the scavenger receptor cysteine-rich superfamily, which is secreted by mature tissue macrophages in mouse in the 361 362 context of inflammation and obesity. Kurokawa et al. [24,25] reported that the AIM/Api6/CD5L protein is incorporated into adipocytes via CD36-mediated 363 364 endocytosis, and induces lipolysis by suppressing the activity of fatty acid synthase (FASN). In our study, CD5L negatively correlates (r = -0.75; P = 0.0007) with FASN, 365 366 the latter of which was strongly associated with the LL group for both sPLS-lipolysis

and sPLS-LPL-activity (Tables 3 and 4). As proposed earlier by Iwamura et al. [26] in 367 adipocytes of mice, we further suggest that in bovine mammary epithelial cells, the 368 highly abundant CD5L binds to cytosolic FASN, inhibiting its enzymatic activity and 369 thus lowering the milk short and medium chain FA from *de novo* mammary synthesis. 370 In other words, CD5L may act by repressing *de novo* synthesis by FASN, favouring a 371 higher fatty acid uptake by both the mammary LPL and NEFA transporters for milk 372 lipid synthesis [27]. The latter being favoured by the high plasma NEFA concentration 373 374 observed due to adipose mobilization which was associated with lipolysis in milk [21]. GP2 was identified in the heat- and acid-stable fraction of ovine milk [28] and was 375 recently listed in all the fractions of bovine milk throughout lactation [15]. The heat-376 377 and acid-stable fraction of bovine milk belongs to the proteose-peptone fraction, which contain potential activators or inhibitors of LPL enzyme [29]. Most of the 378 379 component of proteose-peptone fraction are fragments of caseins produced by the action of endogenous plasmin and the main constituents are recognized as 380 381 components 3, 5, 8 [30,31]. Peptone protease (PP) 5 have been identified both as an activator [10] or an inhibitor of LPL enzyme [9,21] and remain controversial. Among 382 this PP fraction, the potential GP2 role in the lipolysis process has not been yet 383 addressed. However, given its structure of glycosylphosphatidylinositol-anchored 384 glycoprotein, GP2 may be involved in the link of LPL with the MFGM. This hypothesis 385 remains to be investigated and is based on the observations that 386 glycosylphosphatidylinositol-anchored glycoprotein such as GPIHBP1 is involved in 387 the binding of LPL and chylomicrons in mice [32]. Moreover, GP2 is highly positively 388 correlated with the glypican-1 protein (GPC1) in an sPLS discriminant analysis 389 between the LL and HL groups (Supplementary Figure S3 reports the circle plot of 390 component 1 and 2). GPC1 is a cell surface proteoglycan carrying an heparan sulfate 391 moiety, which facilitates or inhibits the interaction of proteins with lipid-rafts. Heparin-392 like glycosaminoglycans have been identified as potential activators of LPL [29,33]. 393 394 Among research focusing on the interactions between LPL and MFGM allowing its access to its substrates, LPL is known to bind to heparan sulfate-type 395 396 glycosaminoglycans present on the surface of MFG [6]. All these assumptions justify analyzing the involvement of GP2 in the localization of LPL close to its substrate, 397 398 supported by GP2 positive correlation with milk LPL activity (r = 0.60; P = 0.01) (Supplementary Table S4). 399

Three proteins were both differentially abundant and related to lipolysis. APOA4, A0A3Q1LRW4 and LBP were identified in the milk from the HL group as strongly associated proteins (Table 3, Figure 3). APOA4 is a known actor in lipolysis, since it is required for efficient activation of LPL by APOC-II [3,34]. A0A3Q1LRW4 protein is an immunoglobulin fragment, but not well described. Lastly, the LBP protein addressing the HL group indicates modification of the immune response and lipid transport in the cows in line with adaptive response to feed restriction [35].

407

408 Dairy cows fed diets covering requirements present low lipolysis levels in milk despite the presence of LPL, thus suggesting that the LPL enzyme is tightly regulated. It is 409 410 therefore of interest to identify not only proteins associated with high levels of lipolysis in milk, but also proteins associated with low levels of lipolysis, the latter of 411 412 which may be putative inhibitors of lipolysis in milk. The cullin 9 protein (CUL9) was identified in the milk of the LL group both in our differential analysis and sPLS-LPL 413 414 activity analysis (Figure 4). CUL9 belongs to the cullin family of proteins, molecular scaffolds that have crucial roles in the homeostasis of cellular proteins through the 415 ubiquitin-proteasome system [36]. Cullins work in concert with RING proteins as 416 docking proteins to add ubiquitin to specific proteins, targeting them for destruction. 417 Such a regulation of lipase activity through ubiquitination has been recently 418 demonstrated for the adipose triglyceride lipase in hepatic cells [37]. 419 Two additional proteins were strongly associated with reduced lipolysis levels in milk: 420 SURF4 (Surfeit locus protein 4) and HID1 (Chromosome 17 open reading frame 28 421 ortholog protein) (Figure 4). SURF4 is an endoplasmic reticulum (ER) cargo receptor 422 423 that mediates the selective export of lipoproteins to facilitate their secretion, thus playing a crucial role for the maintenance of lipid homeostasis [38]. 424 As well as SURF4, HID1 protein is associated with low levels of LPL activity and 425 lipolysis (Figure 4). HID-1 controls formation of large dense core vesicles by 426 427 influencing cargo sorting of neuropeptides and peptide hormones through acidification of the trans Golgi network [39]. HID1 is thus involved in the release of 428 429 insulin by pancreatic cells through the processing of proinsulin to functionally active 430 hormone [40]. Moreover, in our study, the expression of HID1 is positively correlated with the expression of FASN in the LL group (r = 0.72; P = 0.001; Supplementary 431 Table S4), thus favouring the mammary *de novo* FA pathway in the case of a 432 433 sufficient feeding level.

434

435 **4. Conclusions**

In this study, we used feed restriction as a lever to produce highly contrasted 436 samples with regard to lipolysis levels in bovine milk. Following proteomic studies, we 437 combined uni- and multivariate statistical analyses with milk lipolysis values and/or 438 LPL enzyme activities measured in milk to identify key regulators of lipolysis in bovine 439 milk. We identified the CD5L and GP2 proteins as robust biomarkers of high lipolysis 440 in cow milk. HID1, SURF4 and CUL9 are putative inhibitors of the lipolytic process in 441 the milk. The data provided here constitute a robust basis for further tests on a larger 442 443 population to design a quick on-farm diagnosis tool such as strip tests to monitor 444 lipolysis levels in cow milk.

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446 **References**

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	LL	HL	SEM	p-val lipolys is	Significa nce of lipolysis	Signific ance of period
Milk yield and gross composition						
Milk yield (kg)	18.5	16.7	0.62	0.031	*	NS
Milk fat content (g secreted)	710.7	611.5	31.8	0.056	NS	NS
Milk protein content (g secreted)	583.4	486.1	24.2	0.0004	***	NS
Milk lactose content (g secreted)	908.1	825.3	31	0.044	*	NS
Somatic Cell Count (x10 ³ /mL)	34.3	33.5	8	0.967	NS	NS
Milk fat characteristics						
Lipolysis (mEq/100g fat)	0.32	0.84	0.09	0.002	**	NS
Lipoprotein Lipase activity (nmol/min/ml)	514.8	744.2	35.7	0.002	**	NS
Milk fat globule diameter ($d_{4,3}^*$) (µm)	3.74	3.65	0.09	0.587	NS	NS
Milk fat globule diameter $(d_{3,2}^*)$ (µm)	3.31	3.13	0.07	0.185	NS	NS
Milk fat globule area (S*) (m²)	1.97	2.11	0.05	0.147	NS	NS
Milk proteins characteristics						
Protein content (g/kg)	31.2	29	0.5	0.011	*	NS
Nitrogen content (g/kg)	32.5	30.3	0.5	0.01	**	NS
Non-casein nitrogen (g/kg)	6.4	6	0.1	0.046	*	*
Non-protein nitrogen (g/kg)	1.25	1.32	0.04	0.215	NS	NS
Casein content (g/kg)	26	24.3	0.5	0.008	**	NS
Soluble protein content (g/kg)	5.2	4.7	0.2	0.011	*	NS
Casein/protein ratio (%)	82.8	83.6	0.5	0.054	NS	NS

Table 1: Morning milk parameters in LL and HL groups.

 $^{*}d_{4,3}=\Sigma(N_{i}\times d_{i}^{4})/\Sigma(N_{i}\times d_{i}^{3})$

 $^{*}d_{3,2} = \Sigma(N_{i} \times d_{i}^{3}) / \Sigma(N_{i} \times d_{i}^{2})$

*S = 6/($\rho \times d_{3,2}$) (with N_i the number of MFG in diameter class d_i and ρ the density of the particle considered (0.92 for fat))

P-values were significant at <0.001 (***); <0.01 (**) and <0.05 (*)

NS = not significant

Table 2: Differentially regulated proteins in HL group compared with LL group from the parametric univariate differential analysis (Diff-A).

Accession	Gene name	Protein name	Raw abundance ratio (HL/LL)	FC	RSD	Adjusted- Pvalue
A0A3Q1M3 L6	Uncharacterized protein	Immunoglobulin heavy constant mu	2.0	1.6	0.262	0.078
A6QNW7	CD5L	CD5 molecule like	3.1	2.2	0.624	0.078
A0A3Q1LR W4	Uncharacterized protein	Immunoglobulin heavy constant mu	2.7	1.9	0.470	0.078
P06394	KRT10	Keratin, type I cytoskeletal 10	2.7	2.1	0.590	0.078
A0A3Q1M1 93	GP2	Glycoprotein 2	2.1	1.7	0.315	0.078
Q32PJ2	APOA4	Apolipoprotein A-IV	5.6	2.9	0.739	0.078
Q2TBI0	LBP	Lipopolysaccharide- binding protein	2.6	1.9	0.521	0.080
E1BM39	CUL9	Cullin 9	0.3	-2.4	0.760	0.099

			contrib	ance of ution to np1
Accession	Gene Name	Protein Name	HL	LL
P02663	CSN1S2	Alpha-S2-casein	0.338	
Q03247	APOE	Apolipoprotein E	0.314	
A6QNW7	CD5L	CD5 molecule like	0.313	
Q2TBI0	LBP	Lipopolysaccharide-binding protein	0.242	
P02662	CSN1S1	Alpha-S1-casein	0.231	
A0A3Q1LRW 4	Uncharacterize d protein	Immunoglobulin heavy constant mu	0.192	
Q32PJ2	APOA4	Apolipoprotein A-IV	0.140	
P15497 A0A3Q1LQY	APOA1	Apolipoprotein A-I	0.133	
1	CNTFR	Ciliary neurotrophic factor receptor	0.119	
A0A3Q1M193	3 GP2	Glycoprotein 2	0.105	
Q29S21	KRT7	Keratin, type II cytoskeletal 7	0.099	
P17697	CLU	Clusterin	0.070	
P11017	GNB2	Guanine nucleotide-binding protein G	0.065	
P81265	PIGR	Polymeric immunoglobulin receptor	0.054	
F1MKU3	BSPRY	B-box and SPRY domain containing Polyunsaturated fatty acid lipoxygenase	0.032	
P27479	ALOX15	ALOX15		-0.378
P31039	SDHA	Succinate dehydrogenase		-0.345
F1N647	FASN	Fatty acid synthase		-0.224
Q28024	GNG12	Guanine nucleotide-binding protein G		-0.214
A7YY49	SURF4	Surfeit locus protein 4		-0.158
A2VDV2	STK38	Serine/threonine-protein kinase 38 Chromosome 17 open reading frame		-0.139
Q08E22	HID1	28 ortholog Broad substrate specificity ATP-binding		-0.120
Q4GZT4	ABCG2	cassette transporter ABCG2		-0.117
E1BPK6	MYO6	Unconventional myosin-VI Cytochrome b-c1 complex subunit 2,		-0.111
P23004	UQCRC2	mitochondrial Ubiquitin-like modifier-activating		-0.076
A3KMV5	UBA1	enzyme 1 Dolichyl-diphosphooligosaccharide	•	-0.048
A3KN04 A0A3Q1MSN	RPN1	protein glycosyltransferase subunit 1		-0.036
7	COASY	Coenzyme A synthase RAB3 GTPase activating non-catalytic	•	-0.033
A0A3Q1LTV A0A3Q1MFP		protein subunit 2 Rab3 GTPase-activating protein		-0.030
2	RAB3GAP1	catalytic subunit		-0.023

Table 3: List of 30 proteins from component 1 of sparse multi-level multivariate analysis (sPLS – milk lipolysis) contributing to LL or HL group

Accession	Gene name	contrib	ance of ution to np1	
			HL	LL
A0A3Q1M1				
93	GP2	Glycoprotein 2	0.442	•
F1MKU3	BSPRY	B-box and SPRY domain containing	0.305	•
P06394	KRT10	Keratin, type I cytoskeletal 10	0.244	
P20072	ANXA7	Annexin A7	0.208	
P12624	MARCKS	Myristoylated alanine-rich C-kinase	0.191	
		substrate		•
A6QNW7	CD5L	CD5 molecule like	0.164	•
E1B749	SLC5A9	Solute carrier family 5 member 9 Sodium- and chloride-dependent creatine	0.147	
O18875	SLC6A8	transporter 1	0.126	
		Immunoglobulin heavy constant mu	0.400	
L6	protein IDH1	loopitroto dobudrogonogo	0.106	•
Q9XSG3 Q29S21		Isocitrate dehydrogenase	0.104	•
E1BEH7	KRT7	Keratin, type II cytoskeletal 7	0.079	•
A0A3Q1LQ	TC2N	Tandem C2 domains, nuclear	0.079	•
Y1	CNTFR	Ciliary neurotrophic factor receptor Alkaline phosphatase, tissue-nonspecific	0.063	
P09487	ALPL	isozyme	0.056	
Q32LM0	SH3GLB1	Endophilin-B1	0.046	
Q1RMU4	ERLIN2	Erlin-2	0.036	
P81125	NAPA	Alpha-soluble NSF attachment protein Chromosome 17 open reading frame 28	0.015	
Q08E22	HID1	ortholog		-0.344
A5D9A8	SQLE	Squalene monooxygenase		-0.327
E1BM39	CUL9	Cullin 9		-0.275
F1MUP9	VAT1	Vesicle amine transport 1		-0.271
Q2HJ97	PHB2	Prohibitin-2		-0.215
F1MEX9	ACSL3	Acyl-CoA synthetase long chain family member 3		-0.136
A0A3Q1LV G9 A0A3Q1LM	NDRG4	NDRG family member 4		-0.100
J5	ATP13A3	ATPase 13A3		-0.083
Q71SP7	FASN	Fatty acid synthase		-0.081
F1N545	ANKRD13A	Ankyrin repeat domain 13A		-0.032
P63009	AP2B1	AP-2 complex subunit beta		-0.020
Q1RMP9	CMTM8	CKLF-like MARVEL transmembrane domain-containing protein 8		-0.018
A7YY49	SURF4	Surfeit locus protein 4		-0.010

Table 4: List of 30 proteins from component 1 of sparse multi-level multivariate analysis (sPLS – LPL activity) contributing to LL or HL group

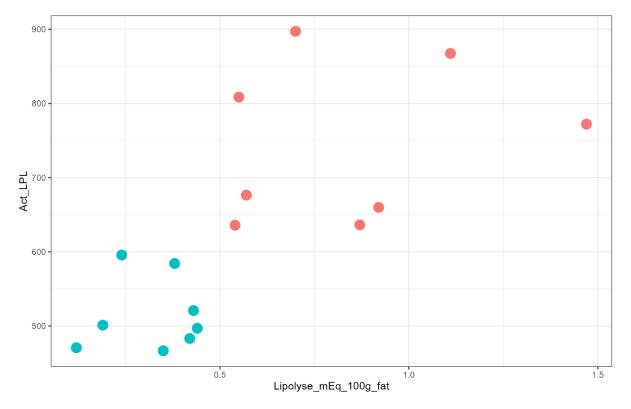


Figure 1: Plot regression between lipolysis (mEq/100g of fat) and LPL activity in milk (nmol/mn/ml). Blue dots are from LL group and red dots are from HL group.

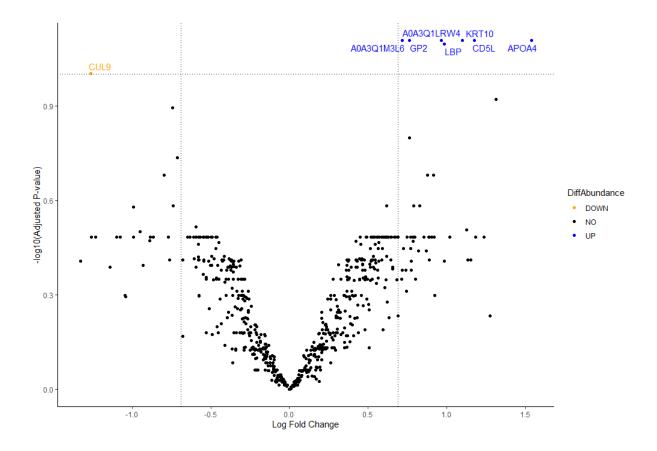


Figure 2: Volcano plot displays log fold changes on the x-axis versus a measure of statistical significance (Adjusted P-value) on the y-axis from the parametric univariate differential analysis (Diff-A). Gene Name of proteins with a higher abundance in HL than LL group are in blue. Gene Name of proteins with a lower abundance in HL than in LL group are in orange.

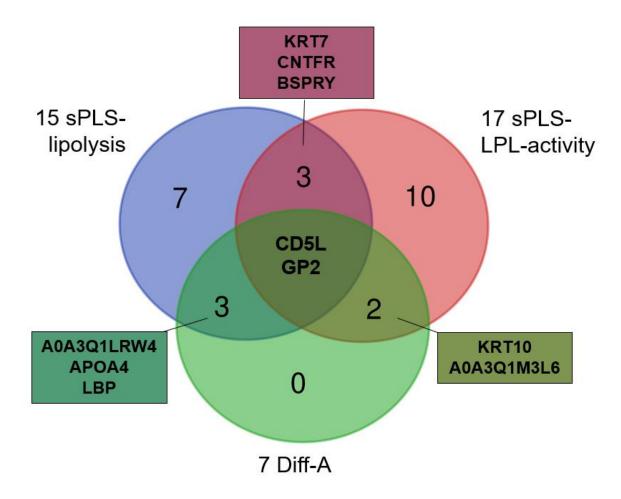


Figure 3: Venn diagram comparing proteins lists addressing HL group from sPLS-lipolysis (n=15), sPLS-LPL-activity (n=17) and differential analysis (n=7).

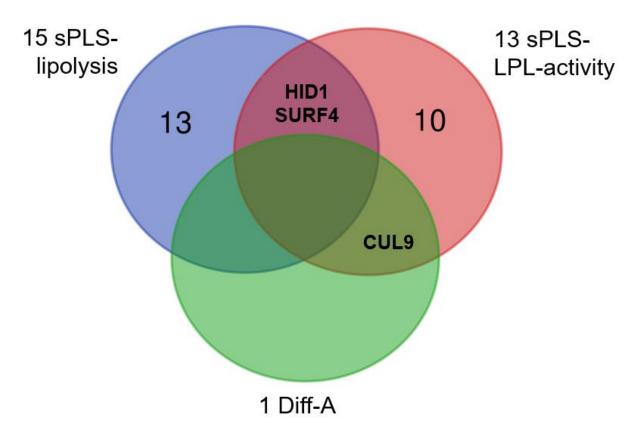


Figure 4: Venn diagram comparing proteins lists addressing LL group from sPLSlipolysis (n=15), sPLS-LPL-activity (n=13) and differential analysis (n=1).

Supplementary Table S1: Dry matter, protein and energy intakes, energy balance and efficiency of protein digestible in intestine for LL and HL groups of cows

	LL	HL	SEM	p-val lipolysis	Signifi cance of lipolysi s	Signific ance of period
DMI (kg/d)	21,1	15,8	0,8	0,000	***	NS
PDI* (g/d)	1761,6	1306,1	74,9	0,000	***	NS
NEL requirements (MJ/d)	19,69	17,56	0,65	0,016	*	NS
PDI efficiency**	0,83	0,84	0,01	0,023	*	**
NEL balance (MJ/kg DM)	-5,7	-21,9	2,8	0,003	**	NS

*PDI = protein digestible in the intestine (INRA, 2018)

**PDI efficiency = (67,5-0,52 x (PDI-100) + 0,014 x (MilkProteins-1000))/100 (INRA, 2018)

								Highest	Lowest																		
Accession	Peptide count	 Unique peptides 	Confiden ce score	Anova (p)	a Value	Max fold change	Power	mean condition	mean condition	Mass	Description	:8 HL cé	iHL c	5 HL c	3 HL o	4 HL c	1 HL c	7 HL c2	HL d	BLL cé	5 LL c5	iLL c	3 LL 04	LL c	1 LL c7	7 LL c2	2 LL
A0A3Q1M3L6 A0A3Q1M3L	3	3	288,6	0,00015	0,07954	2,20488	0,99405	HL	LL	40450	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1	3226518	2621250	4618716	4488714	3744970	4456646	3369445	4974398	2228555	1349347	1586230	2537017	2647998	1919380	2153799	1202398
P81265 PIGR_BOVIN;F1MR E1BM39 E1BM39 BOVIN	9	8	775,38	-,	-,	2,37159	0,98556	HL	LL HL	82383 280394	Polymeric immunoglobulin receptor OS=Bos taurus OX=9913 GN=PIGR PE: Cullin 9 OS=Bos taurus OX=9913 GN=CUL9 PE=3 SV=3	18491661 55721	17827237 42068	16234862 57630	56889382 12035	24959346 63371	13957555 155657	22436490 32947	24789977 24046	6311510 106520	16559764 228090	5968660 731736	10893410 91953	16724980 263421	9122168 136179	7368834 78939	17332069 66437
A5D9A8 A5D9A8_BOVIN	3	3	234,75	.,	0,07954	2,7695	0,97575	LL	HL	63520	Squalene epoxidase OS=Bos taurus OX=9913 GN=SQLE PE=2 SV=1	267138	333860	222873	348292	513451	176116	265883	319247	492317	1316786	1651682	620758	482820	269110	337201	1060616
A6QNW7 A6QNW7_BOVIN	2	2	75,41	.,	0,07954	3,25975	0,97403	HL	LL	50179	CD5 molecule like OS=Bos taurus OX=9913 GN=CD5L PE=2 SV=1	643807	592909	562089	266766	338739	337455	131201	310142	127599	26711	80848	104284	129637	207537	127133	226291
P62935 PPIA_BOVIN;G3X8E Q08E22 Q08E22 BOVIN	2	2	453,78 115,78	.,	0,07954 0,07954	1,91686 2,21171	0,97125	LL	HL HL	17858 88424	Peptidyl-prolyl cis-trans isomerase A OS=Bos taurus OX=9913 GN=PPIA PE: Chromosome 17 open reading frame 28 ortholog OS=Bos taurus OX=9913	4010575 150009	2290016 369420	3584617 149259	6517901 308098	4244459 341137	2079380 135199	4202181 186125	6021004 185060	3740351 414099	8048892 946040	6802231 652788	6978896 336053	4898127 359689	8894368 236875	7140479 380311	12533023 435730
A0A3Q1LRW4 A0A3Q1LRW	3	3	219,5	-,	-,	2,97963	0,96359	HL	LL	47130	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1	4893882	5780402	4249250	9587083	1750842	5222401	9810590	6730173	1070669	1817993	1951621	2026944	2145015	1817171	2387631	4305990
A6QNZ7 A6QNZ7_BOVIN;A0 Q148J4 Q148J4 BOVIN;A0	9	4	749,45 738.22	-,	-,	2,95267 1.6784	0,9589	HL	LL HL	54816 20837	Keratin 10 (Epidermolytic hyperkeratosis; keratosis palmaris et plantaris) C RAB2A, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB2/	883223 10535572	963247 3997409	1133275 7852213	391108 4848207	584185 7005446	748431 4912477	913247 11433758	1961319 9508143	194422 7763388	127432 9786634	142178 10670042	406512 6609125	386029 12262340	943935 18548596	241266 12715467	361512 15876310
E1BNW4 E1BNW4_BOVIN	4	4	260,94	-,	-,	1,61707	0,90393	HL	LL	78539	Transmembrane channel-like protein OS=Bos taurus OX=9913 GN=TMC4 F	1392806	1674433	2569959	1110141	1160836	938296	1818823	1839859	1386477	671131	780583	794407	807036	1223767	1257034	514567
A0A3Q1M193 A0A3Q1M19	3	3	174,07	.,		2,89491 3.14467	0,8958 0.88234	HL	LL	58427 53280	Glycoprotein 2 OS=Bos taurus OX=9913 GN=GP2 PE=1 SV=1	4238810	7983325	6800899	7208158	5478408	6206673	5097694	10608024	2424584	3124936	1604835	2466313	4036523	3978824	2995935	4722875 96054
A0A3Q1LKB0 A0A3Q1LKB0 Q3ZC65 Q3ZC65_BOVIN	6	2	66,75 543,39		.,	3,14467	0,88234	LL	LL HL	45783	Lipopolysaccharide-binding protein OS=Bos taurus OX=9913 GN=LBP PE=4 AUP1, lipid droplet regulating VLDL assembly factor OS=Bos taurus OX=99:	423454 7645294	250048 7533428	120660 7454262	126822 6136405	145365 6756025	106415 7592812	143527 7761627	227590 3795844	39144 6607011	168252 10030098	91116 11771302	79247 8395895	55110 9106829	38138 7854526	32871 7614252	13062908
Q28024 GBG12_BOVIN	3	3	168,18	.,	.,	1,66504	0,86675	LL	HL	8052	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=	769263	514114	879234	596975	948293	1372805	813274	2282752	1951921	2157106	1636973	1337010	1375231	3103622	2503532	1936831
A0A3Q1MB37 A0A3Q1MB3 P09487 PPBT_BOVIN	5	5	334,19 355.76	.,	0,24533 0.24533	1,92418	0,83157	HI	HL	80207 57156	Acyl-CoA synthetase short chain family member 2 OS=Bos taurus OX=991: Alkaline phosphatase, tissue-nonspecific isozyme OS=Bos taurus OX=9913	2114252 8423425	1577784 5029499	2816705 7231044	4387306 4136854	4059671 2849111	4092851 3978422	2617173 10412417	2284696 4162687	4289839 2338748	6310487 403245	10846871 2313361	6608888 1715647	4509270 4935284	2152739 3497869	2854309 3559427	9948758 1783223
A0A3Q1MEI7 A0A3Q1MEI7	2	2	258,92	0,00652	0,24533	1,87271	0,82648	LL	HL	52267	Presenilin OS=Bos taurus OX=9913 GN=PSEN1 PE=3 SV=1	521189	470865	302372	1005377	251318	870944	869947	593459	708107	1510679	1229433	1757367	540016	892899	580572	2039818
A0A3Q1MKC8 A0A3Q1MKC	4	3	244,33 395.17	.,	0,26146	1,81176	0,80978	HL HL		50852 42982	Keratin, type II cytoskeletal 7 OS=Bos taurus OX=9913 GN=KRT7 PE=1 SV=:	348587 4635077	683041 1967503	415822 1984517	326480 1919417	350165 2108630	185141	216983	479894 2446000	147272 930868	224216 528658	99932 360485	253901	203872	184163 1873800	273669 2069573	180670 667784
A0A3Q1LQY1 A0A3Q1LQY1 A0A3Q1M3N0 A0A3Q1M3N	4	8	574,94	.,	-,	4,76744	0,78854	HL	LL LL	42982	Ciliary neurotrophic factor receptor OS=Bos taurus OX=9913 GN=CNTFR P Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1	3104310	1967503	302598	459812	393613	2407122 511824	3502870 1920270	606006	323928	259873	122680	796890 55187	3732271 376609	179461	155496	134563
F1MH40 F1MH40_BOVIN	3	3	134,93		-,	2,05909	0,77494	HL	LL	26318	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=2	1730907	1772626	1371175	776731	263100	960929	1278585	1693129	280019	432583	334921	512970	1446930	717647	1189429	396489
A8YXY3 SEP15_BOVIN P12624 MARCS_BOVIN	2	2	145,18 252.76	-,	-,	1,95847 2.4378	0,76865 0,75468	LL HI	HL	17964 31646	Selenoprotein F OS=Bos taurus OX=9913 GN=SELENOF PE=2 SV=2 Myristoylated alanine-rich C-kinase substrate OS=Bos taurus OX=9913 GN:	239484 1356703	187035 1200599	500675 853963	638425 385107	202178 570318	325442 899710	449553 938623	793840 658359	482354 628734	903434 63997	806062 116997	491656 129379	791788 376576	786618 921401	526637 465689	2228024 48188
G5E601 G5E601_BOVIN;A0	10	10	541	.,		1,76434	0,75059	LL	HL	155520	RAB3 GTPase activating non-catalytic protein subunit 2 OS=Bos taurus OX=	819917	684956	841835	456899	1248151	384583	852648	748010	2727916	682038	1227056	1113708	1389198	1421875	1540285	695999
O18875 SC6A8_BOVIN	3 10	3 10	220,18 641.79	.,		1,47092 1.74728	0,73774	HL	LL	70629 81483	Sodium- and chloride-dependent creatine transporter 1 OS=Bos taurus OX	924262 40183899	1028849 32772747	1354651 36866579	892850 44694265	531101 31218702	805669 19000071	1032097 40310361	853460 24919069	602041 45001505	298207 79828774	556840 113957118	547517 61645104	568751 37061194	903711 34428648	950536 32278390	446262 67655057
A0A3Q1MK38 A0A3Q1MK3 A0A140T831 A0A140T831	3	3	245.17	- ,		1,74728	0,73692	LL	HL	16384	Terpene cyclase/mutase family member OS=Bos taurus OX=9913 GN=LSS Cystatin-B OS=Bos taurus OX=9913 GN=CSTB PE=3 SV=2	40183899	758225	778259	2115827	957953	722953	1490040	931657	1206587	1049224	1509295	1753080	1613617	2093182	1484308	4203706
Q28065 C4BPA_BOVIN;A0A	4	4	182,09	0,02.20	0,26366	3,87951	0,72686	HL	LL	68841	C4b-binding protein alpha chain OS=Bos taurus OX=9913 GN=C4BPA PE=2	384050	498445	288435	66578	10100	465844	297912	85171	36782	129449	69469	15268	20536	48367	29628	228893
A0A3Q1LMJ5 A0A3Q1LMJ5 A0A140T897 A0A140T897	8	8 5	638,27 391.07	.,	0,26366	1,69107 1.86065	0,72537	LL HL	HL	141962	Cation-transporting ATPase OS=Bos taurus OX=9913 GN=ATP13A3 PE=3 S Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1	2184290 552810	2756134 512617	2924505 891593	2993222 498733	2740416 648380	3158768 876041	2080695 918869	2177796 1342093	3893128 393748	10147833 511213	6705968 759848	4910873 246604	3032263 488320	2236400 674346	2576470 347039	3629961 211724
G5E6N4 G5E6N4_BOVIN	2	2	102,95	.,	.,	1,74547	0,70431	LL	HL	41723	Palmitoyltransferase OS=Bos taurus OX=9913 GN=ZDHHC18 PE=3 SV=2	59117	17238	76560	72388	47171	24136	28068	76055	111961	38027	76692	42220	70203	81234	136189	129260
A0A3Q1MJK0 A0A3Q1MJK0	4	4	450,07	.,.	0,27168	1,41322	0,69928	LL	HL	49429	FAS-associated factor 2 OS=Bos taurus OX=9913 GN=FAF2 PE=4 SV=1	3354205	4056370	3685925	3287263	2264581	1312724	3433115	2683479	3526532	4356339	5737916	2979207	3157992	2982014	3688504	6214712
Q71SP7 FAS_BOVIN A0A3Q1MMA1 A0A3Q1MN	44 4	10 4	3766 264.72	0,01812	0,2779 0.298	2,2421	0,69025		HL	274380 31726	Fatty acid synthase OS=Bos taurus OX=9913 GN=FASN PE=2 SV=1 Uncharacterized protein OS=Bos taurus OX=9913 GN=SEC22B PE=3 SV=1	4144732 352640	3426255 309229	5003815 381666	12529573 329112	22749906 671157	18893801 221413	3743940 533578	9727860 1192359	15144389 621532	80382645 931684	39515881 755999	16972339 275161	18101400 1084932	19271271 1466128	5895740 1564941	16435192 437020
A0A140T898 A0A140T898_	6	3	373,85	0,02149	0,298	1,66827	0,6628	LL	HL	22928	Ras-related protein Rab-13 OS=Bos taurus OX=9913 GN=RAB13 PE=4 SV=1	608319	261969	786305	272913	448751	422625	744490	696952	551656	637171	727681	354147	942710	1449530	1101374	1057936
A0A3Q1MD79 A0A3Q1MD	5	5	316,31	0,02239	0,298	1,71259	0,6561	LL	HL	64892	Phosphatidylinositide phosphatase SAC1 OS=Bos taurus OX=9913 GN=SAC	326960	262467	217194	450825	486318	287094	611780	594868	626100	398469	1748787	814410	556407	440818	357876	575303
A0A3S5ZPG9 A0A3S5ZPG9_ A0A3S5ZPI3 A0A3S5ZPI3_B	4	5 4	486,29 327,77	0,02245 0,02315	0,298 0,298	1,89159 2.09506	0,65564 0.65051	LL	LL HL	35661 22238	Mucin-15 OS=Bos taurus OX=9913 GN=MUC15 PE=4 SV=1 Ankyrin repeat domain 22 OS=Bos taurus OX=9913 GN=ANKRD22 PE=4 SV	25843723 2291745	15816447 904395	13939732 2172792	5291420 681096	15021924 2157662	12135382 1502431	13836104 3209587	12234034 1952154	12185499 2119462	689047 2630031	4159545 2829724	5562389 2308755	9853067 6982344	11253964 2478720	12111773 4652210	3874178 2803099
A0A3Q1M8R7 A0A3Q1M8R	2	2	234,45	0,02318		2,18185	0,6503	HL	EL	36855	Secretory carrier-associated membrane protein OS=Bos taurus OX=9913 C	8378051	7153414	1983184	1526808	2980145	5224795	6514626	1663009	947656	246255	3360519	1206023	2750893	4753553	3950952	1170866
P02662 CASA1_BOVIN;A0A	9	9	750,39 92.22	0,02367 0.02386	0,298 0,298	1,77243	0,64681	HL	LL HL	24513 46704	Alpha-S1-casein OS=Bos taurus OX=9913 GN=CSN1S1 PE=1 SV=2 Serine/threonine kinase 26 OS=Bos taurus OX=9913 GN=STK26 PE=4 SV=1	161025009 518338	44936046 640270	46322973 504866	111661782 1738375	36995023 372233	37737358 425815	76215672 184188	52489829 362193	20555789 422672	43708857 1426413	30167063 2125087	63020894 1805481	37541099 523826	33671378 473108	52384591 474466	52396524 5342356
Q32LG5 REEP6_BOVIN	2	2	195,49	0,02380	0,298	1,77797	0,64447	LL	HL	20561	Receptor expression-enhancing protein 6 OS=Bos taurus OX=9913 GN=REE	401554	314594	173301	130999	239592	131499	208868	319564	479905	385261	265245	158140	616112	488483	535379	306931
Q3SZF2 ARF4_BOVIN;A0A3	7	4	498,44	0,02492	0,298	1,62908	0,63807	LL	HL	20515	ADP-ribosylation factor 4 OS=Bos taurus OX=9913 GN=ARF4 PE=2 SV=3	12389670	4717871	7849047	7445385	7546355	6926538	12784481	13513925	7465823	9261434	8443344	9353538	19118788	20588024	19832858	14817677
P10790 FABPH_BOVIN;A0A A0A301MV91 A0A301MV9	10 6	10 6	755,19 563.52	0,02571	0,298	1,78415	0,63277	LL HL	HL	14770 47337	Fatty acid-binding protein, heart OS=Bos taurus OX=9913 GN=FABP3 PE=1 Fibrinogen gamma-B chain OS=Bos taurus OX=9913 GN=FGG PE=4 SV=1	120510636 2805032	89246663 1921266	150313686 1828229	125251540 548270	77807444 485152	183975063 1151472	228480111 7546779	220308398 1453435	124709129 546856	144277778 1105455	183334593 2008564	184228358 504073	295301610 814441	512545569 581835	310699131 3 805344	277180804 296796
A0A3S5ZPM3 A0A3S5ZPM3	3	3	174,01	0,0276	0,298	2,01967	0,62057	HL	LL	60741	6-phosphogluconate dehydrogenase, decarboxylating OS=Bos taurus OX=5	10054736	6641776	12415049	8789050	20652379	10897343	12661578	15311257	4665172	13169664	17590860	5952254	10182792	5153470	6726724	7591456
A0A3Q1LUY5 A0A3Q1LUY5	2	2	144,97	0,02777	0,298	1,43399	0,61949	LL	HL	81834	SEC14 like lipid binding 1 OS=Bos taurus OX=9913 GN=SEC14L1 PE=4 SV=1	159418	93606	135498	85439	259066	179623	158798	140695	185468	183872	290153	124066	155439	251223	129365	236408
A0A3Q1MFE4 A0A3Q1MFE P02584 PROF1_BOVIN:E1B	2	2	103,64 141.13	0,02813 0.02967	0,298 0.30377	2,05134 1.49523	0,61721 0.60785	LL	HL HL	83478 15048	MICOS complex subunit MIC60 OS=Bos taurus OX=9913 GN=IMMT PE=1 S Profilin-1 OS=Bos taurus OX=9913 GN=PFN1 PE=1 SV=2	20233 471111	6714 258068	10030 613479	41886 416788	219950 396919	46374 361165	71597 846161	94989 973792	20052 875670	99555 974451	26173 624776	144090 435757	224086 1056945	107735 1020348	185653 1025505	142857 1455522
E1BEH7 E1BEH7_BOVIN	2	2	94,88	0,02971	0,30377	2,04497	0,60761	HL	LL	55149	Tandem C2 domains, nuclear OS=Bos taurus OX=9913 GN=TC2N PE=4 SV=	57289	42467	106359	11735	58920	106406	75919	37261	41379	8087	6771	11576	73992	24937	53519	15177
A0A3Q1LNZ8 A0A3Q1LNZ8 A0A140T8A5 A0A140T8A5	3	3	274,86 365,48	.,	0,30377	1,42582	0,604 0.60185	LL HL	HL	41045 46729	Transmembrane protein 120B OS=Bos taurus OX=9913 GN=TMEM120B PI Isocitrate dehydrogenase [NADP] OS=Bos taurus OX=9913 GN=IDH1 PE=1	633831 1960074	558013 1789382	646845 1668287	706073 705714	782901 2304733	587792 2194203	1284593 2217150	1337892 2093191	953628 1279630	1375209 390133	1591442 451894	975275 631123	1125357 1516842	1530180 3017134	897881 1786878	2156269 666095
P60712 ACTB_BOVIN;A0A3	10	2	854,53	-,	-,	1,50357	0,58683	HL	LL	41710	Actin, cytoplasmic 1 OS=Bos taurus OX=9913 GN=ACTB PE=1 SV=1	9387976	11076102	7641346	6466282	11028798	7383537	11784602	12667531	9287169	880221	1493721	5333149	9539225	9371053	8998890	5725931
A0A3Q1LRZ4 A0A3Q1LRZ4_	2	2	151,05	-,	0,31069	4,06075	0,58641	LL	HL	33417	Prohibitin-2 OS=Bos taurus OX=9913 GN=PHB2 PE=1 SV=1	24101	63091	1674	120489	163133	20708	59706	136018	37510	392101	39418	81226	516736	39482	165170	1012445
F1N2J7 F1N2J7_BOVIN F1N272 F1N272 BOVIN;A0	2	2	179,61 652,29	.,	0,31213 0,31545	1,45408 1,72305	0,58336	LL	HL HL	51852 133757	Uncharacterized protein OS=Bos taurus OX=9913 GN=ALG1 PE=4 SV=3 Cation-transporting ATPase OS=Bos taurus OX=9913 GN=ATP13A4 PE=3 SV	283061 11301660	190849 17431189	248658 10039576	166397 37907607	274814 13228619	252561 23050734	455966 12129888	217948 10911521	138538 14897056	443816 46385969	271809 44070442	344802 48814806	424717 16243829	243969 15643876	353104 11872096	514535 31600251
F1MEX9 F1MEX9_BOVIN;A	12	12	989,09			1,75888	0,56746	LL	HL	80230	Acyl-CoA synthetase long chain family member 3 OS=Bos taurus OX=9913	10970286	9600273	15584159	17631092	8916733	8645180	10191715	8924628	12679894	24335161	48193756	21521470	8633362	9786557	10582010	20307125
E1BQ28 E1BQ28_BOVIN A0A3Q1MFP2 A0A3Q1MFP	2	2	102,56 282	-,	-,	1,42062 1.64824	0,56467	HL	LL HL	49787	Solute carrier family 39 member 8 OS=Bos taurus OX=9913 GN=SLC39A8 f RAB3 GTPase activating protein catalytic subunit 1 OS=Bos taurus OX=991:	39827879 540560	49597974 365804	46462100 382879	32248307 459335	32306141 669911	38176620 698710	49590814 457234	39781710 410208	31850057 1274081	5058191 472865	14768271 1240601	29966372 988401	51150168 867857	25408522 736963	36322096 1166341	25017637 282998
A0A3Q1LKR8 A0A3Q1LKR8	3	3	324,92	.,	.,	1,41489	0,55923	LL	HL	129371	Ubiquitin-like modifier-activating enzyme 1 OS=Bos taurus OX=9913 GN=U	273060	274384	157084	172117	449520	110861	196528	315133	454241	438996	348356	285284	401517	241697	192039	285953
A0A3Q1MDS4 A0A3Q1MDS	5	3	165,74	.,		1,53487	0,55894	LL	HL	24372	RAB3D, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB3I	1884006	759378	1582352	3393771	1027487	862387	1921571	1480311	1038555	2044450	3748496	3350960	1629244	1338772	2305639	2539981
F1MDT6 F1MDT6_BOVIN;A G5E513 G5E513 BOVIN;A0	15 9	15 3	1250,29 903,27	.,		1,69271 1.57968	0,55571 0.55261	LL HI	HL	93223 48077	Glycerol-3-phosphate acyltransferase 1, mitochondrial OS=Bos taurus OX= Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=2	10929563 19033541	16147365 23036916	11576359 30939797	19521772 49477999	16217480 22155140	11640787 20557234	14336045 23502086	12911469 46776018	19624499 9177365	56683811 58483052	28776539 19444731	20606123 18244026	16724728 18977867	8795682 13158740	16250200 11500995	31798545 20641626
A0A3Q1M4U6 A0A3Q1M4U		4	229,43			1,74992	0,55162	LL	HL	126176		325786	267298	442505	976442	338529	172945	291913	190298	376220	543537	1615914	715445	394362	304655	331011	681998
Q2YDM1 ARL1_BOVIN A0A3Q1LSB2 A0A3Q1LSB2	2	2	144,45 146.54	.,	-,	2,07733	0,54932		HL HL	20414	ADP-ribosylation factor-like protein 1 OS=Bos taurus OX=9913 GN=ARL1 P Translocon-associated protein subunit delta OS=Bos taurus OX=9913 GN=5	28304 73165	98878 128637	139888 142304	303395 228682	70112 226760	131509 150741	33129 187570	150325 590834	98541 268760	497425 460091	282695 191669	207570 98481	125304 472872	229757 472785	163196 464423	1128077 837856
F1MKU3 F1MKU3_BOVIN	5	5	398,67	- ,	0,31545	1,86188	0,5454	HL	LL	44640	B-box and SPRY domain containing OS=Bos taurus OX=9913 GN=BSPRY PE	2603496	977136	1294897	1001547	1744865	724930	3807036	1263800	665228	51885	137041	547652	2436890	506567	1538631	503908
G5E5T5 G5E5T5_BOVIN;A0	7	2	689,54	.,	0,31545	2,1831	0,54429	HL	LL	56008	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=2	275850	395094	1826588	964891	343250	426722	266075	548859	181523	452720	1193891	244244	265675	132523	27307	307305
Q3SYS6 CHP1_BOVIN;A0A3 Q3ZC78 CR032 BOVIN	7	7	597,41 108,13	- , -	0,31545 0.32283	1,76324 1.66762	0,54356		HL HL	22428	Calcineurin B homologous protein 1 OS=Bos taurus OX=9913 GN=CHP1 PE UPF0729 protein C18orf32 homolog OS=Bos taurus OX=9913 PE=3 SV=1	2553243 384360	2146141 108718	3812724 127835	1574298 110635	4200723 112657	3713656 412938	7288614 551312	2871096 187739	2824948 387792	2178195 401344	4121978 100053	2669685 204383	9113256 663209	6013110 243859	6559770 349759	7613262 419447
Q3SZN8 Q3SZN8_BOVIN;H9	3	3	296,08	0,04532			0,53032	LL	HL	48819	Ribonuclease/angiogenin inhibitor 1 OS=Bos taurus OX=9913 GN=RNH1 PE	1780243	1057732	1665154	693359	1810069	1024037	1871270	1789602	1531308	2374688	3525612	2010586	2112486	1161833	1217596	3062571
G3N0V2 G3N0V2_BOVIN;AI P63243 RACK1_BOVIN:A0A		3	387,75 152,79	0,04533			0,53026	HL	LL	63127 35055	Keratin 1 OS=Bos taurus OX=9913 GN=KRT1 PE=1 SV=2 Receptor of activated protein C kinase 1 OS=Bos taurus OX=9913 GN=RAC	840334 687339	564739 280690	824825	374332	580871	604052	406581 673797	930043	345046 297874	62326	293226	449041 715176	461258	761826 393153	267928	480632 414743
A0A3Q1LNU8 A0A3Q1LNU8	-	3	152,75	0,04843	-,	1,5281	-,	LL	HL		Extended synaptotagmin 2 OS=Bos taurus OX=9913 GN=ESYT2 PE=1 SV=1	252726	172319	143362	73471	198040	124239	228711	244149	337043	345377	370038	339694	321314	192705	237160	121413
A0A3Q1MAC3 A0A3Q1MAC		3	315,68	0,04857			0,51717	LL	HL	21128	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1	1414293	476607	1372027	2854271	373019	855774	528278	1013709	624914	2595561	1246285	2045653	439518	1819953	1474259	3321064
P26201 CD36_BOVIN;F1ML A5D7J6 A5D7J6 BOVIN;F1M		5	403,37 278,93	0,04937 0.05049			0,51406 0,50978	HL HL	LL		Platelet glycoprotein 4 OS=Bos taurus OX=9913 GN=CD36 PE=1 SV=5 Calreticulin OS=Bos taurus OX=9913 GN=CALR PE=2 SV=1	143997448 523566	149497712 931652	182819900 890090	83497265 506204	97663915 1333057	83961123 401319	100327738 807130	82265905 1857495	99143455 1357902	61634168 130628	115136234 146462	54075464 226906	77953662 759699	110618412 551178	103384136 1100984	35028991 587882
A0JN43 A0JN43 BOVIN	5	5	314,73	0,05169			0,50526	LL	HL		Extended synaptotagmin 1 OS=Bos taurus OX=9913 GN=ESYT1 PE=1 SV=1	347326	580287	513852	572999	498439	340351	163441	883319	802442	1133274	1533512	701471	309018	588742	528497	468217
Q4GZT4 ABCG2_BOVIN;B2D	17	17	1410,17	0,05169			0,50526	LL	HL	72678			461975398	668353351		479930166	486354648			690853813 1	1158483830 1			477209303	419380640		513711745
A0A3Q1LSB7 A0A3Q1LSB7_ P11017 GBB2 BOVIN;P628	5	2	322,76 314,97		0,33291 0,33291	1,87249 1,3003	0,50462 0,50087	LL HL	HL	26842 37307	Peptidyl-prolyl cis-trans isomerase OS=Bos taurus OX=9913 PE=3 SV=1 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Bos t	512996 40399240	402973 23310644	622600 30192318	316503 23220382	99962 23274841	126843 25213570	285278 37696047	377126 25947838	468454 16629770	269096 8605381	259263 11997878	415424 18469106	901794 31729017	548339 27465899	488485 31008681	1710821 15251271
E1BFV0 E1BFV0_BOVIN	2	2	122,89	0,0529	0,33291	1,50944	0,50083	LL	HL	97165	Karyopherin subunit beta 1 OS=Bos taurus OX=9913 GN=KPNB1 PE=1 SV=2	81326	182891	109470	259132	185854	198606	285029	241734	189836	500764	436592	406919	276931	103418	222706	311477
P02663 CASA2_BOVIN A4IFU2 A4IFU2 BOVIN	7	7	416,35	0,05294 0.05375			0,50069	HL	LL	26002	Alpha-S2-casein OS=Bos taurus OX=9913 GN=CSN1S2 PE=1 SV=2	68732759 340528	31098216	41767609 188510	161472957 255029	20987921 92890	28320301 126794	39679872 191976	29867499	10305392 227064	15672696 383962	15127098 231484	50720013 279424	24510735 192541	29665800 222668	30454229 333280	39601644 717266
P17697 CLUS_BOVIN	3 5	2	192,12 313,79	0,05375			-,	HL	HL LL		RAP2B protein OS=Bos taurus OX=9913 GN=RAP2B PE=2 SV=1 Clusterin OS=Bos taurus OX=9913 GN=CLU PE=1 SV=1	340528 288187	95591 76744	188510 265258	255029 405674	292890	126794 367063	191976 143813	173925 223661	55493	383962 79907	231484 127540	279424 139680	32435	152802	247781	113589
Q3ZCK2 Q3ZCK2_BOVIN	4	2	190,88	0,05666	-,	-,	-,	LL	HL		RAS like proto-oncogene A OS=Bos taurus OX=9913 GN=RALA PE=2 SV=1	2319529	1073963	999288	1371778	751487	758656	1360987	1203761	703850	1464020	3368133	1329147	1090928	1918756	1426424	2528991
F1MIU3 F1MIU3_BOVIN Q08DW1 Q08DW1_BOVIN;	6 2	6 2	367,43 146,43	0,05747 0.0597				HL	LL HL		Transmembrane channel-like protein OS=Bos taurus OX=9913 GN=TMC5 F RAB9A, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB9/	2112956 204756	1884604 118524	1644183 437663	564614 155676	928720 137264	1488567 40271	2025284 102645	1704571 260923	1144658 142924	509800 223822	451640 272606	798961 96323	1228386 195225	1128225 404524	1483802 378151	820244 545616
A2VDV2 STK38_BOVIN;A0A		2	182,43	0,06027	0,3487	1,42473	0,47558	LL	HL	54141	Serine/threonine-protein kinase 38 OS=Bos taurus OX=9913 GN=STK38 PE	142392	214231	352131	119747	235029	147636	155020	307738	277404	424892	666730	227751	201154	198329	235595	213024
P61356 RL27_BOVIN	3	3	159,44	0,06189	0,35191	1,7418	0,47043	LL	HL	15788	60S ribosomal protein L27 OS=Bos taurus OX=9913 GN=RPL27 PE=2 SV=2	43557	49334	20118	113972	195814	34023	87870	389209	165507	240162	69842	46689	492780	292201	313085	194816

A0A3Q1LUS2 A0A3Q1LUS2 4	4	383,58		35191 1,384	2 0,46813		L 5548		1529932	1369942	1369675	1447517	1518536	1217346	1548335	1860894	1173251	454663	600472	1114488	1390209	1271622	1225384	790708
A0A3Q1LVG9 A0A3Q1LVG9 2 F1MLB8 F1MLB8 BOVIN;P1 7	2	121,4 581.16		35191 2,581 35191 1.815	0,46589		IL 4490 IL 5965	 NDRG family member 4 OS=Bos taurus OX=9913 GN=NDRG4 PE=4 SV=1 ATP synthase subunit alpha OS=Bos taurus OX=9913 GN=ATP5F1A PE=1 SV 	101213 121706	103263 177294	31975 261886	703719 1711626	46246 1653075	206094 253816	49559 471179	92051 1258790	61904 300185	905120 1879162	484582 858949	840211 1253484	119490 1213581	163691 782053	141667 1383566	447577 3598483
A0A3O1LYB4 A0A3O1LYB4 6	6			35191 1,815			L 3756		7210758	7375898	8748547	5303185	5933924	9480739	4/11/9 10677219	8954598	4475666	762761	1912742	5025278	8691792	9591049	9093376	4678745
F1N1/6/F1N1/6 BOVIN:40A 8	8	494.54		35239 1,300			L 9202	Gelsolin OS=Bos taurus OX=9913 GN=GSN PE=1 SV=2	2067625	2999108	1296172	1043635	2821905	2544757	3860350	2576334	2307605	336645	697902	1130886	2563257	1799801	3296721	991957
E1BM93/E1BM93 BOVIN 3	3	236.14	-,	35239 1,549			IL 3778		1043871	589269	729724	392841	839921	744151	1271219	948898	872171	1193689	871779	505683	1876601	873333	1063431	1885348
F1MXE4 F1MXE4_BOVIN 2	2	151,91	0,06969 0	35654 1,712	4 0,44722	HL	L 4556	26S proteasome non-ATPase regulatory subunit 6 OS=Bos taurus OX=9913	40571	87417	34102	17438	183269	100301	108902	289243	78429	30111	2598	8830	69989	55934	230717	83966
F2Z4I1 F2Z4I1_BOVIN;A0A3 8	8	498,18	0,0707 0	35771 1,571	0,4444	LL I	IL 2046	GTP-binding protein Rheb OS=Bos taurus OX=9913 GN=RHEB PE=4 SV=1	2380743	1437415	2265168	1667086	1701305	2230678	3003353	3087500	1801138	1465418	2733390	2349452	3889256	4033726	5235709	3496704
A0A3Q1LRL7 A0A3Q1LRL7_ 2	2	148,23	0,07171 0	35823 1,553	3 0,4416	LL I	IL 5822	Xylulose kinase OS=Bos taurus OX=9913 GN=XYLB PE=1 SV=1	53699	140234	47949	222436	140691	62876	50632	111240	117543	344329	175150	125250	98612	51628	109363	177452
Q7YRW9 Q7YRW9_BOVIN 2	2	113,23	0,07233 0	35823 1,581	8 0,43991	LL I	IL 2238	Reticulon OS=Bos taurus OX=9913 GN=RTN4 PE=1 SV=2	247792	124823	295099	113434	316306	219166	240349	469420	287262	476120	323432	196951	408224	389383	460577	520065
A0A3Q1LYE7 A0A3Q1LYE7_ 6	3	478,43	0,07274 0	35823 1,420	1 0,43879		IL 2183		14940887	9712159	7951142	10677674	12095728	12704576	17995602	14063890	11940108	29309739	19392814	16287263	14941060	10903186	15066166	38407563
A7YY49 SURF4_BOVIN;F1Ni 2	2	112,26		36263 1,297	.,		IL 3040		117251	119801	176909	221837	301517	242422	176613	508244	263762	470282	507171	485828	348935	224167	317948	368502
A0A3Q1MWL7 A0A3Q1MW 3	3	128,76	-,	36263 1,576	5 0,43231		L 14822	0 DENN domain containing 3 OS=Bos taurus OX=9913 GN=DENND3 PE=4 SV	39488	70264	110654	12484	116151	89540	81965	134694	67434	4160	36761	19186	95669	102169	94591	914
P80195 GLCM1_BOVIN;Q32 10		953,3		36263 2,841	/8 0,42935		L 1714	Glycosylation-dependent cell adhesion molecule 1 OS=Bos taurus OX=991	640784409	242453861	86826587	87166125	53667656	77562767	586199525	44722289	63050707	23829553	27257874	22508319	145525320	128982789	68494225	69182238
A0A3Q1LUE9 A0A3Q1LUE9 2 Q6WCD5 Q6WCD5 BOVIN 4	2	123,14 174.38		36263 1,467 36263 1.67	0,42/3/		L 1669	Ig-like domain-containing protein OS=Bos taurus OX=9913 PE=1 SV=1	2644865	754844	853854	2186592	1657844	1675448 174774	1209995	2546179	379475 460603	453927 507700	310222 965086	707284	2832810	1937601	1542230	449475 220370
A0A498UZ20 A0A498UZ20 3	4	174,38		36263 1,67	4 0.42676		IL 9595 IL 14856	Toll-like receptor 4 OS=Bos taurus OX=9913 GN=TLR4 PE=2 SV=1 6 Unconventional myosin-VI OS=Bos taurus OX=9913 GN=MYO6 PE=3 SV=1	160478 10037	183403 36362	228006 51343	106237 38681	250525 126248	38441	127766 84672	260131 73291	68853	51807	135122	372129 52344	96261 74541	262055 66021	256146 83872	52634
Q08DN8 FLOT1 BOVIN 6	6	445.71	-,	36263 1,300	••••••		L 4732	· · · · · · · · · · · · · · · · · · ·	2196855	2122085	1457094	1257120	1118278	1964580	2694993	905866	1196429	688761	1503148	1176841	1525996	2426115	843140	1237744
F6R1D7/F6R1D7 BOVIN 5	5	152.16	-,	36482 1.384	.,42337		L 3502		404112	425610	588836	316533	398223	338138	300993	476470	357354	57484	160508	285475	342439	375874	517911	161509
A0A3Q1LN631A0A3Q1LN63 2	2	116.56	0.08113 0				L 4568	Leukocyte elastase inhibitor OS=Bos taurus OX=9913 GN=SERPINB1 PE=1 5	120431	204428	38950	23599	197351	67724	779375	104698	62872	90506	43994	56616	92014	24480	81284	55039
A0A3Q1M9B5 A0A3Q1M9E 2	2	97,06	0,08154 0	36482 2,203	6 0,41632	LL I	IL 13914	5 High density lipoprotein binding protein OS=Bos taurus OX=9913 GN=HDLE	1569	8500	21257	27533	77523	11207	1087	47539	87557	217640	43219	27968	39762	23359	27224	14275
E1BAI0 E1BAI0 BOVIN 2	2	118,44	0,08198 0	36482 1,387	6 0,41526	LL I	IL 2664		500542	101029	212222	93537	199398	250073	709665	291320	187317	323184	498487	221829	507317	233977	259495	699311
Q9BGI1 PRDX5_BOVIN 3	3	106,61	0,08405 0	36874 1,511	1 0,41034	LL I	IL 2323	Peroxiredoxin-5, mitochondrial OS=Bos taurus OX=9913 GN=PRDX5 PE=2 !	340574	227004	258731	68562	246892	166897	436131	431683	373428	296688	230150	161448	569433	609873	541697	333361
Q6B855 TKT_BOVIN 4	4	124,92	0,08433 0	36874 1,57	0,40968		L 6786	Transketolase OS=Bos taurus OX=9913 GN=TKT PE=2 SV=1	209182	292677	129892	123294	384939	214666	305124	183141	229630	17514	26791	150783	232777	166914	239208	55588
F1N545 F1N545_BOVIN 4	4	278,28	-,	37349 1,590	,		IL 6745	Ankyrin repeat domain 13A OS=Bos taurus OX=9913 GN=ANKRD13A PE=4	519344	581017	378113	893732	462972	448416	409824	506996	571214	1675867	1735123	1140098	331211	507913	472645	859738
A0A452DIL6 A0A452DIL6_B 5	5	368,72		37391 1,763	2 0,40282		L 6094	Glypican-1 OS=Bos taurus OX=9913 GN=GPC1 PE=3 SV=1	485916	473572	372440	272496	388935	368220	867623	816994	309868	249384	378606	101973	552167	83227	284686	108966
Q5EA55 GOGA7_BOVIN 4	4	221,82		37391 1,547	4 0,40096		IL 1581	Golgin subfamily A member 7 OS=Bos taurus OX=9913 GN=GOLGA7 PE=2	947646	666227	852003	845599	811846	702891	1238811	1259535	1011604	694390	732416	863795	1571765	1676718	2158893	1539000
A0A3Q1NJP7 A0A3Q1NJP7 2	2	72,63		37458 1,502	.,		L 2667	Ras-related protein Rab-26 OS=Bos taurus OX=9913 GN=RAB26 PE=4 SV=1	161174	235850	125151	20896	125027	63844	209473	149828	149754	37753	10110	32979	215039	67056	177152	27039
A0A3Q1M253 A0A3Q1M25 2	2	82,96		37458 1,478	.,		IL 5368	DENN domain containing 2D OS=Bos taurus OX=9913 GN=DENND2D PE=4	71074	153783	154501 427045	120902	220772	176421 604473	117990	149413	167737	537824	307252 818808	169354 1371408	147686 542812	159115	169426	101026
Q3SZ01 SH3Y1_BOVIN 2 Q0VCI2 STX19 BOVIN 6	2	77,72 603.36	0,09124 0 0.09158 0		,		IL 3704 L 3386	SH3 domain-containing YSC84-like protein 1 OS=Bos taurus OX=9913 GN=: Syntaxin-19 OS=Bos taurus OX=9913 GN=STX19 PE=2 SV=1	3828347	562947 2366125	2439429	1039315 1141314	437571 1909137	3221951	958450 2981171	426234 3060404	548349 1339322	1378049 864736	912557	905172	2116524	349999 3300412	675506 3194500	1293101 864374
Q35X32 Q35X32 BOVIN 10		816.26	0.09209 0				L 3560	-,	32280411	33982030	28701724	9481570	10800805	16603809	44578771	7996695	14203313	9171467	11643365	13055652	11915010	16573889	12481725	9936007
G5E6P3 G5E6P3 BOVIN 10		640.36		1.379 1.312			L 4391	G protein subunit alpha 13 OS=Bos taurus OX=9913 GN=GNA13 PE=4 SV=2	16278876	14217482	17257914	7165632	10600935	13524458	14913602	16412466	8966526	3695555	5116959	5128256	14166120	20774540	16737467	5923403
Q0VBZ9 MRP BOVIN 3	3	222,11	.,	3859 1,485			L 1981	MARCKS-related protein OS=Bos taurus OX=9913 GN=MARCKSL1 PE=2 SV	289266	349559	265223	45403	205010	302786	158752	172783	384397	11158	73272	28886	54641	483383	215261	38605
A0A3Q1MG04 A0A3Q1MG(4	4	243,56		3859 2,341			L 5743	Fibrinogen beta chain OS=Bos taurus OX=9913 GN=FGB PE=4 SV=1	1034499	823341	843464	122246	129581	343169	3461117	540492	132729	905105	1546809	73612	237632	65796	225215	414569
F6RWD2 F6RWD2_BOVIN 2	2	169,44	0,098 0	3859 2,249	6 0,38004	LL I	IL 3857		276697	291111	358534	758436	290931	517221	95986	312007	454158	3285128	1374270	820556	99453	359121	301906	1224345
Q0II59 PDXK_BOVIN 4	4	260,54	0,10091	,391 1,430	6 0,37429	HL	L 3479	Pyridoxal kinase OS=Bos taurus OX=9913 GN=PDXK PE=2 SV=1	2457007	3291746	2746430	901539	2984866	6988500	6121051	3116123	1390050	199859	350028	805641	5736861	2963651	5890834	297865
A0A3Q1M3X3 A0A3Q1M3X 2	2	70,6	0,10091	,391 1,462	5 0,37429		L 2366		455212	416237	379602	153620	472827	621689	395570	553437	248855	52127	146785	137179	459480	437595	505045	206585
F1N647 F1N647_BOVIN;A0. 46	5 8	3609,71	.,	,391 1,759	9 0,37066		IL 27423	6 Fatty acid synthase OS=Bos taurus OX=9913 GN=FASN PE=1 SV=3	6343805	5384548	7994487	2343877	27096882	14995535	7336711	11784053	21894506	16040376	20685331	6017149	39034625	23755405	13152755	4301034
Q3ZBE9 NSDHL_BOVIN 9	9	1159,96		,391 1,379	1 0,37037		IL 3987	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Bos tau	24169884	19651208	25683347	33739170	23890793	20018493	22542889	16802076	21794291	69614069	58232331	30503505	23097801	20454811	25930674	62497121
E1BCI3 E1BCI3_BOVIN;A0A: 9	9	774,11	-,	39266 1,305	,		L 6729	Solute carrier family 7 member 4 OS=Bos taurus OX=9913 GN=SLC7A4 PE=	25223615	37964137	19233095	24177642	33556536	20099670	30897255	44699868	21929177	11320834	12385278	18877015	40047583	13762609	38348174	16948873
P23004 QCR2_BOVIN;A0A3 2 A0A452DIH71A0A452DIH7 4	2	167,07	-,	39266 2,039			IL 4811	-,	4773	67436	66840	825992	759368	69011	271146	320730	59220	170757	198782	676294	554661	233346	435239	1790133
A0A140T881 A0A140T881 7	4	153,62 519.37	-,	39266 1,358 39337 1.698			L 4944 L 3740		588859 13748865	1010508 5625880	659014 11954768	440858 4008162	1455352 6083109	932122 4986925	581053 9082569	1325079 3543134	929266 3304198	642424 2604502	484508 3811198	333724 2933654	851406 4229353	949138 5718625	916070 4335363	569602 5019579
A0A301NCJ7 A0A301NCJ7 2	2	265.08		39681 3.067	,		L 3740	CKLF-like MARVEL transmembrane domain-containing protein 8 OS=Bos ta	88956	226500	106486	1230897	90493	4980923	14509	201463	109424	992816	1149724	660626	217536	245108	4555565	1732033
A0A3O11Y46 A0A3O11Y46 7	7	428.15	-,	40046 1.435			L 9407	MICAL like 2 OS=Bos taurus OX=9913 GN=MICALL2 PE=4 SV=1	461981	667860	668829	232350	887124	654627	732247	803946	501466	73383	155746	202138	652964	704707	783146	158252
A0A301MCH31A0A301MCF 2	2	102,53		40458 1,325			IL 7393	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondria	2605	19084	11388	18668	187389	13155	53364	77281	38431	57157	34149	55257	97185	26821	107660	110546
F1MHC2 F1MHC2_BOVIN 8	6	483,01		40943 1,339	2 0,35071		L 6631	Syntaxin binding protein 2 OS=Bos taurus OX=9913 GN=STXBP2 PE=1 SV=1	4054254	4451862	2029059	2235943	5525779	4040743	4022576	5726599	3816512	1870031	2469318	3293017	3772571	2699685	4665076	1877907
A0A3Q1MRF4 A0A3Q1MRF 4	4	316,93	0,11655 0	41544 1,399	3 0,346		L 3953	NAD-dependent protein deacetylase OS=Bos taurus OX=9913 GN=SIRT2 PI	927585	808541	442946	326967	946021	971216	780906	591149	512204	207413	476424	407992	390248	666404	874145	195943
Q2KIV8 Q2KIV8_BOVIN;A0/ 5	5	345,23	0,11769 0	41752 1,244	9 0,34409	LL I	IL 2683	Glutathione S-transferase OS=Bos taurus OX=9913 GN=GSTM3 PE=1 SV=1	1001450	241378	448729	741248	415349	623578	1122663	857684	840941	856641	1092684	1049478	615509	945031	756688	1053648
F1MHB9 F1MHB9_BOVIN;A 3	3	159,86	0,11874 0	41885 1,221	6 0,34236	HL	L 4766	Inositol polyphosphate-5-phosphatase A OS=Bos taurus OX=9913 GN=INPI	263340	177199	346572	131277	256275	309077	126440	251518	165220	42903	73364	146188	161345	219791	306783	59743
A0A3Q1N308 A0A3Q1N308 10	0 10	757,45	0,11918 0	41885 1,415	5 0,34164	HL	L 5300	Methanethiol oxidase OS=Bos taurus OX=9913 GN=SELENBP1 PE=1 SV=1	9776895	9926574	2229867	2421743	5058559	4492427	7252831	4191776	6995236	5803778	1650338	4012829	3825984	5565690	3687680	2685111
A0A3Q1LFK0 A0A3Q1LFK0_ 2	2	181,49	.,	42003 1,242	- ,		L 6113	Amino acid transporter OS=Bos taurus OX=9913 GN=SLC1A2 PE=3 SV=1	126469	173714	173607	110825	128950	152462	87946	333202	75749	21611	15576	133320	195029	83482	373810	24703
A7MB21 A7MB21_BOVIN 3	3	196,88	-,	42045 1,375	,		IL 7782		137698	103452	173493	90886	231851	145494	78517	198122	382541	205859	161746	259707	109718	77886	186520	215702
A5PKG9 A5PKG9_BOVIN;AC 12		908,72	-,	42045 1,334			IL 5929		6120610	6952135	14187891	4223641	8837368	6616310	6258043	6470083	10597130	3086429	11640203	7783530	11323497	10172703	10674532	7125732
P63097 GNAI1_BOVIN 5	3		0,12426 0		,		IL 4033		323860	521368	445607	1418556	589757	1520796	299026	574647	442257	2789335	2197748	1495118	340110	461961	541464	2243657
P27479 LOX15_BOVIN 10 G3MYK6 G3MYK6_BOVIN;C 3) 10 3	495,72 208.67	-,	42045 1,435 42045 1.805			IL 7507 IL 2500		2174792 163480	3930796 35747	2009879 432674	2387425 221844	3515277 143187	1685146 148825	2235020 347343	2622905 248590	5264626 97579	6948884 206411	3977529 111021	3661055 331300	4588021 281348	2411678 879576	2218614 634679	1642964 606779
OSEA19 ARL15 BOVIN;C 3	4	208,67	-,	42045 1,805.			IL 2300	ADP-ribosylation factor-like protein 15 OS=Bos taurus OX=9913 GN=ARL15	2395654	2363790	2027140	1082544	1392692	968736	2620773	1944480	1449870	1176698	1190792	1156246	2642501	2573302	3352329	3053159
Q3ZCA7 Q3ZCA7 BOVIN 6	4	504.93		42045 1,450			IL 2255		2368901	1795272	1635343	3885368	1756668	2409988	2240896	2102046	1742458	7942804	4391313	3460764	2575034	2451715	1642277	5029675
P15497 APOA1 BOVIN;A0A 10		826,5		42045 1.565	-,		L 3025		13946364	4838576	3586474	3736069	2879454	4374234	10652807	4682469	1171033	3846005	2186233	1247671	4047976	4922640	4598667	4254443
P06623 CN37 BOVIN 8	8	387,41	0,12797 0	42045 1,418	9 0,32779		L 4484	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Bos taurus OX=9913 GN=(1253189	1244795	1152208	305209	702365	732093	1021783	511600	1310668	136064	327892	363868	411430	745973	662405	473539
Q5E946 PARK7_BOVIN 3	3	129,53	0,12809 0	42045 1,452	4 0,3276	HL	L 2002	Protein/nucleic acid deglycase DJ-1 OS=Bos taurus OX=9913 GN=PARK7 PE	525352	221632	84059	240364	254354	377975	1074901	209013	96561	12486	18186	513210	284737	291933	547872	80724
A0A3Q1LLL1 A0A3Q1LLL1_ 4	4	265,99	0,12898 0	42045 1,472	0,32626	HL	L 4980	Endophilin-B2 OS=Bos taurus OX=9913 GN=SH3GLB2 PE=4 SV=1	252623	348154	316273	114516	293313	583752	248279	535443	247615	65454	112761	84459	251516	457707	510148	57875
A3KN04 A3KN04_BOVIN 4	4	343,96		42625 1,640	3 0,32173		IL 6831	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 1 (274628	620148	246058	329935	950186	233800	391650	1272988	999182	2744369	797707	266715	972580	584607	611043	593233
A0A3Q1LVV7 A0A3Q1LVV7 6	6	333,79	.,	42787 3,611	,		L 8979	Fibrinogen alpha chain OS=Bos taurus OX=9913 GN=FGA PE=4 SV=1	1162652	417219	321102	35740	103920	105310	3898346	309869	174584	248729	819838	45557	309395	87625	88467	30952
A0JN39 COPB_BOVIN 2 P68103 FF1A1_BOVIN:F1B56	2	110,51	-,	42967 1,309			IL 10705		53475	75970	62219	141463	343005	211898	42397	474038	261164	443788	286956	140645	192208	161167	230789	156607
F1MOV7 F1MOV7_BOVIN 3	6	614,8 168	-,	42967 1,222 43109 1.395	,		L 5010		215216457 68197	137618376 79556	120797101 94542	106756877 33251	185143076 166108	158814187 42010	251558921 27763	154729579 86512	125109688 126095	35434343 145019	38072623 86226	96784381 30789	307158946 73925	171739984 99155	162146596 119317	70490490 75925
O32LI4 TPRGL_BOVIN:F6OF 5	5	478.15		43109 1.820	,		IL 0220	·····	3546593	2384652	2440162	4004585	1494247	2915596	6128790	2189501	2338464	16351548	6290093	6465232	1774903	2384320	2379185	12583712
A0A3Q1MBS5 A0A3Q1MBS 6	6	269,33		43109 1,620			L 10235	9 Alpha-actinin-1 OS=Bos taurus OX=9913 GN=ACTN1 PE=1 SV=1	530621	875156	226098	761647	643257	565853	880590	742017	858705	372443	402375	271928	544470	329271	500926	204173
Q9N2J2 GPX4_BOVIN 3	3	264,9	-,	43109 1,596			IL 2222		1628370	1244502	1196635	295762	914755	864085	1877287	1799777	1539932	785390	1395462	819868	2570101	3042912	2569271	686895
A0A3Q1LS27 A0A3Q1LS27 3	3	135,05		43259 1,395	6 0,30835		IL 5856	TBC1 domain family member 24 OS=Bos taurus OX=9913 GN=TBC1D24 PE	375847	438867	323336	865782	508481	115670	325145	409965	410742	395662	749495	981717	449887	240350	511164	579096
A0A0A0MPA4 A0A0A0MPA 2	2	103,5	0,14452 0	43783 1,998	0,3043	LL	IL 1347		34641	30150	10894	27007	139987	32743	82929	238312	94481	104348	20243	21002	285877	202086	259349	194978
P04272 ANXA2 BOVIN 12		974.26	0,14496 0	43783 1.288	4 0,30371		L 3858		10998032	6521406	9225836	4045465	6385136	7364266	13242106	10157105	5895738	1714534	5380451	3466061	9675035	8849687	8266358	6284617
P04272[ANAA2_BOVIN 12	2 12							Calnexin OS=Bos taurus OX=9913 GN=CANX PF=1 SV=1	152377	415563	536907	266950	868591	559993	146802	811071	919279		733906					569288
A7Z066 A7Z066_BOVIN;A0/ 5	2 12 5			43783 1,242			IL 6773											465996		295586	459076	705618	574174	
A7Z066 A7Z066_BOVIN;A0/ 5 E1BG25 E1BG25_BOVIN 2		126,81	0,14554 0	43783 1,902	3 0,30294	HL	L 8064	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1	809505	54071	74760	150999	44509	151586	146542	94599	180422	405	38905	63825	98903	251384	71151	14527
A7Z066 A7Z066_BOVIN;A0/ 5 E1BG25 E1BG25_BOVIN 2 E1BE21 E1BE21_BOVIN 2		126,81 101,04	0,14554 0 0,14641 0	43783 1,902 43842 1,329	3 0,30294 4 0,30181	HL LL I	L 8064	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1 Transmembrane and coiled-coil domains 4 OS=Bos taurus OX=9913 GN=TI	809505 103109	54071 49699	55946	37360	97911	44926	146542 161810	94599 66183	180422 126999	405 45156	38905 104328	63825 75578	98903 110011	251384 72776	71151 45794	14527 132589
A72066 A72066_BOVIN;A0/ 5 E1BG25 E1BG25_BOVIN 2 E1BE21 E1BE21_BOVIN 2 A0A3Q1LUG9 A0A3Q1LUG5 2	5 2 2 2	126,81 101,04 164,36	0,14554 0 0,14641 0 0,14827 0	43783 1,902 43842 1,329 44055 1,422	 3 0,30294 4 0,30181 5 0,29938 	HL LL I	L 8064 IL 6751 IL 4777	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1 Transmembrane and colled-coll domains 4 OS=Bos taurus OX=9913 GN=TI Uncharacterized protein OS=Bos taurus OX=9913 GN=TXNDC5 PE=1 SV=1	809505 103109 536003	54071 49699 444914	55946 731413	37360 642012	97911 1386506	44926 733597	146542 161810 866988	94599 66183 1335869	180422 126999 1116928	405 45156 3343514	38905 104328 1310041	63825 75578 590508	98903 110011 1371660	251384 72776 737490	71151 45794 884398	14527 132589 1167076
A72066 A72066_BOVIN;A0/ 5 E1BG25 E1BG25_BOVIN 2 E1BE21 E1BE21_BOVIN 2 A0A3Q1LUG9 A0A3Q1LUG5 2 Q0P5L6 Q0P5L6_BOVIN 3	5 2 2 3	126,81 101,04 164,36 192,92	0,14554 0 0,14641 0 0,14827 0 0,14892 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308	73 0,30294 64 0,30181 52 0,29938 52 0,29855	HL LL I LL I	L 8064 IL 6751 IL 4777 IL 8836	Melanotransferrin OS-Bos taurus OX-9913 GN=MELTF PE=3 SV=1 Transmembrane and colled-coll domains 4 OS-Bos taurus OX-9913 GN=TI Uncharacterized protein OS-Bos taurus OX-9913 GN=TNCOS PE=1 SV=1 Centromere/kinetochore protein zw10 OS-Bos taurus OX-9913 GN=ZW1(809505 103109 536003 234761	54071 49699 444914 163262	55946 731413 225368	37360 642012 375936	97911 1386506 526895	44926 733597 681014	146542 161810 866988 334689	94599 66183 1335869 352741	180422 126999 1116928 550210	405 45156 3343514 667382	38905 104328 1310041 1211303	63825 75578 590508 830467	98903 110011 1371660 367855	251384 72776 737490 246489	71151 45794 884398 407015	14527 132589 1167076 685121
A72066 A72066 BOVIN;A0/ 5 E1BG25 JE1BG25 BOVIN 2 E1BE21 JE1BE21 BOVIN 2 A0A3Q1LUG9 JA0A3Q1LUG9 2 Q0P5L6 Q0P5L6 BOVIN 3 F1MJQ1 JF1MJQ1_BOVIN;A(9	5 2 2 3 8	126,81 101,04 164,36 192,92 449,29	0,14554 0 0,14641 0 0,14827 0 0,14892 0 0,15015 0	43783 1,902 43842 1,329 44055 1,422	73 0,30294 54 0,30181 52 0,29938 52 0,29855 16 0,29697	HL LL LL LL	L 8064 IL 6751 IL 4777 IL 8836 IL 2350	Melanotransferrin OS-Bos tarurs OX-9913 GN-MELTP FE-3 SV-1 Transmembrane and colled-coil domains 4 OS-Bos tarurs OX-9913 GN-811 Uncharaterized protein OS-Bos tarurs OX-9913 GN-71XNC5 ZPE-1 SV-1 Centromere/Anetochore protein avx10 OS-Bos tarurs OX-9913 GN-82N1 C Ras-related protein Rab-7 a OS-Bos tarurs OX-9913 GN-82N2 FE-1 SV-1	809505 103109 536003 234761 7388429	54071 49699 444914 163262 2911712	55946 731413 225368 5109179	37360 642012 375936 2146192	97911 1386506 526895 3471770	44926 733597 681014 2720806	146542 161810 866988 334689 6366472	94599 66183 1335869 352741 4589272	180422 126999 1116928 550210 3867841	405 45156 3343514 667382 5389077	38905 104328 1310041 1211303 4266396	63825 75578 590508 830467 3271934	98903 110011 1371660 367855 6314539	251384 72776 737490 246489 6925502	71151 45794 884398 407015 7799347	14527 132589 1167076 685121 5111146
A72066 A72066 BOVIN;A0/ 5 E1BG25 [E1BG25_BOVIN 2 E1BE21 E1BE21_BOVIN 2 A0A3Q1LUG9 A0A3Q1LUG9 Q0P5L6 [Q0P5L6_BOVIN 3 F1MJQ1 F1MJQ1_BOVIN;A(9	5 2 2 3 8	126,81 101,04 164,36 192,92 449,29 420,76	0,14554 0 0,14641 0 0,14827 0 0,14892 0 0,15015 0 0,151 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308 44112 1,284 44119 1,225	73 0,30294 64 0,30181 52 0,29938 52 0,29855 16 0,29697 17 0,2959	HL LL LL LL HL	L 8064 IL 6751 IL 4777 IL 8836 IL 2350 IL 8315	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1 Transmembrane and colled-coll domains 4 OS=Bos taurus OX=9913 GN=TI Uncharacterized protein OS=Bos taurus OX=9313 GN=TXNDC5 PE=1 SV=1 Centromere/Ainetochore protein zw10 OS=Bos taurus OX=9913 GN=ZMIC Ras-related protein Rab-7a OS=Bos taurus OX=9913 GN=CBPA PE=1 SV=1 Oxysterol-binding protein OS=Bos taurus OX=9913 GN=CBPA PE=3 SV=1	809505 103109 536003 234761	54071 49699 444914 163262	55946 731413 225368 5109179 2064111	37360 642012 375936	97911 1386506 526895 3471770 2496570	44926 733597 681014 2720806 1843618	146542 161810 866988 334689	94599 66183 1335869 352741	180422 126999 1116928 550210	405 45156 3343514 667382	38905 104328 1310041 1211303 4266396 2866147	63825 75578 590508 830467	98903 110011 1371660 367855	251384 72776 737490 246489 6925502 1302443	71151 45794 884398 407015	14527 132589 1167076 685121
A72066 A72065 BOVIN;A0/ 5 E1B625 [E1B625 BOVIN 2 E1B621 [E1B621 BOVIN 2 A0A3Q1LUG9 A0A3Q1LUG5 2 Q0P5L6 [Q0P5L6 BOVIN 3 F1MJQ1 [F1MJQ1 BOVIN;Af 9 A0A3Q1MKV7 A0A3Q1MK, 6	5 2 2 3 8 6 2	126,81 101,04 164,36 192,92 449,29 420,76	0,14554 0 0,14641 0 0,14827 0 0,14892 0 0,15015 0 0,151 0 0,15135 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308 44112 1,284	3 0,30294 64 0,30181 62 0,29938 62 0,29855 66 0,29697 77 0,2959 12 0,29546	HL LL LL LL HL HL	L 8064 IL 6751 IL 4777 IL 8836 IL 2350 L 8315	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1 Transmembrane and colled-coil domains 4 OS=Bos taurus OX=9913 GN=TI Uncharacterized protein OS=Bos taurus OX=913 GN=TXNOS PET=1 SV=1 Centromere/kinetochore protein zw10 OS=Bos taurus OX=9913 GN=AB07A PE=1 SV=1 Oxysterol-binding protein OS=Bos taurus OX=913 GN=AB07A PE=1 SV=1 Oxysterol-binding protein OS=Bos taurus OX=913 GN=OSPL9 PE=3 SV=1 Solute carrier family 29 member 1 OS=Bos taurus OX=9913 GN=SU2912 F	809505 103109 536003 234761 7388429 1876188	54071 49699 444914 163262 2911712 1636604	55946 731413 225368 5109179	37360 642012 375936 2146192 1077032	97911 1386506 526895 3471770	44926 733597 681014 2720806	146542 161810 866988 334689 6366472 2428092	94599 66183 1335869 352741 4589272 3133709	180422 126999 1116928 550210 3867841 1681219	405 45156 3343514 667382 5389077 1123951	38905 104328 1310041 1211303 4266396	63825 75578 590508 830467 3271934 1667393	98903 110011 1371660 367855 6314539 1710952	251384 72776 737490 246489 6925502	71151 45794 884398 407015 7799347 2215774	14527 132589 1167076 685121 5111146 1031319
A72066 JA72066 BOVIN-A0U 5 E1B625 JE1B625 BOVIN 2 BA3301L069 JA0A301LVG 2 A0A301L069 JA0A301LVG 2 QOP5L6 JOVIN 3 F1MI01 JE1MI01 JE0VIN;AL 9 A0A301MV(07 JA0A301MK) 6 A0A301MV(07 JA0A301MV) 2	5 2 2 3 8 6 2 2	126,81 101,04 164,36 192,92 449,29 420,76 96,22 106,8	0,14554 0 0,14641 0 0,14827 0 0,14822 0 0,15015 0 0,151 0 0,15135 0 0,1522 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308 44112 1,284 44119 1,225 44119 1,639	3 0,30294 64 0,30181 52 0,29938 52 0,29855 16 0,29697 17 0,2959 12 0,29546 18 0,29439	HL LL LL LL HL HL LL	L 8064 IL 6751 IL 4777 IL 8836 IL 2350 IL 8315 IL 5436 IL 6966	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1 Transmembrane and colled-coll domains 4 OS=Bos taurus OX=9913 GN=TI Uncharacterized protein OS=Bos taurus OX=9913 GN=TNOC5 PET SV=1 Centromere/Ainetochore protein xv10 OS=Bos taurus OX=9913 GN=ABd7A PE=1 SV=1 Oxysterol-binding protein OS=Bos taurus OX=9913 GN=ABd7A PE=1 SV=1 Oxysterol-binding protein OS=Bos taurus OX=9913 GN=ABd7A PE=1 SV=1 Solute carrier family 29 member 1 OS=Bos taurus OX=9913 GN=SU5914 SV=1 Solute carrier family 29 member 1 OS=Bos taurus OX=9913 GN=SU5914 SV=1 SV=SV=SV=SV=SV=SV=SV=SV=SV=SV=SV=SV=SV=S	809505 103109 536003 234761 7388429 1876188 694370	54071 49699 444914 163262 2911712 1636604 637600	55946 731413 225368 5109179 2064111 1174429	37360 642012 375936 2146192 1077032 597091	97911 1386506 526895 3471770 2496570 1018246	44926 733597 681014 2720806 1843618 775790	146542 161810 866988 334689 6366472 2428092 773644	94599 66183 1335869 352741 4589272 3133709 856207	180422 126999 1116928 550210 3867841 1681219 530771	405 45156 3343514 667382 5389077 1123951 1608978	38905 104328 1310041 1211303 4266396 2866147 1131294	63825 75578 590508 830467 3271934 1667393 519424	98903 110011 1371660 367855 6314539 1710952 698444	251384 72776 737490 246489 6925502 1302443 711731	71151 45794 884398 407015 7799347 2215774 800663	14527 132589 1167076 685121 5111146 1031319 278707
A72066jA72066_BOVIN;A0J S E1B623[E1B625_BOVIN 2 LB623[E1B627_BOVIN 2 A0A301L059[A0A301LUG5 2 Q0P5L6[Q0P5L6_BOVIN 3 FIMU01[F1MU01_BOVIN;AK 9 A0A301LIVG9[A0A301LMK 6 A0A301MKV7[A0A301MK 6 A0A301LP19[A0A301LPH] 2	5 2 2 3 8 6 2 2 3	126,81 101,04 164,36 192,92 449,29 420,76 96,22 106,8 285,69	0,14554 0 0,14641 0 0,14827 0 0,14892 0 0,15015 0 0,1511 0 0,15135 0 0,1522 0 0,15289 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308 44155 1,308 44112 1,284 44119 1,225 44119 1,639 44195 1,480	3 0,30294 64 0,30181 52 0,29938 52 0,29855 66 0,29697 77 0,2959 12 0,29546 18 0,29439 14 0,29352	HL LL LL LL HL HL HL	L 8064 HL 6751 HL 4777 HL 8836 HL 2350 L 8315 L 5436 HL 6966 L 3370	Melanotransferrin OS-Bos taurus OX-9913 GN-MELTF PE-3 SV-1 Transmembrane and colled-coll domains 4 OS-Bos taurus OX-9913 GN-TI Uncharacterized protein OS-Bos taurus OX-9913 GN-TXNDC5 PE-1 SV-1 Centromere/Anetochore protein axv10 OS-Bos taurus OX-9913 GN-ZAVIZ Ras-related protein Rab-7a OS-Bos taurus OX-9913 GN-RaVAR 24 Oxysterol-binding protein OS-Bos taurus OX-9913 GN-BAR2A PE-1 SV-1 Solute carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- Solute carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- Solute Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE Carrier family 29 member 1 OS-Bos taurus OX-9913 GN-BAR2A PI- SOLUTE CARACTER SOLUTE CARACTER PI- SOLUTE CARACTER SOLUTE CARACTER SOLUT	809505 103109 536003 234761 7388429 1876188 694370 73081	54071 49699 444914 163262 2911712 1636604 637600 69972	55946 731413 225368 5109179 2064111 1174429 130143	37360 642012 375936 2146192 1077032 597091 164054	97911 1386506 526895 3471770 2496570 1018246 161556	44926 733597 681014 2720806 1843618 775790 38206	146542 161810 866988 334689 6366472 2428092 773644 107782	94599 66183 1335869 352741 4589272 3133709 856207 61523	180422 126999 1116928 550210 3867841 1681219 530771 97067	405 45156 3343514 667382 5389077 1123951 1608978 320260	38905 104328 1310041 1211303 4266396 2866147 1131294 141740	63825 75578 590508 830467 3271934 1667393 519424 153098	98903 110011 1371660 367855 6314539 1710952 698444 89850	251384 72776 737490 246489 6925502 1302443 711731 70522	71151 45794 884398 407015 7799347 2215774 800663 89932	14527 132589 1167076 685121 5111146 1031319 278707 155106
A72066 JA72066 BOVIN-ADU 5 E18625 E18625 BOVIN 2 E18625 E18625 BOVIN 2 A0A3Q1LUG9 JA0A3Q1LUG 2 A0A3Q1LUG9 JA0A3Q1LUG 3 FIJMUQ1 [FIJMUQ1 BOVIN;AI 9 A0A3Q1LMKV7 JA0A3Q1LMK 6 A0A3Q1LMFV1 JA0A3Q1LHG 2 A0A3Q1LMFV1 JA0A3Q1LHG 2 A0A3Q1LMFV1 JA0A3Q1LHG 2 A0A3Q1LMFV1 JA0A3Q1LHG 4 A0A3Q1LMFV1 JA0A3Q1LHFV 2 P11153 [LIP_BOVIN 10	5 2 2 3 8 6 2 2 3 3 2	126,81 101,04 164,36 192,92 449,29 420,76 96,22 106,8 285,69 155,51 1048,79	0,14554 0 0,14641 0 0,14827 0 0,14827 0 0,1515 0 0,1515 0 0,1515 0 0,1515 0 0,1522 0 0,15289 0 0,15482 0 0,15711 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308 44112 1,284 44119 1,255 44119 1,639 44412 1,544 4415 1,544 4415 1,544 4415 1,544 44195 1,544 44195 1,544	3 0,30294 44 0,30181 52 0,29938 52 0,29855 66 0,29697 77 0,29546 80 0,29439 44 0,29352 52 0,29546 50 0,29546 52 0,29114 52 0,28835	HL LL LL HL HL HL HL HL	L 8064 IL 6751 IL 4777 IL 8836 IL 2350 IL 8315 IL 5436 IL 6966 IL 3370 IL 16143 IL 5334	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 SV=1 Uncharacterized protein OS=Bos taurus OX=913 GN=TMLOS PE=1 SV=1 Uncharacterized protein OS=Bos taurus OX=913 GN=TMLOS PE=1 SV=1 Centromere/indetochore protein zw10 OS=Bos taurus OX=9913 GN=SMLO SN=ZVIC Ras-related protein Rab-7a OS=Bos taurus OX=913 GN=SMLO PE=3 SV=1 Oxysterol-binding protein OS=Bos taurus OX=913 GN=SMLO PE=3 SV=1 Solute carrier family 29 member 1 OS=Bos taurus OX=913 GN=SMLO PE=3 SV=1 Golgi phosphoprotein 3 OS=Bos taurus OX=913 GN=SMLO PH3 PE=2 SV=1 SNLOE DS=Bos taurus OX=913 GN=SMLO PE=3 SV=1 Golgi phosphoprotein 3 OS=Bos taurus OX=913 GN=SMLO PH3 PE=2 SV=1 Upoprotein lipase OS=Bos taurus OX=913 GN=NLP ISS PE=4 SV=1 Nucleoporin 155 OS=Bos taurus OX=913 GN=NLP ISS PE=4 SV=1	809505 103109 536003 234761 7388429 1876188 694370 73081 1856989 65969 45131818	54071 49699 444914 163262 2911712 1636604 637600 69972 1130089 115944 22847767	55946 731413 225368 5109179 2064111 1174429 130143 572663 89125 7187396	37360 642012 375936 2146192 1077032 597091 164054 880790 41444 10134553	97911 1386506 526895 3471770 2496570 1018246 161556 1300402 80776 6435015	44926 733597 681014 2720806 1843618 775790 38206 1261917 127940 7962983	146542 161810 866988 334689 6366472 2428092 773644 107782 668294 42141 15727714	94599 66183 1335869 352741 4589272 3133709 856207 61523 2182337 47323 7242363	180422 126999 1116928 550210 3867841 1681219 530771 97067 1563214 109677 6280426	405 45156 3343514 667382 5389077 1123951 1608978 320260 1527115 201939 16324052	38905 104328 1310041 1211303 4266396 2866147 1131294 141740 934217 468825 12960547	63825 75578 590508 830467 3271934 1667393 519424 153098 799803	98903 110011 1371660 367855 6314539 1710952 698444 89850 732888 53556 6920828	251384 72776 737490 246489 6925502 1302443 711731 70522 753436 151023 5626937	71151 45794 884398 407015 7799347 2215774 800663 89932 593137 37849 2969959	14527 132589 1167076 685121 5111146 1031319 278707 155106 944983 65793 6415555
A72066 JA72066 BOVIN-ADU 5 E1B625 JE1B625 BOVIN 2 E1B621 JE1621 BOVIN 2 A0A301L069 JA0A301L065 2 QAPSL6 JOPSL6 BOVIN 3 FILMI01 JE1MI01 JE1MI01 JE1MI01 JE0VIN;AL 9 A0A301LMC9/JA0A301MK 6 A0A301LMC9/JA0A301MK 6 A0A301MI00JA0A301MK 2 A0A301M00JA0A301MK 2 QIRMW9 J01RMW9 BOVIN 2 QIRMW9 J01RMW9 BOVIN 2 P11151 LIP_BOVIN 10 G3MW18 JG3MW18 BOVIN 2	5 2 2 3 8 6 2 2 3 3 2 3 2 0 10 2	126,81 101,04 164,36 192,92 449,29 420,76 96,22 106,8 285,69 155,51 1048,79 99,31	0,14554 0 0,14641 0 0,14827 0 0,14827 0 0,15015 0 0,15115 0 0,1522 0 0,15289 0 0,15482 0 0,15711 0 0,15782 0	43783 1,902 43842 1,329 44055 1,422 44055 1,308 44112 1,284 44119 1,225 44119 1,639 44115 1,480 44422 1,514 44612 1,735 44659 1,455	3 0,30294 44 0,30181 52 0,29338 52 0,29855 52 0,29559 12 0,29546 18 0,29352 12 0,29439 14 0,29352 12 0,29114 12 0,28145 12 0,2814	HL LL LL HL HL HL HL HL HL HL	L 8064 IL 6751 IL 4777 IL 8836 IL 2350 IL 8315 IL 5436 IL 6966 IL 6966 IL 3370 IL 16143 IL 5334 IL 7022	Melanotransferrin OS=Bos taurus OX=9913 GN=MELTF PE=3 Sy=1 Transmembrane and colled-coil domain4 05=Bos taurus OX=9913 GN=TH Uncharacterized protein 05=Bos taurus OX=913 GN=TMNDC5 PE=1 Sy=1 Centromere/kinetochore protein ax-10 OS=Bos taurus OX=9913 GN=ADXPA DE Solute carrier tamily 29 member 105=Bos taurus OX=9913 GN=ADXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=ADXPA DE Golgi phosphoprotein 305=Bos taurus OX=9913 GN=ADXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=ADXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=ADXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=ADXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=DXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=DXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=DXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=DXPA DE Solute carrier family 29 member 105=Bos taurus OX=9913 GN=DXPA DE Solute carrier family 29 member 25=50 Solute carrier 6=25=50 taurus OX=9913 GN=DXPA DE Solute carrier 6=25 kinard OX=9913 GN=DXPA DE Solute carrier family 29 member 25=50 Solute carrier 6=25 kinard OX=9913 GN=DXA DE=1 SV	809505 103109 536003 234761 7388429 1876188 694370 73081 1856989 65969 45131818 23318	54071 49699 444914 163262 2911712 1636604 637600 69972 1130089 115944 22847767 68795	55946 731413 225368 5109179 2064111 1174429 130143 572663 89125 7187396 41559	37360 642012 375936 2146192 1077032 597091 164054 880790 41444 10134553 57777	97911 1386506 526895 3471770 2496570 1018246 161556 1300402 80776 6435015 79798	44926 733597 681014 2720806 1843618 775790 38206 1261917 127940 7962983 42730	146542 161810 866988 334689 6366472 2428092 773644 107782 668294 42141 15727714 43673	94599 66183 1335869 352741 4589272 3133709 856207 61523 2182337 47323 7242363 61449	180422 126999 1116928 550210 3867841 1681219 530771 97067 1563214 109677 6280426 104621	405 45156 3343514 667382 5389077 1123951 1608978 320260 1527115 201939 16324052 311007	38905 104328 1310041 1211303 4266396 2866147 1131294 141740 934217 468825 12960547 62812	63825 75578 590508 830467 3271934 1667393 519424 153098 799803 170009 6537403 35447	98903 110011 1371660 367855 6314539 1710952 698444 89850 732888 53556 6920828 57308	251384 72776 737490 246489 6925502 1302443 711731 70522 753436 151023 5626937 46811	71151 45794 884398 407015 7799347 2215774 800663 89932 593137 37849 2969959 51764	14527 132589 1167076 685121 5111146 1031319 278707 155106 944983 65793 6415555 35771
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A72066jA72066 BOVIN-ADU 5 E18623 [E1623_BOVIN 2 E18623 [E1623_BOVIN 2 A0A3Q1LUG9]A0A3Q1LUG5 2 A0A3Q1LUG9]A0A3Q1LUG5 2 A0A3Q1LUG9]A0A3Q1LUG5 2 A0A3Q1LUG9]A0A3Q1LUG5 2 A0A3Q1MKV7[A0A3Q1MK) 6 A0A3Q1MKV7[A0A3Q1MK) 6 A0A3Q1MV0[A0A3Q1MK) 6 A0A3Q1MV9[A0A3Q1MF] 2 QIRMWB[Q1RMW9]Q1RMW9[Q0VIN 4 A0A3Q1M9F3]A0A3Q1M9F 2 QISWWB[G3WWB, BOVIN 4 A0A3Q1MV93]A0A3Q1M9F 2 QISWWB[G3WWB, BOVIN 10 G3MWVB, G3WWB, BOVIN 2 QISWEF3[G3WZB8_BOVIN 2 A6QP84[A6QP84_BOVIN 2 A0A3Z8F7[A0A3S2F87] 2 A0A3Z8F87]A0A3S2F87_2 2	5 2 2 3 8 6 2 2 3 2 2 3 2 2 3 2 2 2 2 2 2 2 2 2 2	126,81 101,04 164,36 192,92 449,29 420,76 96,22 106,8 285,69 155,51 1048,79 99,31 114,99 201,95 478,31 235,63	0,14554 0 0,14641 0 0,14827 0 0,14827 0 0,1515 0 0,1515 0 0,1513 0 0,1513 0 0,1528 0 0,1528 0 0,1528 0 0,1521 0 0,1528 0 0,1528 0 0,1548 0 0,15781 0 0,15816 0 0,15782 0 0,15846 0 0,15782 0 0,15846 0 0,15846 0 0,15846 0 0,16363 0 0,16384 0 0,1643 0	43783 1,902 43783 1,329 44055 1,422 44055 1,328 44112 1,284 44112 1,284 44119 1,225 44119 1,639 44226 1,514' 44659 1,700 44659 1,700 44659 1,494 44659 1,494 44659 1,494 44659 1,494 44659 1,439 44659 1,439 44659 1,307	3 0,30294 42 0,30181 42 0,29938 52 0,29938 52 0,29938 52 0,29938 52 0,29938 52 0,29938 52 0,29938 52 0,29597 52 0,29546 58 0,29439 54 0,29352 50 0,28749 56 0,282709 56 0,282701 51 0,28038 88 0,27988	HL LL I LL I HL HL HL HL HL I HL I LL I HL LL I HL LL I HL HL	L 8064 H 6751 H 4777 H 8836 H 8836 L 2350 L 5436 H 6966 L 3370 H 1644 L 5334 H 7022 L 5281 H 7022 L 5281 H 7022 L 5281 H 7022 L 5281 H 7072 L 5281 H 7072 L 5281 H 7072 L 5281 H 707 H 7072 H 707 H 70	 Melanotransferrin OS-Bos taurus OX-9913 GN-MELTF PE-3 SV-1 Transmembrane and colled-coll domains 4 05-Bos taurus OX-9913 GN-TI Uncharacterized protein OS-Bos taurus OX-9913 GN-TXNDC5 PE-1 SV-1 Centromere/Interchore protein xv10 OS-Bos taurus OX-9913 GN-XVDVE Ras-related protein Rab-70 OS-Bos taurus OX-9913 GN-STADS PE-1 SV-1 Oxysterol-binding protein OS-Bos taurus OX-9913 GN-STADS PE-3 SV-1 Solute carrier family 29 member 1 OS-Bos taurus OX-9913 GN-STADS PE-3 SV-1 Golg phosphoprotein 3 OS-Bos taurus OX-9913 GN-EXIDE PE-3 SV-1 Golg phosphoprotein 3 OS-Bos taurus OX-9913 GN-EXIDE PE-3 SV-1 Golg phosphoprotein 3 OS-Bos taurus OX-9913 GN-EXIDE PE-3 SV-1 Uncleoporin 155 OS-Bos taurus OX-9913 GN-HEVE PE-3 SV-1 Uncleoporin Igase OS-Bos taurus OX-9913 GN-EXIDE SPE-4 SV-1 Uncharacterized protein OS-Bos taurus OX-9913 GN-VEFAB FE-1 SV-1 Uncharacterized protein OS-Bos taurus OX-9913 GN-VEFAB FE-3 SV-2 Uncharacterized protein OS-Bos taurus OX-9913 GN-VEFAB FE-3 SV-2 J domain-containing protein OS-Bos taurus OX-9913 GN-VEFAB FE-1 SV Leucine rich repeat containing 47 OS-Bos taurus OX-9913 GN-REFLO2 PE-2 SV-1 	809505 103109 536003 234761 7388429 1876188 694370 73081 1856989 65569 45131818 23318 826829 2080625 473424 78062	54071 49699 444914 163262 2911712 1636604 637600 69972 1130089 115944 22847767 68795 844869 1068752 496464 124726	55946 731413 225368 5109179 2064111 1174429 130143 572663 89125 7187396 41559 159295 1375136 574656 37706	37360 642012 375936 2146192 1077032 597091 164054 880790 41444 10134553 57777 34403 2965373 926670 198586	97911 1386506 526895 3471770 2496570 1018246 161556 1300402 80776 6435015 79798 237278 1376708 470104 277719	44926 733597 681014 2720806 1843618 775790 38206 1261917 127940 7962983 42730 72876 653270 369705 58316	146542 161810 866988 334689 6366472 2428092 773644 107782 668294 42141 15727714 43673 374211 2132566 955479 106420	94599 66183 1335869 352741 4589272 3133709 856207 61523 2182337 47323 7242363 61449 239781 2001051 814908 194579	180422 126999 1116928 550210 3867841 1681219 530771 97067 1563214 109677 1263214 109677 1280426 104621 203805 1197879 426795 229163	405 45156 3343514 667382 5389077 1123951 1608978 320260 1527115 201939 16324052 311007 143079 1754243 609703 132068	38905 104328 1310041 1211303 4266396 2866147 1131294 141740 934217 468825 12960547 62812 56734 2189602 450443 199395	63825 75578 590508 830467 3271934 1667393 519424 153098 799803 170009 6537403 35447 55427 3320316 916910 329797	98903 110011 1371660 367855 6314539 1710952 698444 89850 732888 53556 6920828 57308 267779 1727979 1727979 642064 283366	251384 72776 737490 246489 6925502 1302443 711731 70522 753436 151023 5626937 46811 194848 1930018 1070165 92214	71151 45794 884398 407015 7799347 2215774 800663 89932 593137 37849 296959 51764 211781 992610 1652413 193696	14527 132589 1167076 685121 5111146 1031319 278707 155106 944983 647593 6415555 35771 31126 5869917 1264608 94184

A5D7E1 A5D7E1_BOVIN;F1 4	1 2	284,31		0,44659		0,2791	HL LL	60893	EH domain containing 3 OS=Bos taurus OX=9913 GN=EHD3 PE=2 SV=1	388266	373334	823949	402997	480448	269928	436708	396840	381803	180416	172987	371462	394255	301959 4914	
A0A3Q1MG98 A0A3Q1MG9 10		925,33	0,16509	.,	, .	0,27898	HL LL	77965	Sodium-dependent phosphate transport protein 2B OS=Bos taurus OX=99:	236827348 53703	264178040 45417	326263369 49147	152179282	174927907	205031360 32185	221108685		269477265 271703	52990663	132256718 26627	142303132		235955165 1788402	
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A0A301MHC41A0A301MHi 8	, , , ,	585.21	.,	.,	,	0,27354		99047	Cytoplasmic aconitate hydratase OS=Bos taurus OX=9913 GN=AP2B1 PE=3 3V=2	5236061	5930019	4579988	4653283	6168644	5873107	6097265	5334314	7482555	27110242	7730289	420343 8151194	5095960	4677056 43853	
F1MPK7 F1MPK7 BOVIN:F1 1		667.45		0,44039		0,27334	HL LL	81875	Uncharacterized protein OS=Bos taurus OX=9913 PE=3 SV=3	17859227	19548280	20691620	4055285	14147042	27374865	16568307	16805477	14841569	4936340	16915539	9511297	19609325	22693939 182160	
A0A3Q1M2B2 A0A3Q1M2E 19		1428,7	.,	0,45297	,	0.26863	HL LL	183629	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1	6728540	3322776	4891430	3608629	6512458	5408736	8298953	2624170	6175490	1075971	1303389	1305611	15867058	3137885 35048	
A5D7E8 A5D7E8 BOVIN 9	9 9	510,82		0,45297		0,2684	HL LL	56894	Protein disulfide-isomerase OS=Bos taurus OX=9913 GN=PDIA3 PE=2 SV=1	547516	1237351	776943	438247	1617206	788404	1004802	2615387	1506315	467421	369818	263689	1641596	930938 14413	
Q2TA08 BAG5_BOVIN 4	1 4	306,09		0,45353		0,26753	LL HL	50923	BAG family molecular chaperone regulator 5 OS=Bos taurus OX=9913 GN=	438172	451076	436828	559754	415341	738319	419470	326362	725838	1327022	1359468	750837	500416	314293 2783	
F1MX05 F1MX05 BOVIN;Q 3	3 2	122,63	0,17632	0,45412	1,21686 0	0,26664	HL LL	47285	Saccharopine dehydrogenase-like oxidoreductase OS=Bos taurus OX=9913	1449379	832315	1538013	1003695	959205	740794	999799	1045294	890523	387647	583034	699722	1173098	888230 8962	74 861527
Q3ZBG9 PLS2_BOVIN 2	2 2	94,17	0,17951	0,45676	1,48955 0	0,26331	LL HL	32555	Phospholipid scramblase 2 OS=Bos taurus OX=9913 GN=PLSCR2 PE=2 SV=:	968816	890374	785301	529104	498366	1041543	1269158	1106113	765364	443522	1308440	783408	925692	2495199 20042	99 1912983
F1MDM4 F1MDM4_BOVIN 2	2 2	84,84	0,1797	0,45676	3,39223	0,2631	LL HL	21415	Receptor expression-enhancing protein OS=Bos taurus OX=9913 GN=REEP	15017	13248	69335	14239	30585	144779	24212	134361	24360	3415	318473	14927	37645	279249 4331	98 78696
A0A452DJ82 A0A452DJ82 4	1 4	584,09	0,17973	0,45676	1,2666 0	0,26308	LL HL	32777	Rho GDP-dissociation inhibitor 1 OS=Bos taurus OX=9913 GN=ARHGDIA PE	3545652	1968444	1353978	4235984	1379554	1397954	3224491	2119936	3530288	1317391	4091810	3809350	2339273	4232623 21559	49 3348550
F1MUP9 F1MUP9_BOVIN 8	3 8	458,87	0,18076	0,45676	1,37499 (0,26201	LL HL	42803	Vesicle amine transport 1 OS=Bos taurus OX=9913 GN=VAT1 PE=1 SV=3	10683860	11383993	25566700	22451491	10202879	9543991	10160930	11011629	12772956	19477049	45692138	28826269	10048573	12874906 106282	21 17344947
A0A3Q1MF55 A0A3Q1MF5 4	1 4	255,91	0,18099	-,	1,75391 0	0,26178	LL HL	32700	ADP/ATP translocase 2 OS=Bos taurus OX=9913 GN=SLC25A5 PE=3 SV=1	364375	539780	974434	427704	1878378	1222199	1294868	1963788	606459	561916	844783	1043525	2076412	1875274 63593	
F1MMK8 F1MMK8_BOVIN 2	2 2	86,51	0,1831	0,4583	-,	0,25963	HL LL	87698	LysinetRNA ligase OS=Bos taurus OX=9913 GN=KARS1 PE=1 SV=2	400994	1118513	743484	318825	1158356	1128843	616816	466341	667562	255026	113082	311365	790585	794724 9424	
E1BA29 E1BA29_BOVIN 9	9 8	352,84	0,18504	0,4583	-,	0,25768	HL LL	42115	G protein subunit alpha q OS=Bos taurus OX=9913 GN=GNAQ PE=4 SV=1	4594396	4226714	6873066	1947814	4445113	6461293	4620980	6431487	3149972	1985573	1794414	1821387	5037695	5784925 68442	
F1MXX6 F1MXX6_BOVIN;G 1 F1BCP6 F1BCP6 BOVIN 4	7 17	2190,4		0,4583	-,	0,25754	LL HL	47815	Lactadherin OS=Bos taurus OX=9913 GN=MFGE8 PE=4 SV=1	1807715376 1	464682655		3330843349	1802404868	1571095540	1836718502		237389842	2981670009	1785543040	2755876345		160338996 14309659	
	4 	204,05	.,	0,4583 0.4583	1,28104 (0,25711	HL LL	130/9/	Tyrosine-protein kinase OS=Bos taurus OX=9913 GN=JAK2 PE=3 SV=2	260198	479129	561701	193854	542150	476332	170066	544992	496301	118129	405342	246409	124267	377473 5359	
P04896 GNAS2_BOVIN;A0A 5 Q2HJG5 VPS35 BOVIN 7	5 5	320,32 499,96		.,	,	0,25693	LL HL	45080	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=E Vacuolar protein sorting-associated protein 35 OS=Bos taurus OX=9913 GI	21084159 1674657	15160228 2403559	19932104 1588423	35071183 4496673	15594337 3372195	15177219 2571700	20121086 2606410	16224557 2108498	12843660 2516700	29582469 4102247	23613590 6006971	28182029 6702151	18579977 2607912	20152080 160958 2571872 21148	
A0A3011KE21A0A3011KE2 9	, , , ,	641.5	0,18047	.,	,	0,25558		52662	Aldehyde dehydrogenase OS=Bos taurus OX=9913 GN=LOC508879 PE=3 S	3270466	4814507	5046585	1623347	8149796	7563720	4652539	4111958	7294153	6330672	6743299	5380471	5192421	4385015 76149	
ASD7R91ASD7R9 BOVIN 6	5 4	356.81	.,	.,	-)	0.25459	LL HL	21216	NRAS protein OS=Bos taurus OX=9913 GN=NRAS PE=2 SV=1	2682940	1543656	1429853	1832535	1343744	1064054	2457544	1923018	1505098	3200305	1904262	1523229	1342563	1955872 19702	
A0A3Q1MDY5[A0A3Q1MD] 4	1 4	162.07	.,	.,	,	0 25278	LL HL	119134	Ubiguitin conjugation factor E4 A OS=Bos taurus OX=9913 GN=UBE4A PE=	193644	250075	358604	503068	368822	525323	243346	246634	617233	1344191	838562	779907	167933	290958 2073	
F1MD661F1MD66 BOVIN 3	3 3	126.65		.,		0.25269	HL LL	54177	Annexin OS=Bos taurus OX=9913 GN=ANXA11 PE=3 SV=3	211466	236161	75980	34923	216863	17133	221993	160647	245901	21388	23046	21189	276040	84758 1233	
F1N0F7 F1N0F7_BOVIN 2	2 2	115,91	0,19209	0,46306	1,36657 (0,25079	LL HL	48941	Eukaryotic translation initiation factor 5 OS=Bos taurus OX=9913 GN=EIF5	87832	151226	194312	148557	259144	108349	110429	331759	316793	103071	105786	151750	310159	360829 3203	62 150908
E1BM16 E1BM16 BOVIN 3	3 3	279,66	0,19321	0,46306	1,45733 0	0,24972	LL HL	55584	Family with sequence similarity 83 member F OS=Bos taurus OX=9913 GN:	682599	1635705	156176	551227	1307626	498712	1570645	489451	874989	1315810	1973756	909448	1547084	411962 3664	53 1867358
A0A3Q1LLH1 A0A3Q1LLH1 2	2 2	85,8	0,19441	0,46306	1,18015 0	0,24859	LL HL	18957	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1	86075	102971	83271	191144	350771	111768	155988	445277	160283	211416	115689	105754	315133	144422 2426	39 273817
A0A3Q1LL79 A0A3Q1LL79_ 3	3 3	190,34	0,19812	0,46306	1,45117 (0,24514	HL LL	51584	Neuroplastin OS=Bos taurus OX=9913 GN=NPTN PE=4 SV=1	449957	860296	675515	412317	463975	652823	320945	679940	323480	296325	125374	282990	522411	747955 4851	78 64165
E1BPM0 E1BPM0_BOVIN;A 10	0 10	548,18				0,24499	HL LL	93979	RAS protein activator like 1 OS=Bos taurus OX=9913 GN=RASAL1 PE=4 SV=	2309013	1510912	2325345	1392469	2064227	1859592	2762977	1709027	2395714	1764372	2657297	1722932	1011355	845065 17454	
F1MZ03 F1MZ03_BOVIN;A(5	5 5	265,17	.,	0,46306	,	0,24225	HL LL	63768	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2 OS=Bos taurus C	271190	414706	556870	136664	407801	293433	272418	530473	454628	26687	104495	114698	349286	391569 3666	
E1BAV3 E1BAV3_BOVIN;A0 2	2 2	128,63	., .	0,46306	,	0,24123	LL HL	42806	Stomatin like 1 OS=Bos taurus OX=9913 GN=STOML1 PE=4 SV=2	75833	92223	107195	161774	206179	147933	107836	50060	208818	805729	203117	170463	83441	77819 1097	
E1BJQ7 E1BJQ7_BOVIN;A0/ 4	1 4	380,63				0,24115	HL LL	35943	GIPC PDZ domain containing family member 1 OS=Bos taurus OX=9913 GN	387432	470827	1040538	378534	481578	953543	527344	558280	297042	72322	159673	339096	522953	547100 8774	
A0A3Q1LKJ2 A0A3Q1LKJ2_I 6	5 6	463,48			,	0,24103	HL LL	48251	Flotillin-2 OS=Bos taurus OX=9913 GN=FLOT2 PE=4 SV=1	2380852	2200792	898329	944843	751818	714755	2677846	747766	1108403	307399	559027	442221	1544272	1458039 6342	
F1MQ37 F1MQ37_BOVIN;A 6	5 6	300,78	.,	.,	-/	0,2409	HL LL	227063		177287	316550	97675	90412	611496	170802	273185	277588	107153	312035	92935	120904	311927	157104 1900	
F1MHH9 F1MHH9_BOVIN;/ 6 A0A301MU33 A0A301MU: 1:	5 6	359,66	.,	0,46306	,	0,2408	HL LL	35147	Uncharacterized protein OS=Bos taurus OX=9913 GN=FCGR2B PE=4 SV=3 Annexin OS=Bos taurus OX=9913 GN=ANXA5 PE=1 SV=1	11052162 13195648	2233687 6092051	2485288 8933596	1669942	1985562 10015976	4196682	2272822 8132045	6720757 20399137	9223405 3209101	232981 6676038	410062 5407506	1056561 4561266	2136419 10607811	1494340 48902 5658814 88576	
A0A3Q1MU33 A0A3Q1MU: 1: P81125 SNAA BOVIN:A0A3 6	1 11 5 6	903,8 417.55	0,20421		1,33379 (1,29093	0,23964	HL LL	35853	Alpha-soluble NSF attachment protein OS=Bos taurus OX=9913 GN=NAPA	2810925	1867567	3562338	4932989 1289745	1496409	7631467 2909201	2854346	20399137 2308121	1538034	436830	1758097	4561266	1705971	2916148 21922	
F1MM83 F1MM83 BOVIN 2		75,73	0,20032	0,46495	,	0,23639	HL LL	27514	6-phosphogluconolactonase OS=Bos taurus OX=9913 GN=PGLS PE=3 SV=1	234556	99953	291014	63921	176612	173601	180297	161953	94028	430830	20520	45819	173309	320505 1749	
P68002 VDAC2 BOVIN;A0A 4	1 4	266.92	.,	.,	-,	0,23035	LL HL	31600	Voltage-dependent anion-selective channel protein 2 OS=Bos taurus OX=9	74478	188207	139288	407913	809766	84206	791787	610566	122064	438790	394743	437918	1127000	527932 12409	
E1B749 E1B749 BOVIN:A0/ 4	1 3	329.51	.,	.,	, .	0.23514	HL LL	73734	Solute carrier family 5 member 9 OS=Bos taurus OX=9913 GN=SLC5A9 PE=	3368735	3355511	6004460	1060345	2795337	3389908	3706915	2640027	2898400	1261759	2047990	883008	3312032	2476218 22767	
A0A3Q1LMM6[A0A3Q1LM] 2	2 2	114.64		0.46528	1.335	0.2341	LL HL	50901	Parvin alpha OS=Bos taurus OX=9913 GN=PARVA PE=4 SV=1	220150	71368	75355	351692	106232	42911	206506	143524	73655	161641	324537	284798	194644	102601 1187	
A0A3Q1M4W1 A0A3Q1M4 3	3 3	174,02	0,21096	0,46528	1,36378 (0,23376	LL HL	25440	MOB kinase activator 1A OS=Bos taurus OX=9913 GN=MOB1A PE=4 SV=1	637739	218889	335285	113863	407195	314721	786573	448489	326264	276633	304196	327918	362543	1055834 9841	69 376949
A4FUX1 A4FUX1_BOVIN;G3 5	5 5	640,77	0,21385	0,4689	1,28317 (0,23132	LL HL	24525	CIDEA protein OS=Bos taurus OX=9913 GN=CIDEA PE=2 SV=1	254221616	89732855	117581919	73887543	112245315	97707817	285878442	163126554	149748471	113752545	159733476	97898627	266576901	145161392 2628737	08 215963442
A0A3Q1MJ97 A0A3Q1MJ97 2	2 2	152,79	0,21385	0,4689	1,1857 (0,23132	HL LL	25980	Synaptophysin like 1 OS=Bos taurus OX=9913 GN=SYPL1 PE=4 SV=1	3140724	2044049	1788271	2124580	2106227	2007548	3505816	3255214	2395637	1923435	1527258	2509896	2661144	1406183 27397	06 1274759
A0A3Q1LTU6 A0A3Q1LTU6 7	7 7	301,17	0,2152	0,46913	1,39611 0	0,23019	LL HL	89021	Tax1-binding protein 1 homolog OS=Bos taurus OX=9913 GN=TAX1BP1 PE	376309	323683	562483	159893	474670	714155	689623	207747	632967	132471	489528	466026	628883	556109 5517	52 454319
G3X743 G3X743_BOVIN 2	2 2	196,37	0,2188	0,47298	1,51041 0	0,22723	LL HL	72095	Arginyl aminopeptidase OS=Bos taurus OX=9913 GN=RNPEP PE=4 SV=2	85621	294912	221567	412503	363663	217055	118006	290800	255110	974834	558015	458393	150827	164321 2589	93 272554
Q0VCQ6 Q0VCQ6_BOVIN;A 3	3 3	181,8	0,22001	0,47411	1,19666 0	0,22625	HL LL	24700	Programmed cell death 10 OS=Bos taurus OX=9913 GN=PDCD10 PE=2 SV=	1308150	529158	716889	437578	568518	407265	624285	873293	249841	88715	273822	324807	734407	969662 10197	
A0A3Q1MPF1 A0A3Q1MPF 9	9 9	697,81	.,	.,	1,3696 0	0,22158	HL LL	51036	Rab GDP dissociation inhibitor OS=Bos taurus OX=9913 GN=GDI2 PE=3 SV=	5259054	4515261	1315036	6401667	7814903	3803855	4923081	3370085	3596017	8325308	3317223	7926111	2756353	1894332 21589	
Q9XSA7 CLIC4_BOVIN 3	3 3	136,15	.,	.,	,	0,22124	HL LL	28709	Chloride intracellular channel protein 4 OS=Bos taurus OX=9913 GN=CLIC4	716320	514966	1141488	643879	667654	929933	618531	1477478	466812	171262	295961	347101	635551	1334857 13439	
E1BIE9 E1BIE9_BOVIN;A0A: 5	5 5	385,96	.,	.,	,	0,21953	HL LL	65536	Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC100337457 PE=	207092	3981215	3059184	1081630	575638	1971493	1249024	6788053	325822	943632	1053212	933520	479366	3805604 44011	
A0A3Q1LHT7 A0A3Q1LHT7 8	3 8	548,52	., .	.,	,	0,21628	HL LL	166675	Ribosome binding protein 1 OS=Bos taurus OX=9913 GN=RRBP1 PE=1 SV=	159902	614816	467004	162189	807162	469213	352380	1196113	692321	62894	92849	112259	618510	595996 8593	
A0A3Q1LN89 A0A3Q1LN89 2	2 2	89,23	0,23388	., .	-,	0,21544	LL HL	144844	Calcium dependent secretion activator 2 OS=Bos taurus OX=9913 GN=CAL	53026	34514	97538	46428	237903	203104	69408	197450	280328	51703	528462	127191	106605	67741 1804	
E1BH06 E1BH06_BOVIN;F1 3 P00727 AMPL BOVIN 2	3 3	172,88		0,49838		0,21222	LL HL HL LL	1926/6	Uncharacterized protein OS=Bos taurus OX=9913 GN=C4A PE=1 SV=3 Cvtosol aminopeptidase OS=Bos taurus OX=9913 GN=LAP3 PE=1 SV=3	150069 48982	139371 38551	352314 35270	84126 41048	50321 103306	122325 65568	188042 58644	87149 14794	97739 27383	405989 16379	1297906 3910	116019 80284	157512 30001	62940 1568 36962 173	
O3ZCI2 AKIA1 BOVIN 4	2 2 1 4	127,02	.,	0,49838	,	0,21215	HL LL	30254	Aldo-keto reductase family 1 member A1 OS=Bos taurus OX=9913 GN=LAP3 PE=1 SV=3	48982	416412	206961	41048	300532	378973	695763	309000	2/383	95580	3910	80284 148197	374081	604627 4289	
40A301M2I5 A0A301M2I5	4 1 2	267.71		0,49838		0,2115	HL LL	30594	Keratin, type I cytoskeletal 14 OS=Bos taurus OX=9913 GN=KRT14 PE=1 SV	686361	416412 488307	611359	560198	807411	282768	807046	1372127	487779	256205	499295	678328	471465	496652 3886	
A0A3Q1NEU9 A0A3Q1NEU! 8	8 8	436,37	-,		,	0.20882	LL HL	533236	Dynein cytoplasmic 1 heavy chain 1 OS=Bos taurus OX=9913 GN=DYNC1H	58024	21429	21898	53511	438593	257612	248831	152617	225706	252773	148621	80212	510466	475159 1247	
P24627 TRFL_BOVIN;A0A3(12		904		0,50159		0.20847	HL LL	78006	Lactotransferrin OS=Bos taurus OX=9913 GN=LTF PE=1 SV=2	4168335	2643051	1156651	5284606	1026528	842460	5251915	1063843	647901	3430734	2259074	2216261	877979	412168 4283	
A0A3Q1M4H2 A0A3Q1M4ł 2	2 2	285,97				0,20768	LL HL	90585	ADAM metallopeptidase domain 9 OS=Bos taurus OX=9913 GN=ADAM9 P	72553	1281	1218360	1110054	476090	455184	30189	373722	458641	2118172	499738	1369367	63558	1322772 6160	
A0A3Q1MBG6 A0A3Q1MBC 3	3 3	92,62	0,24621	0,50173	1,42024	0,2065	HL LL	75538	Sphingosine kinase 2 OS=Bos taurus OX=9913 GN=SPHK2 PE=4 SV=1	201655	107147	435459	125890	254788	217699	146111	294241	211327	312171	229676	155928	42088	113333 1560	62 97491
P05307 PDIA1_BOVIN;A0A: 7	7 7	402,27	0,24977	0,50173	1,42121 (0,20403	HL LL	57230	Protein disulfide-isomerase OS=Bos taurus OX=9913 GN=P4HB PE=1 SV=1	757019	1184551	908435	552323	1274873	686640	1310318	2790518	837129	246976	451406	813814	1415290	807366 11509	48 466915
F6RWK1 F6RWK1_BOVIN 3	3 3	186,66	0,2509	0,50173	1,39999 0	0,20326	HL LL	50445	Rho GTPase activating protein 1 OS=Bos taurus OX=9913 GN=ARHGAP1 PE	103338	114434	179349	50212	208056	172562	87625	180553	110716	50417	57397	68619	116814	124636 1909	67 33881
A0A3Q1M6K1 A0A3Q1M6K 8	3 8	459,98	0,25523	0,50173	1,28047 0	0,20032	HL LL	147062	Peptidylprolyl isomerase OS=Bos taurus OX=9913 GN=PTPRJ PE=4 SV=1	2121873	2538274	2960369	619779	1662603	3063373	2056944	1744437	1884802	483142	1175193	983494	1496263	2460533 32564	
Q5EA79 GALM_BOVIN 3	3 3	138,82	.,		,	0,20017	HL LL	37591	Aldose 1-epimerase OS=Bos taurus OX=9913 GN=GALM PE=2 SV=1	2155125	1906724	2163833	624998	2226785	3245281	1862554	2963621	2271767	711414	2683539	1411791	1777157	1420004 26438	
A0A452DIG0 A0A452DIG0_ 4	4 4	188,53	,	-,	-/	0,19859	LL HL	15155	Cytochrome b5 OS=Bos taurus OX=9913 GN=CYB5A PE=1 SV=1	123300	73846	246463	91673	294420	191047	281304	439769	178510	77835	81766	77868	471800	939427 7293	
A0A3Q1LMU9 A0A3Q1LML 2 A0A3Q1LVC7 A0A3Q1LVC7 6	2 2	64,53 357.82	0,25954	-,	-,	0,19747	HL LL	37115 78703	Eukaryotic translation initiation factor 3 subunit H OS=Bos taurus OX=991: Ezrin OS=Bos taurus OX=9913 GN=EZR PE=1 SV=1	21589 746908	51671 394763	5652 502947	123876 168099	115409 318630	0 247212	7 569383	201869 568751	57847 516535	3254 97215	20288 94541	19498 176975	73874 470819	1234 1104 586452 5074	
A0A3Q1LVC/ A0A3Q1LVC/ 6 A0A3Q1LJQ9 A0A3Q1LJQ9 2	2 2	357,84		0,50173	-,	0,19683	HL LL	78703	EZrin OS=BOS taurus OX=9913 GN=EZR PE=1 SV=1 Mevalonate kinase OS=Bos taurus OX=9913 GN=MVK PE=3 SV=1	746908 36816	394763	502947	168099	318630 171026	247212 59958	56896	568751 96108	25346	97215 4553	94541 20242	3301	470819	57387 1563	
0170W3IRDH14 BOVIN 2	- 2	97.49	0,26083		,	0,19662	HL LL	36603	Retinol dehydrogenase 14 OS=Bos taurus OX=9913 GN=MVK PE=3 SV=1	171181	218426	177016	56551	145583	160532	225421	152868	100600	4553	20242	47296	168622	225217 2024	
F1MTP5 F1MTP5 BOVIN 3	3 3	200,26	0,2654	0,50173	,	0.19368	HL LL	66235	WD repeat-containing protein 1 OS=Bos taurus OX=9913 GN=WDR1 PE=4	263755	583423	214718	264100	561300	92647	462881	395682	622974	250140	144155	58369	272819	414401 3091	
A0A3Q1M119 A0A3Q1M11 7	7 7	495,39				0,19353	HL LL	27402	14-3-3 protein epsilon OS=Bos taurus OX=9913 GN=YWHAE PE=1 SV=1	3426483	2112376	2346892	1140915	2591909	2671535	4327958	4077090	2088479	331204	535800	1036323	4084237	4243732 48504	
A0A3Q1M8J9 A0A3Q1M8J5 2	2 2	102,88	0,26638	0,50173	1,16103 (0,19306	HL LL	40494	Glyceraldehyde-3-phosphate dehydrogenase OS=Bos taurus OX=9913 GN=	1735669	705252	1046240	575491	774839	527800	1461664	1156006	996678	136466	110968	454513	1183960	1282043 13350	76 946455
A0A3Q1MCE5 A0A3Q1MCE 7	7 7	399	0,26696	0,50173	1,33703	0,1927	LL HL	70190	Acetoacetyl-CoA synthetase OS=Bos taurus OX=9913 GN=AACS PE=4 SV=1	1028030	1033128	1522822	306951	2317461	1001822	961745	1736724	2367948	978777	1965317	926314	1873902	2148430 20168	76 510725
Q5E947 PRDX1_BOVIN;A0A 5	5 5	256,66	0,26708	0,50173	1,52563 (0,19262	LL HL	22195	Peroxiredoxin-1 OS=Bos taurus OX=9913 GN=PRDX1 PE=2 SV=1	1934709	807439	936085	574787	1202437	727298	2429135	2440444	1738087	700931	571219	996490	2794102	3893387 31508	82 1456290
A3FPG8 GPAT4_BOVIN;A6H 13		1166,5			1,16451 (0,19243	LL HL	52021	Glycerol-3-phosphate acyltransferase 4 OS=Bos taurus OX=9913 GN=GPA1	7329314	6548366	12856352	6338846	11345946	9123932	9899607	5901378	10157908	6626837	13119993	7614234	12936811	8841076 72279	
P17248 SYWC_BOVIN 4	1 4	216,08		0,50173		0,19223	HL LL	53778	TryptophantRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=WARS	955311	1208735	681372	337407	1665677	1246558	1393198	1097585	897146	112496	197086	464308	1291040	1651961 19202	
A0A3Q1MQS3 A0A3Q1MQ: 7	7 2	346,74				0,1914	HL LL	29036	14-3-3 protein theta OS=Bos taurus OX=9913 GN=YWHAQ PE=1 SV=1	496456	284010	590079	236620	405244	394443	763064	677170	284862	61420	189372	190366	664313	709997 7331	
F1MPP1 F1MPP1_BOVIN 3	3 3	365,22			1,21938 (.,	LL HL	23506	RAB21, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB21	4269504	2669470	1855555	939244	1533810	1540699	4081923	2473018	2322875	2133850	4738884	2322450	3436102	3180766 23736	
F1MU79 F1MU79_BOVIN 2		113,47	., .			0,1899	HL LL		Peptidylprolyl isomerase OS=Bos taurus OX=9913 GN=FKBP4 PE=4 SV=2	24789	31058	89046	24952	77311	163605	55167	52433	42445	2384	16966	22603	44346	152864 785	
A0A3Q1MCG3 A0A3Q1MC(14		1435,3		-,	1,26118 (-,	HL LL		5'-nucleotidase OS=Bos taurus OX=9913 GN=NT5E PE=3 SV=1	4243928	2385241	11254490	7071548	3252225	5009836	11961192	5690714	1490580	681090	7982956	5877164	7989894	8245212 70327	
A0A3Q1LY00 A0A3Q1LY00_ 3 A0A3Q1M0U9 A0A3Q1M0L 7	337 77	173,8 360,96	., .		1,42099 (1,32038 (.,	LL HL		Membrane palmitoylated protein 5 OS=Bos taurus OX=9913 GN=MPP5 PE Transitional endoplasmic reticulum ATPase OS=Bos taurus OX=9913 GN=V	20403 1061286	76119 1286799	147911 510414	123324 880626	158414 1096980	83740 811035	47437 1111561	207236 734010	49518 1868138	233059 2798644	339825 1519544	145116 1399923	36517 1004545	160482 1498 491024 7559	
A0A3Q1M0U9 A0A3Q1M0U / A0A452DIS9 A0A452DIS9_E 3	/ / 3 3	360,96			1,32038 (HL HL	40209	(Lyso)-N-acylphosphatidylethanolamine lipase OS=Bos taurus OX=9913 GN=V		224704	510414 496260	361458	487154	390922	1111561 384696	734010 409802	1868138 331291	462124	238523	1399923 321245	307721	248885 4312	
A0A3Q1MQ90 A0A3Q1MQ 4		139,41 376,97			1,15518 (HL LL	40209	(Lyso)-N-acylphosphatidylethanolamine lipase OS=Bos taurus OX=9913 GN Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1	309460 890995	224704 986857	496260 506725	361458 318779	48/154 170695	390922 1031090	384696 122735	409802 506581	331291 1124895	462124 893169	238523	321245 478209	307721	248885 4312 1485830 4589	
A0A3Q1MQ90 A0A3Q1MQ 4 A0A140T8A9 A0A140T8A9 3	+ 2	224,79					HL LL		Kappa-casein OS=Bos taurus OX=9913 GN=CSN3 PE=4 SV=1	47148359	30412557		318779	39154554	53771033	88484445	35487387	16038459	28703738	50796962	478209 53400384	30309807	21038012 350970	
A0A301M238 A0A301M23 2		107.13			,	0.1861		64435	Signal peptide peptidase like 2A OS=Bos taurus OX=9913 GN=SPPL2A PE=4	18021	185924	241668	506231	173152	254724	30778	272514	303979	242159	357552	407241	35239	220616 1924	
P15396 ENPP3_BOVIN;A0A 1:		1202,8				0,18543	LL HL	99459	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS	16859508	13819687	29087672	31269029	14986517	25036971	15763760	15858877	21252691	74176507	54778235	32639309	12727895	16496263 145305	
F1MHI1 F1MHI1_BOVIN;F1 2:		2264,5				0,1843	LL HL	49043			170644059		4541495610					195808929	6350759763			854750807 1		
E1BP71 E1BP71_BOVIN;P52 3	3 3	176,88	.,	0,50173	,	0,18387	LL HL	37126	Aldo_ket_red domain-containing protein OS=Bos taurus OX=9913 GN=LOC	117378	3650	11710	53628	2712	24723	59114	96845	21731	0	40053	8871	0	2387427 359	
F1MD24 F1MD24_BOVIN;E 5	5 5	383,36				0,18189	HL LL	73054	Solute carrier family 5 member 1 OS=Bos taurus OX=9913 GN=SLC5A1 PE=		4901714	11225281	9047344	7921977	5706859	5575202	9741337	6225515	2916786	4150599	8816407	6824252	8316539 98211	
A5D7F2 A5D7F2_BOVIN 7	· ·	443,74			1,13211 (HL LL		SYT4 protein OS=Bos taurus OX=9913 GN=SYT4 PE=2 SV=1	1861486	1873431	2551187	1625530	2081646	2057834	2372014	3073017	1882269	589337	731006	1416712	2496184	2771991 39299	84 1340362
Q58D08 P5CR3_BOVIN 2	2 2	128,87	.,		1,39678 (.,	LL HL		Pyrroline-5-carboxylate reductase 3 OS=Bos taurus OX=9913 GN=PYCR3 P	132526	115511	59453	21755	83242	111259	113178	131201	72119	5342	21285	12440	332527	339267 2745	
F1MES6 F1MES6_BOVIN 5	5 5	350,05	0,29651	0,51527	1,26604 0	0,17531	HL LL	49775	UBX domain-containing protein 6 OS=Bos taurus OX=9913 GN=UBXN6 PE=	242671	580515	885259	455211	672854	334627	197200	630603	527061	165078	340684	322245	142852	753689 6543	09 199512

A0A3Q1LYU3 A0A3Q1LYU3 3		248,67	.,	0,51527		0,17531	LL	HL	60027	Atlastin GTPase 3 OS=Bos taurus OX=9913 GN=ATL3 PE=4 SV=1	227119	282151	261322	102667	314103	100179	303898	345889	397388	227084	281091	126279	786595	107398	303589	69662
F1ME65 F1ME65_BOVIN 2 F1MZ04 F1MZ04 BOVIN:E 10	-	126,02 638,71	0,29876	-,	1,46757	0,17408	HL	LL	64491 59194	Cytoskeleton associated protein 4 OS=Bos taurus OX=9913 GN=CKAP4 PE=	25907 8641352	73147 6634432	25547 1146288	80960 729871	71386 8209046	114264 6794326	56295 1137136	81575 2151752	74050 9116541	60812 2055057	28961 3155260	20112 1329236	71210 7317347	141841 3139222	63064 10979446	19476 1956588
Q3MHW6 MOT1 BOVIN 8) 8	638,71 875,91	0,29885	0,51527 0,51527	1,3278 1,18261	0,17403	LL	HL LL	59194 54262	Butyrophilin subfamily 1 member A1 OS=Bos taurus OX=9913 GN=BTN1A1 Monocarboxylate transporter 1 OS=Bos taurus OX=9913 GN=SLC16A1 PE=	8641352 5605344	4966618	1146288 6925547	1535135	8209046 3036553	4212299	113/136 5908878	2151752 4152466	9116541 5916135	2055057 517022	3155260 2527484	1329236 1236596	/31/34/ 4917209	3139222 5504892	4898356	1956588
A0A3Q1MZJ6 A0A3Q1MZJ6 3	2	189.44	0,29911		1,18201	0,17333	пL Ш	LL	32326	DnaJ heat shock protein family (Hsp40) member B2 OS=Bos taurus OX=99:	217888	143746	345770	94889	169246	4212299	174983	252780	150320	50409	68047	80966	144100	280193	302984	141106
E1BA03/E1BA03 BOVIN 2		75,34	0.30452		1,23447	0.171	LL	HL	74332	Non-specific serine/threonine protein kinase OS=Bos taurus OX=9913 GN=	181306	190974	169532	104077	177646	126016	232199	300733	225971	150800	146657	138656	262407	303849	345332	77818
F1N261 F1N261 BOVIN 4	3	270.21	0.30466	.,	1,26755	0.17093	н	LL	58698	Tyrosine-protein kinase OS=Bos taurus OX=9913 GN=LYN PE=1 SV=1	1981523	1158525	1960883	824080	1162780	739253	936299	1320093	1134146	1284359	620119	782700	916942	757986	1120555	778441
Q2HJ94 DNJA2 BOVIN:A0A 4	4	225.75	0.30471	0.51787	1.19419	0.1709	HL	LL	45733	DnaJ homolog subfamily A member 2 OS=Bos taurus OX=9913 GN=DNAJA	824820	1008853	1023074	332828	967021	1267523	439795	841476	760329	90973	326929	270961	632641	1145527	1270410	283089
A0A3Q1NJE9 A0A3Q1NJE9 2	2	126,13	0,3071	0,51787	1,08012	0,16965	HL	LL	36482	Cell cycle control protein OS=Bos taurus OX=9913 GN=TMEM30A PE=3 SV	609763	434018	637305	494838	978193	488004	379555	517195	568213	78431	144008	444100	1248816	505704	728808	246075
A0A452DIU9 A0A452DIU9_ 2	2	125	0,30711	0,51787	1,16265	0,16964	LL	HL	86811	Protein transport protein SEC23 OS=Bos taurus OX=9913 GN=SEC23B PE=:	73134	117989	75445	134147	274324	137933	113270	180389	273992	377507	184873	297758	184284	109015	134752	59755
F1N2L5 F1N2L5_BOVIN 2	2	92,65	0,31026	0,51844	1,2559	0,16801	LL	HL	76275	Maestro heat like repeat family member 6 OS=Bos taurus OX=9913 GN=M	10051	32427	15677	12165	45543	35694	21664	22985	60975	11994	42470	69239	21634	12332	36682	16784
Q3T0S6 RL8_BOVIN 2	2	88,21	0,31056	0,51844	1,02864	0,16785	HL	LL	28007	60S ribosomal protein L8 OS=Bos taurus OX=9913 GN=RPL8 PE=2 SV=3	154894	144645	156296	77428	227810	299441	283282	410312	206569	26275	47258	35033	550544	335635	372694	154071
A2VDZ9 VAPB_BOVIN;A0A3 3	2	292,41	0,31068	0,51844	1,54374	0,16779	LL	HL	27141	Vesicle-associated membrane protein-associated protein B OS=Bos taurus	349727	95078	200437	118529	268524	373327	442807	462357	160843	129575	145447	172638	701982	1235039	986834	384648
A0A3Q1M9B3 A0A3Q1M9E 2	-	183,39	0,3138	0,51844	1,85498	0,1662	LL	HL	22994	60S ribosomal protein L18 OS=Bos taurus OX=9913 GN=RPL18 PE=1 SV=1	29631	63394	85477	93889	254267	14932	53041	454444	177852	43071	54641	5167	184455	220821	561944	521253
A0A3Q1LW82 A0A3Q1LW8 5	5	438,73	0,31407	0,51844	1,33676	0,16606	LL	HL	45191	Protein NDRG1 OS=Bos taurus OX=9913 GN=NDRG1 PE=4 SV=1	1375195	1000759	1223182	2827323	1652561	2628271	1542422	1393787	936259	2742518	2610219	4525181	909093	1856084	1891984	1640000
A0A140T894 A0A140T894_ 6	2	480,95	0,31462	0,51844	1,0699	0,16578	HL	LL	28065	14-3-3 protein beta/alpha OS=Bos taurus OX=9913 GN=YWHAB PE=3 SV=1	1089141	656148	1289887	389105	948259	935249	1715704	1592363	606720	75045	397944	349574	1600872	1586896	1978573	445941
A0A3Q1MHG7 A0A3Q1MH 2	2	206,43	0,31503	0,51844	1,20953	0,16558	HL	LL	35882	Annexin OS=Bos taurus OX=9913 GN=ANXA4 PE=1 SV=1	225423	89208 868865	131080 987446	82784	191829 985405	70734	162431	316152	51539	67871	20653	31449	172410	197481	305335	84948
A0A3Q1M3N4 A0A3Q1M3P 9 A0A3Q1MM65 A0A3Q1MN 4	9	503,18 162.79	0.31779	0,52071 0.52116	1,16445	0,1642 0.16371	LL	LL HL	43243	Unconventional myosin-Ic OS=Bos taurus OX=9913 GN=MYO1C PE=1 SV=1 60S ribosomal protein L4 OS=Bos taurus OX=9913 GN=RPL4 PE=1 SV=1	852127 273106	414242	325270	322778 578463	985405 1389707	767737 583095	1012381 335969	1181523 1243814	1047165 698080	283304 1490632	296186 269655	359860 382992	967473 1019701	1279058 687728	1111295 831350	265081 816913
A0A3Q1LUI41A0A3Q1LUI4 6	6	524.79	0.32167	.,	1.32174	0,16228	11	HL		Calcium-transporting ATPase OS=Bos taurus OX=9913 GN=ATP2B2 PE=3 S'	1816583	2649842	1647297	4855848	1736805	1827257	565354	2082049	1552601	5645133	3313724	4045983	1594532	1614218	1331404	1720929
G3N0Q81G3N0Q8 BOVIN 3	3	129.58	0.32379	.,	1.04023	0.16125	HI	LL		Azurocidin 1 OS=Bos taurus OX=9913 GN=AZU1 PF=1 SV=2	354	47892	5562	14299	7905	1410	321597	5313	0	96767	0	1727	49785	1567	10529	255942
A0A3Q1M588 A0A3Q1M58 2	2	113,11	0,32512	0,52698	1,46409	0,16061	HL	LL	15289	Histone domain-containing protein OS=Bos taurus OX=9913 PE=3 SV=1	234820	861385	199173	324296	624285	120927	4437917	448780	34070	249957	13605	271235	2110094	278126	552106	1235442
F1MFD9 F1MFD9_BOVIN;G 4	4	286,86	0,32629	0,52773	1,08321	0,16005	HL	LL	83898	Oxysterol-binding protein OS=Bos taurus OX=9913 GN=OSBPL10 PE=3 SV=	541593	332080	1082105	461549	774981	922942	772661	1057246	669208	96431	474106	369480	457419	1103624	1340495	289230
A0A452DJA8 A0A452DJA8_ 2	2	105,44	0,32827	0,52965	1,36612	0,1591	LL	HL	36450	Purine nucleoside phosphorylase OS=Bos taurus OX=9913 GN=PNP PE=4 S	84079	19604	59378	201749	42648	249896	82477	78759	81404	240332	423022	225019	31752	158813	64004	263891
A0A3Q1M643 A0A3Q1M64 2	2	92,71	0,33019	0,52965	1,41424	0,15819	LL	HL	33814	ELMO domain-containing protein 2 OS=Bos taurus OX=9913 GN=ELMOD2	157083	107342	443249	746952	180750	633550	183452	550768	142633	831273	114457	776473	165913	734743	380594	758566
M0QVY0 M0QVY0_BOVIN;I 4	2	296,97	0,33155	0,5297	1,42605	0,15755	HL	LL		IF rod domain-containing protein OS=Bos taurus OX=9913 GN=KRT6A PE=:	244853	31707	298069	285459	432738	79553	86104	753886	109863	161629	379957	709289	109307	90324	38546	206592
A0A3Q1LPS9 A0A3Q1LPS9_ 3	3	258,08	0,33376	0,5297	1,15919	0,15652	LL	HL	44594	Uncharacterized protein OS=Bos taurus OX=9913 GN=TMEM43 PE=1 SV=1	302607	367253	379725	887189	455246	460530	602790	633427	456102	469976	566037	590279	836357	380194	412207	1072325
A0A3Q1M9K4 A0A3Q1M9K 4	4	250,37	0,33378	0,5297	1,08512	0,15651	HL	LL	31145	Elongation factor 1-delta OS=Bos taurus OX=9913 GN=EEF1D PE=4 SV=1	287156	344821	307316	209184	801745	370983	345030	610244	223583	125408	96806	97883	611213	665479	898022	239867
A0A3Q1N7N1 A0A3Q1N7N 2	2	119,1	0,33455	0,5297	1,2147	0,15616	HL	LL	95782	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 OS=Bos taurus	54238	70504	170977	32453	132317	70909	49916	105613	76497	8831	35947	31410	83475	92159	141404	27541
E1BPI3 E1BPI3_BOVIN 3 A5PK13 LRC8C BOVIN 7	2	146,2 793.86	0,33832	0,53205	1,27273	0,15443	LL	HL HL	59243 92260	Tyrosine-protein kinase OS=Bos taurus OX=9913 GN=FRK PE=3 SV=2 Volume-regulated anion channel subunit LRRC8C OS=Bos taurus OX=9913	49932 8987201	39324 9242699	53936 8846242	12957 22096903	79120 9506391	3153 6728047	16285 11103416	40601 6137405	88160 11708237	15970 23509665	9088 18016076	26793 19868175	79429 9462428	44773 11013986	60561 5901637	30695 22266962
A0A301M2A1 A0A301M2/ 2	2	90.32	0.33886	-,	1,22007	0,15418	LL 111	LL	56759	Tissue specific transplantation antigen P35B OS=Bos taurus OX=9913 GN=1	107717	192241	103937	78530	209406	143426	90491	153759	11/08257	47791	60579	93874	126993	172230	108966	22200902
A60LG51RS9 BOVIN:A0A3C 2	2	169.6	0.34466	-,	1,58216	0.15158	11	HL	22578	40S ribosomal protein S9 OS=Bos taurus OX=9913 GN=RPS9 PF=2 SV=1	148083	70304	17820	21804	215527	38473	179315	425463	220387	131559	35407	30300	482865	321616	415206	50895
A0A3Q1LUU0 A0A3Q1LUU(2	2	98,95	0,34658		1,41469	0,15073	LL	HL	86592	Inositol polyphosphate-5-phosphatase B OS=Bos taurus OX=9913 GN=INPI	130455	126270	94920	145487	159894	91903	121505	122221	166794	261334	230036	242423	69980	56879	82594	187917
Q27965 HS71B_BOVIN;POC 13	9	691,23	0,34741	0,53762	1,16816	0,15037	HL	LL	70185	Heat shock 70 kDa protein 1B OS=Bos taurus OX=9913 GN=HSPA1B PE=2 5	1601916	1371376	1876003	700347	1352462	900125	694484	1401270	2111315	547440	718786	728155	848800	1638971	1607648	366297
F1MYX6 F1MYX6_BOVIN 2	2	110,06	0,35101	0,54095	1,14154	0,14881	HL	LL	57657	Solute carrier family 7 member 8 OS=Bos taurus OX=9913 GN=SLC7A8 PE=	288069	185696	386623	116293	139555	354301	216480	242889	239249	106337	274444	38919	163716	262407	197809	241010
F1MY82 F1MY82_BOVIN 4	4	415,35	0,35507	0,54479	1,15186	0,14707	HL	LL	77698	Protein kinase C eta type OS=Bos taurus OX=9913 GN=PRKCH PE=3 SV=1	1187404	1138957	1209542	564779	1303424	726763	1190745	773684	997500	188212	282704	543407	1838958	552035	1341301	498511
A0A3Q1M912 A0A3Q1M91 2	2	79,72	0,35857	0,54811	1,35093	0,1456	LL	HL	37274	Abhydrolase domain containing 5 OS=Bos taurus OX=9913 GN=ABHD5 PE=	128100	242204	219494	104783	279575	157602	207060	304114	200806	104231	429915	97314	389483	192900	307753	370415
Q3ZCA1 LRAT1_BOVIN 2	2	151,51	0,35967	0,54867	1,23573	0,14514	LL	HL	33106	Protein LRATD1 OS=Bos taurus OX=9913 GN=LRATD1 PE=2 SV=1	128786	116101	134176	15621	53979	31817	45734	181983	90602	110814	159608	29699	106025	99357	109579	19203
A0A3Q1MWA3 A0A3Q1MV 6	-	444,67	0,36267	0,54962	1,45737	0,1439	LL	HL	32281	Ras-related protein Rab-1B OS=Bos taurus OX=9913 GN=RAB1B PE=4 SV=1	2931030	1142091	2602037	1313001	1895323	1918133	3211462	2638486	1355772	1481812	2372936	1495974	3461535	4530849	4825124	3543662
A6H7F6 GLP3L_BOVIN 4	3	286,14	0,36529	0,54962	1,16133	0,14283	LL	HL	32794	Golgi phosphoprotein 3-like OS=Bos taurus OX=9913 GN=GOLPH3L PE=2 S	1565718	827981	981815	2244341	1477568	1774472	1292330	1639223	1246630	3554343	2534271	2342337	1477326	1184270	1114635	2655321
A0A3Q1LWT5 A0A3Q1LWT 9	/	425,37	0,36642	0,54962	1,23828	0,14237	HL	LL	80019 37706	Cyclin and CBS domain divalent metal cation transport mediator 3 OS=Bos	1077884	905895	689993	306999	856773	375802	1694754	1021932	773540	394756	406272	240401	1483226	794868	1090788	227939
Q1RMU4 ERLN2_BOVIN;A0 2 Q148L0 Q148L0 BOVIN 2	2	103,59 83,94	0,36907	0,54962	1,52586	0,1413	HL	LL	37706 23492	Erlin-2 OS=Bos taurus OX=9913 GN=ERLIN2 PE=2 SV=1 Charged multivesicular body protein 6 OS=Bos taurus OX=9913 GN=CHMP	511341 431935	511856 374567	415864 529266	164387 247420	256060 398233	559721 352738	516709 425226	358533 442378	340478 246810	45373 101464	72730 111393	127516 324312	540899 326741	266587 420075	305099 608304	131176 87601
F1N334 F1N334 BOVIN:07 4	4	368.24	0.37274	0,54962	1,19885	0,13985	HI	LL	33509	Short-chain dehydrogenase/reductase 3 OS=Bos taurus OX=9913 GN=DHR	7355212	3304955	3081445	1083571	2769045	864777	6336392	442378	2781260	101464	1297842	762488	4351180	6762955	4374762	865542
Q08E421Q08E42 BOVIN 7	7	433.88	0.37286	0.54962	1,08057	0.1398	11	HL	93951	Leucine rich repeat containing 8 VRAC subunit A OS=Bos taurus OX=9913 (3101283	2694355	1721895	2310617	3831847	2194458	4104028	2521656	3653899	3292744	4116490	3263449	3880344	2597524	2681827	1923321
A0A301LPY41A0A301LPY4 2	2	123.36	0.37473	-,	1.12847	0.13906	HL	LL	43940	Poly(rC) binding protein 2 OS=Bos taurus OX=9913 GN=PCBP2 PE=1 SV=1	343792	217411	373015	405435	465414	392060	355272	594113	290779	274531	281000	342514	598298	314106	389780	368287
A0A3Q1NEH7 A0A3Q1NEH 4	4	264,37	0,3753	0,54962	1,14409	0,13884	HL	LL	157137	Capping protein regulator and myosin 1 linker 1 OS=Bos taurus OX=9913 G	48775	240458	138913	955907	568197	78529	67071	446320	358415	317582	356820	419463	308297	179420	355975	211627
F1MNY2 F1MNY2_BOVIN 7	7	468,47	0,37674	0,54962	1,35831	0,13828	HL	LL		Cell migration inducing hyaluronidase 2 OS=Bos taurus OX=9913 GN=CEM	643306	591511	582491	399490	406151	410708	202037	759960	859364	288301	169261	160131	329667	532595	705832	76687
Q1LZA3 ASNS_BOVIN 5	5	331,93	0,37709	0,54962	1,16147	0,13815	HL	LL	64179	Asparagine synthetase [glutamine-hydrolyzing] OS=Bos taurus OX=9913 GI	705043	882389	975750	274863	1415487	622329	1033421	1306495	1013541	421775	436088	308480	1687107	876696	1080508	289137
Q2KI18 PLPL2_BOVIN 6	6	242,84	0,37921	0,55012	1,47236	0,13733	HL	LL	53382	Patatin-like phospholipase domain-containing protein 2 OS=Bos taurus OX	3011037	3532769	2395467	352697	1050195	1701234	3545251	758703	1300822	1032894	606766	494695	1940568	1339258	2147901	898017
A0A3Q1LUA9 A0A3Q1LUA9 2	2	92,68	0,37963	0,55012	1,20167	0,13717	LL	HL	48404	Target of myb1 like 1 membrane trafficking protein OS=Bos taurus OX=99:	706070	811580	315890	744687	640185	229595	613206	455717	702051	730733	564971	903577	497355	141230	491358	728364
A0A3Q1M757 A0A3Q1M75 3	3	178,52	0,38218	.,	1,15165	0,1362	HL	LL	41170	Mitogen-activated protein kinase OS=Bos taurus OX=9913 GN=MAPK13 PI	968187	811913	914154	341797	653854	559780	975546	799397	642834	369556	346212	531476	907742	651523	1025929	269151
A0A3Q1LXL9 A0A3Q1LXL9_ 3	3	154,98	0,38652	0,55795	1,29493	0,13456	HL	LL	86546	Transmembrane protein 63A OS=Bos taurus OX=9913 GN=TMEM63A PE=4	168836	237737	423525	79887	290365	364817	392753	339155	225401	18080	87628	166591	209320	319333	439292	125713
A7Z024 A7Z024_BOVIN;Q5: 6	6	290,8	0,3875	.,	1,17566	0,1342	HL	LL	39434	Protein XRP2 OS=Bos taurus OX=9913 GN=RP2 PE=2 SV=1	2662179	3048154	4611882	1183261	3242550	3285045	3077082	4232105	1996615	812435	1700868	1250684	3147671	3834301	4998354	1413434
A6H704 A6H704_BOVIN 4	4	245,01	0,3925	.,	1,25062	0,13236	LL	HL	50613 83993	CHMP7 protein OS=Bos taurus OX=9913 GN=CHMP7 PE=2 SV=1	597289	1153600	488726	206140	512983	481807	1058043	766405	1289409	740534	1291862	697627	1080154	658528 647946	536603 788429	158810
A0A3Q1MDC6 A0A3Q1MDI 3 A0A3Q1LUG5 A0A3Q1LUG5 4	3	135,09 207.01	0,3926	-,	1,19471	0,13232	11	HL		Nicastrin OS=Bos taurus OX=9913 GN=NCSTN PE=1 SV=1 Sorting nexin OS=Bos taurus OX=9913 GN=SNX9 PE=3 SV=1	710934 430682	608373 581075	927554 442893	1397805 1077067	405069 622040	590173 528809	1259397 411839	401980 597469	546273 609460	955878 1716090	1746305 821430	2561913 890746	729400 436537	333892	355836	303636 1059981
A0A3Q1L003 A0A3Q1L003 4 A0A3Q1LR68 A0A3Q1LR68 2	2	72.32	0.39703	.,	1,54945	0.13073		LL		E3 ubiguitin-protein ligase OS=Bos taurus OX=9913 GN=ITCH PE=4 SV=1	84157	122723	153392	41918	87873	164027	169614	87833	80413	11499	38493	35507	140696	72268	99003	9456
P61284/RL12 BOVIN:G3MZ 3	3	142.05	0.39706		1,71759	0.13072	11	HL	17808	60S ribosomal protein L12 OS=Bos taurus OX=9913 GN=RPL12 PE=2 SV=1	34137	32202	14828	26652	98506	49991	136175	265041	79042	188338	4270	20269	265529	144798	230972	250696
A0A3Q1MLH4 A0A3Q1MLH 3	3	187,54	0,39856		1,59522	0,13018	LL	HL	34500	Very-long-chain 3-oxoacyl-CoA reductase OS=Bos taurus OX=9913 GN=HS	71265	98971	69154	26318	253948	99432	352028	283615	151730	57325	97226	35109	610499	293118	397010	258034
A0A3Q1M280 A0A3Q1M28 3	3	174,56	0,39893	0,56137	1,16476	0,13005	LL	HL	24452	Ubiquitin domain-containing protein 1 OS=Bos taurus OX=9913 GN=UBTD:	1208316	794827	480485	129138	521642	423591	1129702	975505	828027	272306	846262	540525	1301811	776017	1003845	202912
Q3MHE8 SRPRA_BOVIN 3	3	119,3	0,39934	0,56137	1,08606	0,1299	HL	LL	69852	Signal recognition particle receptor subunit alpha OS=Bos taurus OX=9913	878980	859229	687500	107658	926286	534638	645249	857997	1277436	227777	195688	170633	1028977	914551	895834	125633
A0A452DIB1 A0A452DIB1_I 8	8	648,18	0,40101	0,56248	1,26461	0,12931	LL	HL	25952	Ras-related protein Rab-18 OS=Bos taurus OX=9913 GN=RAB18 PE=4 SV=1	86889952	41644239	55294414	37893521	51988411	52538875	82784605	70450944	60094696	33160127	48793998	44029210	98665403	107225748	118876544	42672066
A7MBH9 A7MBH9_BOVIN 6	4	597,99	0,40246	0,5625	1,0174	0,1288	LL	HL	40451	G protein subunit alpha i2 OS=Bos taurus OX=9913 GN=GNAI2 PE=2 SV=1	2610103	1561623	2278230	3871594	4039050	2657625	2447274	2949237	4022541	6783303	4129759	4466256	4106389	2016788	2731777	4668808
A0A3Q1LVE7 A0A3Q1LVE7 3	3	155,52	0,40388	0,5625	1,05407	0,12831	HL	LL	69572	Polyadenylate-binding protein OS=Bos taurus OX=9913 GN=PABPC1 PE=1	14624	23819	51213	35007	182128	23627	2224	157358	39049	91722	0	5379	111105	105809	146361	15632
A0A3Q1LQ02 A0A3Q1LQ02 2 A0A3Q1M994 A0A3Q1M99 2	2	86,51 106.54	0,40802	0,56513 0.56979	1,14221 1.20927	0,12688 0.12497	HL HL	LL	53627 59498	Vitamin D-binding protein OS=Bos taurus OX=9913 GN=GC PE=4 SV=1 Polypyrimidine tract-binding protein 1 OS=Bos taurus OX=9913 GN=PTBP1	193888 12873	61756 85483	76868 26997	154352 8471	115559 144844	106845 102093	35442 109196	188439 169919	88795 108385	148108 52783	143711 10880	216517 4138	12598 139534	39253 35264	79076 161562	33565 18262
A0A3Q1M994 A0A3Q1M99 2 A0A3Q1LQD0 A0A3Q1LQD(2	2	106,54	0,41366	0,56979	1,20927	0,12497	LL	HL	59498 29363	40S ribosomal protein S4 OS=Bos taurus OX=9913 GN=PTBP1	128/3	85483 91205	26997	8471 37530	144844 189149	102093 8970	227469	260678	108385	35424	10880	4138 23011	139534 394443	35264 20525	400968	18262
A0A301M200 A0A301M2(2	2	108.23	0.42103	0.57186	1.08159	0.12253	н	LL	48881	E-box/LRR-repeat protein 20 OS=Bos taurus OX=9913 GN=FBXI 20 PE=4 SV	692766	603649	614787	171952	481754	650119	733836	365601	379850	177311	155480	149428	822700	760801	772149	271052
Q0P5A6 PSMD5_BOVIN 2	2	115,76	0,42277	0,57186	1,05441	0,12197	HL	LL	56007	26S proteasome non-ATPase regulatory subunit 5 OS=Bos taurus OX=9913	18844	77801	66359	8457	160446	50034	43606	123992	80773	41071	18684	2635	3653	132031	131087	9070
A0A3Q1LV44 A0A3Q1LV44 3	2	243,02	0,4258	0,57282	1,18094	0,12099	LL	HL	56274	Aldehyde dehydrogenase OS=Bos taurus OX=9913 GN=ALDH3A2 PE=1 SV=	140353	163984	57028	44422	266463	188110	185744	323442	181127	75240	325693	173148	390086	99861	214723	96305
A0A3Q1MIK4 A0A3Q1MIK4 2	2	220,35	0,42634	0,57282	1,0572	0,12082	HL	LL	32129	Phospholipid phosphatase 1 OS=Bos taurus OX=9913 GN=PLPP1 PE=4 SV=	584146	324914	1141752	308658	499778	509295	672983	794543	608335	72522	238545	148140	709589	819171	1058023	338910
A0A452DII8 A0A452DII8_B(7	7	578,2	0,42787	0,57282	1,18962	0,12033	LL	HL		ATP synthase subunit beta OS=Bos taurus OX=9913 GN=ATP5F1B PE=3 SV:	428718	985397	744464	1002386	3306460	524057	1514109	2758033	915406	832516	540749	1381678	3390757	1809383	3137438	1610202
A0A3S5ZPX3 A0A3S5ZPX3_I 3	2	313,12	0,42881		1,27312	0,12004	HL	LL		Mitogen-activated protein kinase kinase 2 OS=Bos taurus OX=9913 GN=M.	1340658	1646129	2746069	662909	718161	3112468	2596888	568109	873793	640855	3281537	744503	1899490	3408710	692228	938980
A7MB32 A7MB32_BOVIN 3		250,21		0,57282		0,11989	HL	LL		Non-specific serine/threonine protein kinase OS=Bos taurus OX=9913 GN=	344610	497765	658496	549027	398430	290815	398337	403362	451384	650063	228354	568658	371401	254147	437143	231369
A0A3Q1M4K3 A0A3Q1M4K 5	5	369,73	., .		1,05476	.,	HL	LL	8629	Ubiquitin-like domain-containing protein OS=Bos taurus OX=9913 GN=LOC	32063131	25420589	38960640	14941353	26841077	23084397	29532599	27352362	31394633	5122200	22610205	14672450	33838597	39439830	40000537	13591545
Q0VD16 Q0VD16_BOVIN 4 A0A3Q1MFG3 A0A3Q1MFG 3	-	366,68 258.11	0,43122		· · ·	0,11928	HL	LL HL		MAP2K1 protein OS=Bos taurus OX=9913 GN=MAP2K1 PE=2 SV=2	216322	417698 163294	859034 119487	265268 134956	763784	405863 137331	264121 160176	456611 628860	351107 241397	140052	116578 180576	244224 86011	333306 374046	570272 202551	889421	91068 321559
A0A3Q1MFG3 A0A3Q1MFC 3 A0A3Q1NDH3 A0A3Q1NDH 2	3	258,11 84,88	0,43152 0,4346		· · ·	0,11918 0,11823	HL	LL		40S ribosomal protein SA OS=Bos taurus OX=9913 GN=RPSA PE=1 SV=1 Endophilin-B1 OS=Bos taurus OX=9913 GN=SH3GLB1 PE=4 SV=1	123439 35428	163294 16871	119487 285946	134956 11726	247196 70659	137331 30375	160176 93528	628860 58277	241397 11365	294522 321	180576 20772	86011 8932	374046 51866	202551 17177	219380 137605	321559 14392
A0A3Q1NDH3 A0A3Q1NDH 2 A0A3Q1LSW8 A0A3Q1LSW; 4		84,88 139,5	0,4346	0,57282		0,11823	HL	LL		Serine/threonine-protein kinase N1 OS=Bos taurus OX=9913 GN=SH3GLB1 PE=4 SV=1	51332	87194	285946 84417	55309	313068	140825	62616	213707	248868	104754	48477	111478	232393	60697	137605	14392
G3MXZ0 G3MXZ0 BOVIN 4		303.52	0,436		· · · ·	0,11779	HL	LL		Lactoperoxidase OS=Bos taurus OX=9913 GN=LPO PE=1 SV=2	799751	751902	777468	1245440	1427445	794097	2389125	1828835	248868 830184	3851284	48477 1888942	1356978	1206807	703902	439768	2094564
A0A3Q1LVE3 A0A3Q1LVE3 2		202,14	-,	0,57282			LL	HL		Leukocyte surface antigen CD47 OS=Bos taurus OX=9913 GN=CD47 PE=4 5	4126832	5466289	6775698	9060640	2162107	2104076	4527530	2577275	4359214	6120957	7682398	8812877	3431524	3523605	2725248	5820995
077834 PRDX6_BOVIN;A0A 4		320,08		0,57282			LL	HL		Peroxiredoxin-6 OS=Bos taurus OX=9913 GN=PRDX6 PE=1 SV=3	387499	156460	291026	162015	149295	164945	219399	413213	199078	196798	84367	126803	372170	377796	574512	513839
A0A3Q1M909 A0A3Q1M90 2		118,93	0,44068	0,57282	1,2682	0,11637	LL	HL		Mitochondrial peptide methionine sulfoxide reductase OS=Bos taurus OX=	167940	7441	74223	101721	50547	30752	77976	101326	13105	53966	86016	60269	72992	122171	191262	135905
A0A3Q1M483 A0A3Q1M48 57	57	3913,65				0,11597	HL	LL	259248	Acetyl-CoA carboxylase 1 OS=Bos taurus OX=9913 GN=ACACA PE=4 SV=1	20454389	39590692	22588704	8165981	48701261	51716730	26388899	23409615	22234935	34940222	21825629	8468522	32663474	28016578	21805362	6691112
Q3ZCK1 EIF3L_BOVIN 2	2	80,54	0,44307			0,11565	HL	LL		Eukaryotic translation initiation factor 3 subunit L OS=Bos taurus OX=9913	3583	29838	45502	6051	46092	23496	9439	63591	36927	5201	2513	9910	25847	45610	40644	8079
F1MXJ5 F1MXJ5_BOVIN 2		97,5	0,44401	.,	,	0,11537	HL	LL		IST1 homolog OS=Bos taurus OX=9913 GN=IST1 PE=4 SV=3	9061	89826	16800	62329	13766	69434	0	28669	40066	38111	31367	4534	13142	107193	10643	23873
A0A3Q1LJM0 A0A3Q1LJM0 14		839,09	0,44546			0,11494	LL	HL		Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC100848700 PE=	1563686	1995186	964482	75236	1056287	1847226	347025	1154033	2471067	1441159	1210484	203920	1534192	2252619	1431337	231406
F1MMV6 F1MMV6_BOVIN; 3	-	142,28	0,44642			0,11465	HL	LL		Calcium binding protein 39 like OS=Bos taurus OX=9913 GN=CAB39L PE=4	136921	122863	121081	16255	115579	61388	117121	140550	58785	39821	53425	35202	148196	97816	156874	58113
P05631 ATPG_BOVIN 2 A0A301M6Y5 A0A301M6Y 6	2	92,35	0,4474 0.44874		1,80164 1.06019	0,11436 0.11397	LL HL	HL		ATP synthase subunit gamma, mitochondrial OS=Bos taurus OX=9913 GN=	4946 8565907	8321 5069006	19534	1675	70365	16472	60313	76250	19113	1582	3584	7600 3883009	156855	80128 11139010	143411 8240092	28091 4199868
A0A3Q1M6Y5 A0A3Q1M6Y 6 A0A3Q1N6D1 A0A3Q1N6D: 5		335,5 294,5	0,44874			0,11397 0,11329	HL	LL		Guanine nucleotide-binding protein G(o) subunit alpha OS=Bos taurus OX= Macrophage-capping protein OS=Bos taurus OX=9913 GN=CAPG PE=1 SV=	215195	217069	7276419 206219	4364126 192291	5880222 644624	3769010 318870	8352418 233987	7049364 511108	6492314 285343	1377770 87724	3977906 65095	160247	7790202 402490	276548	555740	4199868 104457
Q2KIS4 Q2KIS4_BOVIN;A0A 7		443,54					HL	LL		Dehydrogenase/reductase (SDR family) member 1 OS=Bos taurus OX=9913	4002119	1061026	2369728	3314348	4137221	5111220	4974180	5967995	4334056	6839259	3730257	4531327	2643759	7727021	6964703	6354844
			2,4323	-,	_,,	-,0,				,										3233						

Q08D86 GLPK5_BOVIN 3	3	109,3	.,		663 0,11284			727 Putative glycerol kinase 5 OS=Bos taurus OX=9913 GN=GK5 PE=2 SV=1 727 Terretoria 262 OS Destaurus OX 0012 CN TM/M262 DF	885881 4365100	813651 2776695	573714 2439239	1714239	1051665	1831005	1248348 4822262	1552208 2858689	1033541	2369053	1658108	1727776 2196388	892988 4163800	424095 5083917	1248130 4118984	1839194 1810357
A0A3Q1M8R8 A0A3Q1M8F 5	5	372,78	-,	.,	558 0,11273	LL		754 Transmembrane protein 263 OS=Bos taurus OX=9913 GN=TMEM263 PE= C22 Construction of the protein of the construction of t				1699710	1684194	2387345			3065403	2881585	2961243					
A0A3Q1MSN7 A0A3Q1MSN 2 G3N2S4 G3N2S4 BOVIN 4	2	93,82 235.87		0,57282 1,06 0.57282 1.18		LL	HL 65	636 Coenzyme A synthase OS=Bos taurus OX=9913 GN=COASY PE=3 SV=1	21913	75814 174593	38538 137979	18784 203269	147496 598702	52472 432356	44116 542942	108370 522597	91278 149805	92964 203084	50495 36228	53711 332823	124427 603233	39965 157288	51381 317048	91176 411297
Q76LV21HS90A BOVIN:A0A 13		235,87	.,	0,57282 1,18 0.57282 1.13				398 Leucine rich repeat containing 26 OS=Bos taurus OX=9913 GN=LRRC26 PE 678 Heat shock protein HSP 90-alpha OS=Bos taurus OX=9913 GN=HSP90AA1	1937635	1722759	2072921	739589	3109930	432356	1658066	4094833	2977991	203084	1385644	630653	3747236	2343857	3023382	411297
F1MGK8 F1MGK8_BOVIN 2	2	1003,46	.,),57282 1,13),57282 1,27		LL		678 Heat shock protein HSP 90-alpha OS=Bos taurus OX=9913 GN=HSP90AA1 140 Oncostatin M receptor OS=Bos taurus OX=9913 GN=OSMR PE=4 SV=3	1937635	283606	238046	165856	201750	51483	207227	160098	168637	271266	299063	298064	238344	2343857 31847	227994	316985
P68138 ACTS BOVIN; G8JKX 12		1005,34		0.57282 1.08				Actin, alpha skeletal muscle OS=Bos taurus OX=9913 GN=ACTA1 PE=1 SV=	13544638	18355798	8733833	14172765	18661697	22708149	17045928	19785706	13167254	20504513	22083120	18712412	10109555	10950581		14260464
A0A3O1NJ45 A0A3O1NJ45 2	2 3	137.42	.,	0.57282 1.08	,			Palmitoyltransferase OS=Bos taurus OX=9913 GN=ZDHHC20 PE=3 SV=1	551885	309176	355325	321219	155605	206603	339736	345997	389484	56216	140563	310469	133885	470197	333620	339469
A0A3Q1M343[A0A3Q1M343] 2 A0A3Q1MS82[A0A3Q1MS8 5	2	467.76	-,),57282 1,2	,			Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit 2	526441	986431	290805	1227796	1062458	924048	956911	1581004	1243013	2543871	1183404	1083130	1623092	432264	633551	1434047
A3KN51 A3KN51 BOVIN 3	3	204.55	.,			11	HL 44	TSG101 protein OS=Bos taurus OX=9913 GN=TSG101 PF=2 SV=1	656273	418514	136968	179476	341710	316171	634837	353776	385279	510092	382486	407463	462706	303094	238658	299903
A3KN51 A3KN51 BOVIN 3 A0A452DIW1 A0A452DIW1 3		204,55	.,	0,57282 1,03 0.57282 1.32	,	LL	HL 44 HL 34	517 60S ribosomal protein L10 OS=Bos taurus OX=9913 GN=15G101 PE=2 SV=1	274831	215779	271668	173178	460338	185417	398478	768417	385279	303035	382486 144108	407463	462706 896783	303094 606945	238658	685518
	3		.,	0,57282 1,32 0.57282 1.07		HL															26400686	18034936		10688852
	2 12	1008,21	.,					8F	24156575	18731553	20683868	9702983	13178444	15738149	23520110	20193277	13428170	5699257	12742010	9841077			29829476	
A0A3Q1M656 A0A3Q1M65 2	2	98,88	.,	0,57282 1,08 0.57282 1.31	,	LL		40S ribosomal protein S2 OS=Bos taurus OX=9913 GN=RPS2 PE=3 SV=1 Tetratricopeptide repeat domain 39C OS=Bos taurus OX=9913 GN=TTC39	66272	64431	51362	19798	168852	30718	85331	242330	101640	178548	62056	39129	193035	125812	191307	289971
F1N480 F1N480_BOVIN 2 A0A140T856 A0A140T856 8	2	57,32 474.54	-,	-,,		HL		837 Tetratricopeptide repeat domain 39C OS=Bos taurus OX=9913 GN=TTC39 8257 Coatomer subunit alpha OS=Bos taurus OX=9913 GN=COPA PE=4 SV=1	6828 109388	20401 141755	84733 86453	16547 122843	79683 569718	15671 137057	13475 125764	73253 615257	52552 620108	3217 451255	2917 381540	19580 191345	32961 383507	17083 128308	84217 261083	3713 157587
Q6EWQ71IF5A1 BOVIN:F1N 2	2	474,34	., .),57282 1,16).57282 1.30		LL		Eukarvotic translation initiation factor 5A-1 OS=Bos taurus OX=9913 GN=	2037412	1684866	1481287	928981	2187940	1668968	1778909	2361375	1927061	1149145	792417	776689	3052732	3562657	3758783	1520208
0170701017070 BOVIN;FIN 2	2	1/5,18	-,	0,57282 1,30 0.57609 1.04			LL 64	244 Non-specific serine/threonine protein kinase OS=Bos taurus OX=9913 GN=		540243	644082	253066	446464	734355	767010	567182	535008	36894	136196	333370	708649	701997	1306522	172270
F6R0H3 F6R0H3 BOVIN 4	3	194.09	-,	0,57609 1,04 0.57609 1.36			LL 68			247073	128278	154547	390088	140678	97902	310519	87839	142066	40968	145516	127410	171756	277698	31115
	4		.,		,	HL		692 Syntaxin-binding protein 1 OS=Bos taurus OX=9913 GN=STXBP1 PE=3 SV= 919 26S proteasome non-ATPase regulatory subunit 3 OS=Bos taurus OX=991														133036		343803
Q2KJ46 PSMD3_BOVIN 4 A8E4P3 A8E4P3 BOVIN:F1! 9	9	236,99 812,36	.,	0,57761 1,11 0.57797 1.20				265 proteasome non-Arrase regulatory subunit 5 05-805 taulos 0A-991 268 STOM protein OS=Bos taurus OX=9913 GN=STOM PE=1 SV=1	113075 60373522	156298 91349651	80040 45803924	280821 43134514	511390 39847355	160373 25209749	267055 144435301	791264 93181780	364975 19864629	298997 81614509	286559 30327742	222471 31838312	419829 67066620	56668220	435775 98576100	69267585
A5PJM41AIFM2 BOVIN;A0A 2	2	155.65	.,	0.58184 1.11	,	н		451 Apoptosis-inducing factor 2 OS=Bos taurus OX=9913 GN=AIFM2 PE=2 SV=	140791	313468	202998	75011	271145	64003	225860	177576	128856	4932	11869	83330	204921	149209	491355	100302
OS8DW6IRAB25 BOVIN, ADA 2	5	303.63	-,),58227 1.05		HI		522 Ras-related protein Rab-25 OS=Bos taurus OX=9913 GN=RAB25 PE=2 SV=		1783318	3110348	1868010	2112387	1669386	4357330	3551078	120030	836751	1237432	2080896	4922255	3521649	5000819	2100148
A0A301LMX01A0A301LMX 13	-	1031.05),58227 1,05).59134 1.16		HL	LL 31	 NADH-cytochrome b5 reductase OS=Bos taurus OX=9913 GN=(NB25 FE=2 SV= 		22467884	24836033	12809855	15500960	20073457	44437268	18138008	22849867	9369769	15504552	12491978	29385753	21111300	32602674	12730610
A0A140T886 A0A140T886 5	5 5	198.42	.,	0.59186 1.15	507 0.00097	- 12 - 11	LL 97	337 Coatomer subunit gamma OS=Bos taurus OX=9913 GN=COPG1 PE=3 SV=		41491	66704	87039	294607	53841	36794	263784	160704	63856	76644	100806	66541	127465	155327	25560
Q3T0D7 SAR1A BOVIN 7	3	504.39	-,),59186 1,15).59186 1.32	939 0.09986	LL	HL 22	395 GTP-binding protein SAR1a OS=Bos taurus OX=9913 GN=Cor G1 PE=5 SV= 395 GTP-binding protein SAR1a OS=Bos taurus OX=9913 GN=SAR1A PE=2 SV=	6168849	3370327	5310904	805108	2583967	1740227	7634330	4739220	4901527	2012760	1896708	1508192	7998505	9629022	8519503	2941069
A0A301ML891A0A301ML8 16		1057.09	-,	0.59186 1.04		11	HL 13	Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC100299180 PE	1531101	2346252	1064929	1373230	2252867	3462122	349561	958416	1177477	2324857	1421763	1063437	2569770	3413401	1223265	800798
A0A301LMS51A0A301LMS! 13		1094.99	-,	0.59206 1.04	,	HI	LL 71	720 Heat shock cognate 71 kDa protein OS=Bos taurus OX=9913 GN=HSPA8 P		11078066	11955207	6117322	14415107	6326820	11445384	12064999	17909468	3651884	4215081	10563883	14311828	14816749	12424865	3998545
A0A140T8881A0A140T888 3	3	150.06	-,	0.59206 1.33		11		129 Phosphatidylinositol 4-kinase alpha OS=Bos taurus OX=9913 GN=PI4KA PE		45241	103300	81442	179310	61323	185851	161970	175769	129863	359770	203565	144380	31431	44482	264051
F6PXR51F6PXR5_BOVIN 7	7	450.19	.,	0.59295 1.10	,			Toll like receptor 5 OS=Bos taurus OX=9913 GN=TLR5 PE=3 SV=1	656318	385818	1274207	427366	857929	349742	440053	1433580	706510	313342	684928	336954	661733	754843	1552446	112707
0170E5 CIB1 BOVIN:A0A3 5	5	291.96	-,	0.59301 1.11		LL	HL 21	715 Calcium and integrin-binding protein 1 OS=Bos taurus OX=9913 GN=CIB1	265167	183733	417259	428224	248885	354553	631412	571397	297206	666838	143540	478809	422136	499323	790716	1026173
A0A3Q1MF86 A0A3Q1MF8 2	2	96,1	-,	0,5944 1,15	,			429 Actin related protein 1A OS=Bos taurus OX=9913 GN=ACTR1A PE=1 SV=1	191938	107710	232921	252069	452020	135794	183952	262743	308385	249434	165431	108231	173004	120645	224291	213771
Q3ZC84 CNDP2_BOVIN;A0/ 6	6	258,27		0,5944 1,04		LL		622 Cytosolic non-specific dipeptidase OS=Bos taurus OX=9913 GN=CNDP2 PE	1282737	894065	806696	481506	2155611	685300	1067291	1620978	956320	1397613	821232	751984	1272702	855639	1746161	824225
F1MX65 F1MX65 BOVIN 2	2	134,64		0.59537 1.13		HL		218 Protein OS-9 OS=Bos taurus OX=9913 GN=OS9 PE=4 SV=2	45008	67773	58630	11090	151594	5891	39569	218347	90686	13223	6389	18021	166857	108513	143356	5305
Q3SWY3 IMDH2 BOVIN 2	2	120,64	0,51635 0	0,59537 1,33	092 0,09644			728 Inosine-5'-monophosphate dehydrogenase 2 OS=Bos taurus OX=9913 GN	76659	164622	31652	38016	639270	10468	81030	796480	276784	40862	6508	11796	574528	237172	219263	4392
A0A3Q1LRW8 A0A3Q1LRW 4	3	234,59	0,51671 0	0,59537 1,48	841 0,09636	HL	LL 49	60S ribosomal protein L3 OS=Bos taurus OX=9913 GN=RPL3 PE=1 SV=1	33139	257138	130663	54578	779114	273887	59626	724769	336010	15209	59783	29794	301483	339901	636034	194924
Q6QRN7 Q6QRN7 BOVIN 2	2	207,5	0,51975	0,5956 1,30	879 0,09567	LL	HL 33	926 PP1201 protein OS=Bos taurus OX=9913 GN=TMBIM1 PE=2 SV=1	3370472	3089234	5843183	6582117	3440695	4106714	3422831	3065683	3264034	4091763	10676616	5215582	2099299	4647436	2161232	5113864
A0A3Q1MJY5 A0A3Q1MJY5 2	2	126,39	0,52015	0,5956 1,24	572 0,09558	HL	LL 45	486 Arrestin domain containing 1 OS=Bos taurus OX=9913 GN=ARRDC1 PE=4	280237	244679	357735	85660	267558	317503	409323	189169	206970	80911	94129	108331	273063	391600	301144	61788
A0A3Q1LM10 A0A3Q1LM1 2	2	111,72	0,52031	0,5956 1,05	693 0,09554	LL	HL 77	D68 Erythrocyte membrane protein band 4.1 like 4A OS=Bos taurus OX=9913	27676	29560	93351	24527	39395	56816	13149	29033	6631	3299	95426	67610	21765	92212	46755	23792
A0A3Q1MB98 A0A3Q1MB9 2	2	83,55	0,52172 0	0,59632 1,34	309 0,09523	HL	LL 43	744 Haptoglobin OS=Bos taurus OX=9913 GN=HP PE=3 SV=1	20091	285530	0	22740	83954	2843	743480	3290	0	144280	0	3744	88792	0	10667	718876
Q3T165 PHB BOVIN 2	2	83,8	0,53246 0	0,60674 1,43	319 0,09287	LL	HL 29	786 Prohibitin OS=Bos taurus OX=9913 GN=PHB PE=2 SV=1	11874	20584	1839	0	66227	17803	106700	118644	10659	4938	1886	9056	194518	47652	180651	77754
E1BEI2 E1BEI2 BOVIN 2	2	91,7	0,53436 0	0,60799 1,29	346 0,09246	HL	LL 24	872 Signal peptidase complex subunit 2 OS=Bos taurus OX=9913 GN=SPCS2 PI	135671	159671	117867	15647	39631	325063	0	143388	131922	907	53421	16593	3589	223570	163739	37337
F1MLD7 F1MLD7_BOVIN 3	3	139,07	0,54325 0	0,61275 1,15	676 0,09059	HL	LL 92	780 Uncharacterized protein OS=Bos taurus OX=9913 GN=EFR3A PE=4 SV=3	178347	118961	295706	257086	357917	174148	268779	405775	332612	281574	490639	568182	216912	103423	157656	199377
A0A3Q1M0I1 A0A3Q1M0I1 9	2	509,75	0,54853 0	0,61341 1,08	262 0,08951	HL	LL 13	669 Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC523126 PE=4 S	1065745	1477946	646204	196696	1989193	1739839	407895	620399	855817	191091	227373	221424	2969060	1651339	748959	103564
Q9TT94 ACOD_BOVIN 6	6	586,17	0,54863 0	0,61341 1,28	501 0,08949	LL	HL 41	678 Acyl-CoA desaturase OS=Bos taurus OX=9913 GN=SCD PE=2 SV=2	3630632	2946491	5747437	1492075	5180964	3113087	4626246	7881150	4043073	1727600	2442522	2836704	8153637	8443483	8810477	2158846
Q29455 DNJC5_BOVIN 3	2	335,38	0,54932 0	0,61341 1,10	0,08935	LL	HL 22	118 DnaJ homolog subfamily C member 5 OS=Bos taurus OX=9913 GN=DNAJ	1308176	984098	832374	367905	858664	1291355	1474264	972871	681640	58893	431983	329303	1742903	1889869	2496823	483664
A0A3Q1LYA8 A0A3Q1LYA8 3	3	258,97	0,55361 0	0,61577 1,33	612 0,08849	LL	HL 47	844 Oxysterol-binding protein OS=Bos taurus OX=9913 PE=3 SV=1	2201329	2714295	2773410	2002752	3894743	4953606	3081049	2639453	1939456	7800893	8487524	3852569	2708286	783261	2423449	4186404
A0A3Q1M3K3 A0A3Q1M3K 2	2	142,16	0,55646 0	0,61577 1,09	348 0,08792	LL	HL 52	225 Mothers against decapentaplegic homolog OS=Bos taurus OX=9913 GN=S	340383	505609	684289	1028252	415659	172371	443834	334296	513613	297640	713664	1057811	600635	260854	668248	371562
A0A3Q1M633 A0A3Q1M63 4	3	255,8	0,55648 0	0,61577 1,10	562 0,08792	LL	HL 65	604 Mucin-1 OS=Bos taurus OX=9913 GN=MUC1 PE=4 SV=1	32937354	12212498	12342770	10262314	36385894	29800963	15946485	13838021	8006172	16694669	30610284	14781640	54134426	16145773	31338311	16658913
A0A3Q1LUA4 A0A3Q1LUA4 3	3	199,63	0,55729 0	0,61577 1,22	262 0,08776	LL	HL 51	074 Proteasome 26S subunit, ATPase 1 OS=Bos taurus OX=9913 GN=PSMC1 P	59095	89539	54810	61317	124732	107824	160777	234246	154404	198816	247658	107550	216988	14011	156556	146183
E1BPW1 E1BPW1_BOVIN 5	5	511,94	0,55758 0	0,61577 1,02	408 0,0877	HL	LL 89	082 Oxysterol-binding protein OS=Bos taurus OX=9913 GN=OSBP PE=3 SV=3	1646903	2377610	2174433	658696	2271451	993770	2314284	2038215	2124947	270630	1177295	761870	3048370	2170336	2951380	560370
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A0A3Q1LPN6 A0A3Q1LPN6 3	3	234,03	0,0000000000	0,61806 1,02		LL	HL 43	404 26S proteasome regulatory subunit 8 OS=Bos taurus OX=9913 GN=PSMC	18156	67535	49881	43	191671	95938	12560	208420	137921	89870	60778	13177	98196	104504	99262	53798
A0A3Q1NHB5 A0A3Q1NHB 2	2	129,59	- ,	0,61806 1,22				262 Phosphomannomutase OS=Bos taurus OX=9913 GN=LOC782057 PE=3 SV		1029517	535552	258840	721975	872045	761289	494787	521161	183042	246167	297012	733106	876485	840218	263016
A0A3Q1LMB7 A0A3Q1LMB 2 A0A3Q1LWT4 A0A3Q1LWT 18	2	103 1469.59	-,	0,62082 1,10 0.62088 1.20	,		LL 22	175 Myosin-1 OS=Bos taurus OX=9913 GN=MYH1 PE=3 SV=1	219688 92232224	308099 105966818	84714 78487739	43202 123208931	221273 70911409	257751 86602355	140525 97695277	150592 42901902	280402 94441569	74573 227854949	84034 109786938	98772 132747080	357329 57151521	161677 56516954	174831 44491906 14	92328 46211325
A0A3Q1LWT4 A0A3Q1LWT 18 Q5E954 DNJA1 BOVIN:A0A 5	3 18 5	269.54	-,	0,62088 1,20 0.62088 1.16		LL	HL 81	390 Acyl-CoA synthetase long chain family member 1 OS=Bos taurus OX=9913		3488045	967006	735815	2052796	726195	3160813	42901902	3058838	380588	1309565	308439	3569657	2080061	2265210	238723
A5PKH1 A5PKH1 BOVIN 2	2	269,54 91,61),62088 1,16),62088 1,16	,	LL		853 DnaJ homolog subfamily A member 1 OS=Bos taurus OX=9913 GN=DNAJ/ 065 GRTP1 protein OS=Bos taurus OX=9913 GN=GRTP1 PE=2 SV=1	448727	216549	242263	79668	2052/96	121464	220258	457108	287997	121730	115806	114901	342954	433123	517048	189416
A0A3Q1LIA4 A0A3Q1LIA4 4		272,34),62088 1,10),62088 1,00				732 Dynactin subunit 1 OS=Bos taurus OX=9913 GN=DCTN1 PE=1 SV=1	130694	62027	61723	14415	201754	88971	119593	140183	207501	37106	35706	23110	246947	433123	128207	13400
A0A3Q1NNA0 A0A3Q1NNA 3	3	303.09),62088 1,00).62088 1.09			LL 50	986 Seipin OS=Bos taurus OX=9913 GN=BSCL2 PE=4 SV=1	2679941	3367688	4161972	1891451	3656691	3671687	2867332	3335340	3045523	1754831	4229038	2460065	4409893	3728225	2046348	776452
A0A3Q1N0D1 A0A3Q1N0D 2	2	121.11	-,),62088 1,09				500 Sepin 05-b05 taul 05 0X-5515 GN-5512 CV-65CL2 FE-4 SV-1 5113 Synaptotagmin-like protein 2 OS=Bos taurus OX=9913 GN=SYTL2 PE=4 SV	89064	163110	195946	13144	173887	89647	124358	113923	157282	142829	55231	162103	172904	91504	113761	74609
G5E507 G5E507_BOVIN;Q7 17	7 8	1297.47	-,	0.62088 1.19		LL	HL 81	671 Heat shock protein HSP 90-beta OS=Bos taurus OX=9913 GN=HSP90AB1 F		2656053	2799471	1343856	4322433	2075867	3825603	4976140	6162502	2218059	4335561	1235108	6363572	3574515	3578425	1408769
A0A301MIA41A0A301MIA4 6	6	312.98	.,	0.62088 1.26	465 0.08401		LL 99	582 26S proteasome non-ATPase regulatory subunit 2 OS=Bos taurus OX=991		162162	158205	71007	463441	40064	161964	910576	395577	49597	87125	100279	440528	185191	450104	67204
P379801IPYR BOVIN 2	2	131.42	-,	0.62591 1.21	889 0.08255	HI		793 Inorganic pyrophosphatase OS=Bos taurus OX=9913 GN=PPA1 PE=1 SV=2	41568	7860	86278	41249	213498	283072	53469	104013	49540	281129	43734	186330	4068	145724	139921	27462
E1BAT3 E1BAT3 BOVIN 4	4	199.9	-,	0.62591 1.23		HL		1090 LIF receptor alpha OS=Bos taurus OX=9913 GN=LIFR PE=4 SV=2	80314	182319	137762	68447	152320	142748	136395	106952	99097	27171	40672	55973	100107	138121	185714	31528
A0A301LZT9 A0A301LZT9 2	2	139.74	0.58901 0	0.62591 1.10	583 0.08187			791 WW domain binding protein 2 OS=Bos taurus OX=9913 GN=WBP2 PE=4 S	261250	148292	342326	70697	207201	312973	247910	248405	176004	10710	153189	150893	187912	327338	300270	144044
A0A452DJG2 A0A452DJG2 7	7	446,6	0,59096 0	0,62591 1,18	158 0,08153	LL		145 Guanine nucleotide-binding protein subunit alpha-11 OS=Bos taurus OX=9	9231667	5623221	9390527	17653928	9913264	11891035	9051586	16463690	7909995	49210929	21594494	22167875	6049802	6937945	7374048	19836901
E1BLZ8 E1BLZ8 BOVIN 3	3	304,38	0,59116 0	0,62591 1,14	935 0,08149	LL	HL 40	870 Eukaryotic translation initiation factor 3 subunit F OS=Bos taurus OX=991	95198	229111	11596	66360	375510	73886	204906	609717	428141	293005	213237	121052	547658	49719	274499	141072
A7YY28 ABHEB_BOVIN 2	2	114,56	0,59256 0),62591 1,34	886 0,08125	LL	HL 22	441 Protein ABHD14B OS=Bos taurus OX=9913 GN=ABHD14B PE=2 SV=1	494414	202528	198543	25550	310280	300221	463073	591464	406555	301688	194495	172564	597399	256183	910275	146706
F1N6C2 F1N6C2_BOVIN 2	2	106,94	0,59758 0	0,62798 1,13	387 0,08039	LL	HL 24	984 Transmembrane p24 trafficking protein 4 OS=Bos taurus OX=9913 GN=TM	763787	800943	474037	684733	733847	504022	1313519	778044	870832	346928	1285175	801930	1250542	597192	705421	209906
Q0VCJ8 METL9_BOVIN 4	4	232,3	0,59766 0	0,62798 1,14	865 0,08038	LL	HL 36	513 Methyltransferase-like protein 9 OS=Bos taurus OX=9913 GN=METTL9 PE	3713559	1734740	2108129	667701	2395410	1592340	4978480	2754483	2661607	1264056	2312600	1519000	4998346	3418642	3271728	1531519
A6QL75 A6QL75_BOVIN;G5 3	3	156,2	0,59792 0	0,62798 1,20	914 0,08033	HL	LL 19	115 PTP4A2 protein OS=Bos taurus OX=9913 GN=PTP4A2 PE=2 SV=1	563233	231016	306735	384929	238453	462597	1448922	325287	198355	217317	120784	240188	295518	736064	522412	529546
A0A3Q1NLW9 A0A3Q1NLW 2	2	110,61	0,60654 0	0,62836 1,09	372 0,0789	HL	LL 31	639 VPS37 C-terminal domain-containing protein OS=Bos taurus OX=9913 GN	163797	75320	154212	42180	92066	136297	16202	149988	78464	8951	34623	31343	101379	232099	127544	43887
P61585 RHOA_BOVIN;Q1RI 2	2	191,91	0,60702 0	0,62836 1,16	879 0,07882	HL	LL 21	754 Transforming protein RhoA OS=Bos taurus OX=9913 GN=RHOA PE=1 SV=	9007613	2094431	3871108	2831882	1946600	1515539	7883258	3702601	2146164	1927163	545277	2148576	5866321	3726098	4356393	3362180
F1MG05 F1MG05_BOVIN 6	6	444,03	0,60978 0	0,62836 1,16	744 0,07837	HL	LL 50	330 Elongation factor 1-gamma OS=Bos taurus OX=9913 GN=EEF1G PE=4 SV=	480627	855513	802553	780845	2112237	557363	780569	2391456	1047386	992930	447287	431051	1435238	1237736	1573634	623739
A0A3Q1LXL6 A0A3Q1LXL6_ 5	3	217,62	0,61043 0	0,62836 1,08	915 0,07826	LL	HL 46	075 Casein kinase I isoform gamma-3 OS=Bos taurus OX=9913 GN=CSNK1G3 I	48721	106741	73195	83812	156274	69826	25366	158083	106586	167759	47750	145247	13467	116528	140262	82519
A0A3Q1LVE4 A0A3Q1LVE4 2	2	225,45	0,61102 0	0,62836 1,11	507 0,07817	LL	HL 55	692 Sequestosome 1 OS=Bos taurus OX=9913 GN=SQSTM1 PE=1 SV=1	729260	615425	1042975	200782	367462	617165	1400582	258186	942148	428215	397438	123575	908422	628696	658112	569347
A5D977 A5D977_BOVIN 5	3	318,4	0,61112 0	0,62836 1,03	386 0,07815	HL	LL 23	424 RALB protein OS=Bos taurus OX=9913 GN=RALB PE=2 SV=1	1352498	407678	526221	210060	390626	381684	561779	752652	548400	77895	475404	294633	1019645	706688	680788	114478
F1N650 F1N650_BOVIN 3	3	210,55		0,62836 1,01		LL		955 Annexin OS=Bos taurus OX=9913 GN=ANXA1 PE=3 SV=1	811366	1455216	400520	1291154	1066584	382265	4694573	792913	206252	3788864	932980	740594	1420121	151405	465353	4186541
A0A3Q1MW62 A0A3Q1MV 5	3	312,16		0,62836 1,60				ADP-ribosylation factor 2 OS=Bos taurus OX=9913 GN=ARF2 PE=3 SV=1	838085	1787873	1059829	714753	969110	2724549	685343	1654886	1144034	502683	612362	677118	752419	2853352	3753320	1503067
A0A3Q1LSJ7 A0A3Q1LSJ7_E 2	2	186,06	-,	0,62836 1,18	,	LL		791 Dynactin subunit 2 OS=Bos taurus OX=9913 GN=DCTN2 PE=1 SV=1	194442	285525	170277	98716	600917	77500	220662	386566	400244	17275	93240	35096	470129	617642	618796	42070
F1MK30 F1MK30_BOVIN 2	2	142,34	.,	0,62836 1,10		LL		666 60S ribosomal protein L13 OS=Bos taurus OX=9913 GN=RPL13 PE=3 SV=2		166744	281849	575558	613284	235244	143688	679708	348312	185857	117169	383522	598449	658411	942082	321015
Q3T057 RL23_BOVIN 2	2	105,51	0,61435 0					60S ribosomal protein L23 OS=Bos taurus OX=9913 GN=RPL23 PE=2 SV=2		156713	48648	104326	288197	386139	2690124	713347	491479	247233	109906	192173	917804	312708	525596	165267
Q2HJ33 OLA1_BOVIN;A0A3 3		149,29		0,62836 1,20				715 Obg-like ATPase 1 OS=Bos taurus OX=9913 GN=OLA1 PE=2 SV=1	204674	150110	173984	259423	520722	157134	198615	493076	302142	215928	151903	427437	319609	170072	315580	151118
A4IFE6 A4IFE6_BOVIN 2	2	244,41		0,6294 2,08				ABCE1 protein OS=Bos taurus OX=9913 GN=ABCE1 PE=2 SV=1	19667	36566	22577	1231	65729	21710	29896	73185	189151	0	0	1733	215226	41731	67962	7704
G3X7N4 G3X7N4_BOVIN 2	2	103,58	- ,	0,62951 1,26	,			096 Phosphoglycerate kinase OS=Bos taurus OX=9913 GN=PGK1 PE=1 SV=2	64886	109210	34133	77255	183540	30151	151309	75846	113644	130237	28558	75044	36491	68298	56537	54502
A0A3Q1LN77 A0A3Q1LN77 3	3	231,62		0,62988 1,08	,			NBR1 autophagy cargo receptor OS=Bos taurus OX=9913 GN=NBR1 PE=4		423251	827888	129377	363285	1459334	493895	273242	736727	75683	177415	460163	303598	825400	712589	311098
Q3MHH4 SYQ_BOVIN 3	3	101,44	.,	0,62988 1,08	,			GlutaminetRNA ligase OS=Bos taurus OX=9913 GN=QARS PE=2 SV=1	9125	17771	21113	16657	392414	8406	40495	177775	154189	43624	16094	14723	217939	57496	110372	3247
E1BJV0 E1BJV0_BOVIN 14		895,4	-,	0,62988 1,08				987 EH domain containing 4 OS=Bos taurus OX=9913 GN=EHD4 PE=3 SV=1	20782693	25265097	19100907	8939703	23245075	16082108	20009907	17368036	23239360	10527622	21946354	12926388	21811025	11648266	20294485	9475827
A0A3Q1NA69 A0A3Q1NA69 8	8	427,82	-,		278 0,07484			Gamma-soluble NSF attachment protein OS=Bos taurus OX=9913 GN=NA	3109396	2270925	2121419	802806	2935738	2105415	2308264	3388547	1741199	1066506	708769	1811629	2189561	5264303	4025204	674711
E1BIB8 E1BIB8 BOVIN 2 OOVCX2 BIP BOVIN 6	2	52,63 382.54	.,	0,63286 1,31	901 0,07442 698 0.07414			243 Lysophospholipase 2 OS=Bos taurus OX=9913 GN=LYPLA2 PE=4 SV=3 Endeployment optimum shaperone Bib OS=Bos taurus OX=0013 CN=USDA	133861 572346	82438 346232	94761 573653	68519	168048 964068	154098 566072	202149 412065	186544 2126841	124630	133529 1377908	43497 824625	96780 386661	142859 692921	206606 703074	326373 680818	102646 686967
QUVCX2 BIP_BOVIN 6 Q3SZ54 IF4A1 BOVIN:A0A3 7	6	382,54 499.61	0,63723 0	,,	239 0.07414			356 Endoplasmic reticulum chaperone BiP OS=Bos taurus OX=9913 GN=HSPA Eukarvotic initiation factor 4A-I OS=Bos taurus OX=9913 GN=EIF4A1 PE=2	548097	346232 1098919	573653 768564	895422 562083	964068 1416528	777638	412065	2126841 1335992	499580 1150066	1377908 631810	824625 912882	386661 376135	692921 1478776	634533	680818 1109567	827065
Q35254 IF4A1_BOVIN;AUA3 / Q0VCY1 VAPA BOVIN;AUA3 3	2	499,61		0,63286 1,04 0.63286 1.63				125 Eukaryotic initiation factor 4A-I OS=Bos taurus OX=9913 GN=EIF4A1 PE=2 838 Vesicle-associated membrane protein-associated protein A OS=Bos taurus		1098919	277847	73129	1416528 178945	300340	163803	236805	1150066	52763	912882 189999	376135 115539	308993	634533 777450	1109567 544498	136026
E1BJ18 E1BJ18_BOVIN 15		1127,63	.,		018 0,07403	LL		932 Calpain 6 OS=Bos taurus OX=9913 GN=CAPN6 PE=3 SV=1	9421357	9327532	21992351	8510289	2847652	1779080	2319491	1589652	14297110	4303160	30605756	16206766	3661400	3085590	2607850	1182414
		,00	-,	., 1,50	,0,404		/*							2										

A0A3Q1MSA1 A0A3Q1MSA 3	2	242.87	0 64149	0.63286	1 25754	0.07252	HL	ц :	8122	Lectin, mannose binding 1 OS=Bos taurus OX=9913 GN=LMAN1 PE=1 SV=1	1019398	2209016	437660	182709	924559	1615876	1082359	911079	984176	128320	734779	273637	1849892	1621569	915736	277342
E1BIE4 E1BIE4 BOVIN:F1M 2	2	242,87	0,64148		1,25754	0.07333				EPH receptor B4 OS=Bos taurus OX=9913 GN=EMAN1 PE=1 SV=1	62003	2209016	63411	15340	924559	39863	34012	50250	984176	28880	77943	63871	45680	19568	915736	27983
A0A3S5ZPB0 A0A3S5ZPB0_ 3	3	287,37	0,64348		1,13283	0,07324			5620	Fructose-bisphosphate aldolase OS=Bos taurus OX=9913 GN=ALDOC PE=1	294489	255725	110672	302863	506334	368105	246247	296909	362698	382851	241463	422968	190030	118613	264872	269578
Q5E9R3 EHD1_BOVIN 4	3	275,11	0,04574	-,	1,07833	0,0732				EH domain-containing protein 1 OS=Bos taurus OX=9913 GN=EHD1 PE=1 S	472442	751860	1153038	600971	744703	470674	283198	679234	546653	793411	787700	610511	317755	737550	869415	438904
A0A3Q1MXV0 A0A3Q1MXV 2 Q0IIG7 RAB5A BOVIN 4	2	248,21 341.77	0,64662	-,	1,11948	0,0728				IGv domain-containing protein OS=Bos taurus OX=9913 GN=CEACAM19 PI Ras-related protein Rab-5A OS=Bos taurus OX=9913 GN=RAB5A PE=1 SV=1	80191 3115387	62369 1354030	541125 1892520	37566 747012	116481 1308026	133248 910916	258103 3292361	122835 1958250	71753 2111636	5153 261155	237968 503270	46132 800937	127386 2531574	297094 4128671	188152 2953947	106242 987443
0863B3 SND1 BOVIN:A0A3 11	-	636.96			1,00085	0.07263				Staphylococcal nuclease domain-containing protein 1 OS=Bos taurus OX=9	942955	2133009	2008000	1455160	2916953	1716543	997474	2434240	2936626	988732	628475	1290278	2025929	2162604	1981271	1005702
F6QH94 F6QH94_BOVIN 2	2	211,75	0,65465	0,6393	1,25807	0,07168	LL	HL ·		Protein disulfide isomerase family A member 6 OS=Bos taurus OX=9913 GI	160215	436321	225664	849714	351756	310769	177599	599070	324504	1129740	564994	432198	273673	188857	144232	1052149
Q3SYU2 EF2_BOVIN;A0A3C 14	14	939,4	0,65486	0,6393	1,04808	0,07165	HL	LL S		Elongation factor 2 OS=Bos taurus OX=9913 GN=EEF2 PE=2 SV=3	7183725	11073785	8917337	4414080	14781514	5831716	9421023	11144934	13042671	4797582	5294546	5303297	13935176	9690355	14420427	3619512
Q1RMI2 Q1RMI2_BOVIN 5	5	257,04	0,65563		1,54067	0,07155				Ras homolog family member G OS=Bos taurus OX=9913 GN=RHOG PE=1 S	1254600	368131	542606	591257	447326	511550	918334	975324	528647	86182	249528	759617	1370005	1919086	1601750	1076456
Q3SYZ4 SYDC_BOVIN;F1MT 3 A0A3Q1M273 A0A3Q1M27 2	3	121,6 135,19	0,65633	0,6393 0.63958	1,1471	0,07145			7000 0124	AspartatetRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS PE: Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Bos tauru	27315 29341	93996 71834	41923 91420	74142 182268	312847 100253	56223 147240	46981 20845	277443 90650	150630 122127	134112 25139	52900 68967	53982 112129	211317 80233	83717 36145	92014 74241	96520 182893
A0A301LMK8 A0A301LMK 3	3	107.06	0.6593	0.6398	1,02040	0.07105				Prostaglandin reductase 2 OS=Bos taurus OX=9913 GN=PTGR2 PE=1 SV=1	544989	693297	383030	172473	946078	287700	797223	820865	682592	509093	269110	582592	714746	1154935	711861	248653
Q0VCH9 Q0VCH9_BOVIN 2	2	201,77	0,66408	0,64057	1,46738	0,07042	LL	HL :	7199	GLI pathogenesis-related 2 OS=Bos taurus OX=9913 GN=GLIPR2 PE=2 SV=1	141033	161777	386839	36081	133448	54638	227819	97279	201858	76665	193907	23681	196681	569137	68684	497167
Q3ZBA8 NDRG2_BOVIN;F1! 3	3	369,09	0,66538	0,64057	1,26215	0,07025			9183	Protein NDRG2 OS=Bos taurus OX=9913 GN=NDRG2 PE=2 SV=1	2333883	682471	1393652	171935	833607	837400	1734455	114999	2028388	298733	723413	144302	983302	633629	222615	619059
E1BL67 E1BL67_BOVIN 2 F1MSE7 F1MSE7 BOVIN 5	2	126,78 320.05	0,66586	0,64057 0.64057	1,09597	0,07018			4949 9996	Oxysterol-binding protein OS=Bos taurus OX=9913 GN=OSBPL2 PE=3 SV=1 Sushi domain containing 2 OS=Bos taurus OX=9913 GN=SUSD2 PE=4 SV=1	32349 58551	374619 195537	250156 347221	144199 280605	177377 846752	122468 556197	30986 80794	171947 183068	136336 110795	249397 751923	149173 169304	149985 151767	25209 162094	88888 121958	313314 103565	75283 174264
Q2YDJ41HINT3 BOVIN 2	2	110.12	0.66741	.,	1.0373	0,07002			0457	Histidine triad nucleotide-binding protein 3 OS=Bos taurus OX=9913 GN=H	219539	201209	434973	139148	335674	437000	103143	389797	270610	203963	334989	300170	352161	491461	527973	250820
A0A3Q1MWU8 A0A3Q1MV 3	3	131,67	0,66861	-,	1,34485	0,06983				Syntaxin binding protein 3 OS=Bos taurus OX=9913 GN=STXBP3 PE=3 SV=1	160725	305100	132936	56564	100523	183203	39490	65944	192979	23927	91639	70758	120671	151923	119118	24551
E1BEV7 E1BEV7_BOVIN 2	2	84,01	- ,		1,07428	0,06951	LL	HL 1	11699	Metalloendopeptidase OS=Bos taurus OX=9913 GN=BMP1 PE=4 SV=3	66958	60412	95830	14067	126131	21561	101184	109824	55064	12551	8263	17160	68824	24712	181411	7784
F1MQ96 F1MQ96_BOVIN 2	2	107,69	0,67449		1,25388	0,06908		HL I	8255	Protein kinase C OS=Bos taurus OX=9913 GN=PRKCI PE=3 SV=3	103502	192313	104102	268296	113938	234838	113392	102955	241154	443085	113873	319185	69749	76646	64509	179062
A4FV45 TM214_BOVIN 2 Q2T9M8 Q2T9M8 BOVIN;4 6	2	104,53 684,79	0,6772		1,04106 1.12313	0,06874			6967 3212	Transmembrane protein 214 OS=Bos taurus OX=9913 GN=TMEM214 PE=2 Synaptosomal-associated protein OS=Bos taurus OX=9913 GN=SNAP23 PE	4177 5635039	6362 2962044	13160 5496460	21602 3220168	70236 2939193	8546 3113544	3696 5632162	71197 4761244	28354 2848559	71521 1991414	0 3153270	9631 3155983	32381 4754673	56696 6689147	29117 7723499	0 4016365
Q2KIW91KCY BOVIN:A0A45 3	3	247.43	.,	.,	1.04336	0.06772			2265	UMP-CMP kinase OS=Bos taurus OX=9913 GN=CMPK1 PE=2 SV=2	1125244	596455	1316237	483015	820209	825639	1320489	1318510	772124	193981	450097	336912	1011597	1739813	1808461	557426
A0A3Q1LSE5 A0A3Q1LSE5 2	2	92,35	0,68569	0,65113	1,12262	0,0677	HL	LL a	5456	N-ethylmaleimide sensitive factor, vesicle fusing ATPase OS=Bos taurus OX	54974	81617	140568	37598	135405	87283	75086	139627	115425	3761	50602	40325	171927	103212	116182	11782
F1N3M3 F1N3M3_BOVIN;A 3	3	177,25	0,68733	.,	1,10207	0,0675		HL 1	36855	Protocadherin gamma subfamily A, 3 OS=Bos taurus OX=9913 GN=PCDHG	295705	22171	238006	484890	222996	168269	109037	274675	224702	153833	907333	202618	259681	246998	183797	139229
P18892 BT1A1_BOVIN 8	2	469,3	0,68753		1,12178	0,06747		LL !	9239	Butyrophilin subfamily 1 member A1 OS=Bos taurus OX=9913 GN=BTN1A1	23855104	30476236	33642721	9601544	25590865	12476234	14429006	22677516	38693052	21363211	15328410	9191386	14773589	20692618	21159283	6420978
A60P05 DHR12_BOVIN;A0/ 2 A60PG6 A60PG6 BOVIN 3	2	129,6 174,53	0,69236		1,10055	0,06679			5043 9135	Dehydrogenase/reductase SDR family member 12 OS=Bos taurus OX=991: LANCL2 protein OS=Bos taurus OX=9913 GN=LANCL2 PE=2 SV=1	31436 437356	158335 446958	177439 414240	18184 907155	192237 661142	188002 915640	23123 559646	252307 710054	159299 744277	21589 1340277	58128 919434	37591 1116700	121796 262090	254150 562165	301663 477632	62510 529013
A6QLS91A6QLS9 BOVIN 5	3	319.73	0.69407	-,	1,15893	0.0667			2527	RAB10 protein OS=Bos taurus OX=9913 GN=RAB10 PE=1 SV=1	2517363	1620866	2818424	802049	1829274	2033900	2474059	3199170	1777649	276385	963052	894774	262090	4984169	4519566	2017678
A0A3Q1MNH4 A0A3Q1MN 5	5	264,16	0,69535	0,65127	1,06086	0,06655			0512	Ethylmalonyl-CoA decarboxylase OS=Bos taurus OX=9913 GN=ECHDC1 PE	419891	250109	278907	182138	604808	428155	786045	401083	307388	164584	159046	314325	406623	714886	473729	425423
E1BDK9 E1BDK9_BOVIN 2	2	105,12	0,69584	-,	1,00728	0,0665				Retinol saturase OS=Bos taurus OX=9913 GN=RETSAT PE=4 SV=1	23081	242591	223142	111365	172421	137323	93929	21742	97741	10440	91752	112030	213787	199944	74471	123870
A5PKL2 A5PKL2_BOVIN;A0/ 5	4	285,2	0,69882		1,05106	0,06615		HL :		RAS related 2 OS=Bos taurus OX=9913 GN=RRAS2 PE=2 SV=1	2741323	990606	2271980	688917	1109513	1325179	3143845	2314053	1232406	447457	867922	602520	2000524	3910900	3318367	1116200
A0A3Q1LTG9 A0A3Q1LTG9 3	3	185,19	0,70178		1,03397	0,06582				TBC1 domain family member 9B OS=Bos taurus OX=9913 GN=TBC1D9B PE 14-3-3 protein zeta/delta OS=Bos taurus OX=9913 GN=YWHAZ PE=1 SV=1	45371	58930	156802	17417	110323	213128	68138	69461	107464	14398	73412	27254	5594	289054	94815	29583 3843039
P63103 1433Z_BOVIN;E1BE 6 A0A3Q1LZC0 A0A3Q1LZC0 2	5	422,8 87,71	0,70223		1,02774 1.02879	0,06577				Glycerol kinase OS=Bos taurus OX=9913 GN=TWHA2 PE=1 SV=1	2798671 67728	1926326 36274	2484904 12562	1805951 3112	3176037 44804	2594787 6130	3668015 95229	3916035 29228	2316213 42162	2805288 11954	2528040 52014	1953337 19360	4257735 94762	3766574 14140	4947371 23114	3843039
A0A3Q1M591 A0A3Q1M59 4		206,47	0,70724	.,	1,06564	0,06521			3074	Uncharacterized protein OS=Bos taurus OX=9913 GN=RAB43 PE=4 SV=1	791780	490001	651421	205050	388318	557607	733671	446795	481652	84128	201891	264686	736038	1044985	966638	466431
A0A452DIW4 A0A452DIW4 2	2	102,34	0,7103	0,65669	1,05141	0,06487	HL	LL :	5833	Malate dehydrogenase OS=Bos taurus OX=9913 GN=MDH1 PE=1 SV=1	244939	209534	236543	97465	375100	362242	349548	177802	158091	105591	145162	208699	312422	435970	358336	284229
E1BJ42 E1BJ42_BOVIN 2	2	135,01	0,7114	0,65669	1,36431	0,06475		HL (9959	ZP domain-containing protein OS=Bos taurus OX=9913 GN=ENG PE=4 SV=:	344426	597720	318736	832466	383772	570628	400056	315105	385809	2153397	613432	566091	297657	207687	182310	825449
A0A3Q1LRI7 A0A3Q1LRI7_E 4	4	197,79	0,71204	0,65669	1,09047	0,06469		HL :	2766	Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC521224 PE=4 SV	478878	105466	96514	18636	353905	20113	280787	303974	532258	38451	322937	63805	341056	266666	207439	69652
Q1RMH8 SNX3_BOVIN 3 Q0II86 SNP29 BOVIN 5	2	113,23 380.05	0,71219	0,65669	1,65068	0,06467			8751 8472	Sorting nexin-3 OS=Bos taurus OX=9913 GN=SNX3 PE=2 SV=3 Synaptosomal-associated protein 29 OS=Bos taurus OX=9913 GN=SNAP29	81215 3865041	39803 2847702	87406 1999560	15020 646371	54389 1881200	69629 816867	86064 4787441	93060 3315317	49232 2922785	43654 428001	21404 1456492	16601 648661	123793 3779502	245745 3866978	205120 4980381	58105 964713
F60NX41F60NX4 BOVIN 3	3	244.01	0,7123	-,	1.08919	0.06454				Endoplasmic reticulum-golgi intermediate compartment 1 OS=Bos taurus (36175	104828	231925	37023	298555	236697	11888	516088	196932	112711	72153	40607	145035	207911	333148	43604
G3N0S9 G3N0S9_BOVIN 2	2	106,72	0,71791	0,65875	1,53479	0,06406				Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=2	817105	90012	121416	42479	32318	20972	551920	106752	27982	87583	25466	24510	108116	39791	85810	578168
A5D984 A5D984_BOVIN;Q1 2	2	154,07	0,7224		1,19972	0,06359	HL	LL :	7912	Pyruvate kinase OS=Bos taurus OX=9913 GN=PKM PE=1 SV=1	123790	411282	97051	94245	628817	250152	289976	323055	358627	148425	233003	166248	439593	218791	164524	36042
A0A3Q1LNT7 A0A3Q1LNT7 8	7	339,87	-,		1,12173	0,06356			13691	Unconventional myosin-Id OS=Bos taurus OX=9913 GN=MYO1D PE=3 SV=	1461534	1630468	1241404	636448	1274442	949143	795602	1160826	1100105	712253	981609	778238	1230195	1435321	1215905	309549
Q2TBQ5 RL7A_BOVIN 3 A0A3Q1MBN5 A0A3Q1MBI 3	3	193,48	0,72283		1,18932	0,06355				60S ribosomal protein L7a OS=Bos taurus OX=9913 GN=RPL7A PE=2 SV=3	193130	283287	139807	106496	608888	150123	471547	683561	305388	170836	101781	105109	739830	476210	809728	279173
A0A3Q1MBN5 A0A3Q1MBI 3 A0A3Q1LYU9 A0A3Q1LYU9 4	3	209,44 238.65	0,72338		1,45229	0,06349			3911 8454	Histone H2B OS=Bos taurus OX=9913 PE=3 SV=1 Casein kinase I isoform gamma-1 OS=Bos taurus OX=9913 GN=CSNK1G1 P	420842 89885	1963123 638	336584 100447	233942 8320	1755583 164973	375631 49385	8892989 2033	1443285 141177	211272 3335	1989644 40528	62946 47551	631062 126431	4716116 6441	965530 146709	1540189 188424	3327804 13863
F1MND1 F1MND1 BOVIN;(2	2	150,87	.,		1,05168	0,06338				Cell division control protein 42 homolog OS=Bos taurus OX=9913 GN=CDC	4077034	1753022	2500532	1012253	1888460	2192863	4135801	4001035	1938440	597471	936132	776171	3139481	5881261	4765304	1804314
A5PJY9 A5PJY9_BOVIN 2	2	241,08	0,72461	0,65875	1,43333	0,06336	HL	ш :	9579	CPNE3 protein OS=Bos taurus OX=9913 GN=CPNE3 PE=1 SV=1	188728	462502	31086	58583	192329	128938	77097	156793	332496	39393	164126	76650	159495	112518	42819	138541
Q3ZBG1 Q3ZBG1_BOVIN 4	4	262,41	0,72465		1,38269	0,06336		HL :	3882	RAB14 protein OS=Bos taurus OX=9913 GN=RAB14 PE=1 SV=2	341238	590218	545780	92522	753316	655183	537925	871584	974139	277543	429444	229401	464381	1922231	1332841	416330
A0A452DII2 A0A452DII2_B(7	7	468,09	0,7254	.,	1,08264	0,06328			0946	Protein FAM49A OS=Bos taurus OX=9913 GN=FAM49A PE=4 SV=1	1037847	487809	1933182	572840	509401	518362	494971	750545	612951	482816	1143939	458992	624875	1466821	824444	1211189
A0A3Q1N3F5 A0A3Q1N3F5 3 A6QPT4 A6QPT4 BOVIN 3	3	294,35 126,72	0,72676		1,07069	0,06315			3916 1840	Hydroxysteroid 17-beta dehydrogenase 7 OS=Bos taurus OX=9913 GN=HS MPO protein OS=Bos taurus OX=9913 GN=MPO PE=1 SV=1	4962324 15407	3696485 391865	6128516 25313	2206093	3621906 100721	3350091 4415	3637504 951076	4193835 16397	3020610 2352	649793 256193	2087957	3040388 6081	5422342 167866	5495813 0	6898964 9243	5092902 644540
F1MIN4 F1MIN4 BOVIN 3	3	319.66	.,	.,	1,15954	0.0626			7142	Amino acid transporter OS=Bos taurus OX=9913 GN=SLC1A1 PE=3 SV=1	2831521	3728189	4396202	3186340	1729950	5850055	3037712	2176220	4401816	7935890	5829210	9566377	1379657	1917516	1888047	4091772
A4FUD7 A4FUD7_BOVIN;E1 3	2	147,71	0,73724	0,66482	1,18321	0,06211			5602	RAB33B protein OS=Bos taurus OX=9913 GN=RAB33B PE=2 SV=1	455706	339733	181125	23192	107518	168794	370756	190843	223536	24720	72041	35048	533853	538581	468349	95846
A0A3Q1MKR2 A0A3Q1MKF 2	2	150,06	0,74284	0,66778	1,77184	0,06157	HL	LL 1	70636	Glutamyl-prolyl-tRNA synthetase OS=Bos taurus OX=9913 GN=EPRS1 PE=1	13034	14018	2253	79729	215505	74188	1934	128428	20851	77326	23394	55497	50595	42545	13701	32417
F6RFP6 F6RFP6_BOVIN 3	3	246,52	- ,	0,66778		0,06145		LL :		Basigin OS=Bos taurus OX=9913 GN=BSG PE=1 SV=1	2010134	2792154	1896139	502689	638822	1654447	2129458	820467	2212628	1114246	2029907	416514	2078416	2073633	959751	754208
A0A3Q1LFR2 A0A3Q1LFR2_ 3 Q58CS7 CHMP3 BOVIN;A0. 4	3	139,14 174,6	0,7449 0.74568		·· ··	0,06138			5639 5001	Uncharacterized protein OS=Bos taurus OX=9913 GN=GSTM2 PE=1 SV=1 Charged multivesicular body protein 3 OS=Bos taurus OX=9913 GN=CHMP	389879 874397	108779 807021	321291 723362	212354 348624	211678 541504	177468 793972	332968 1029538	274244 692706	294864 645600	251288 212735	153178 362652	338614 472312	180402 1087237	619870 839616	448923 1112242	417063 346887
E1BNE1 E1BNE1 BOVIN;Q3 3	3	338.86	0,74585	.,		0.06129			7535	Lipid droplet associated hydrolase OS=Bos taurus OX=9913 GN=LDAH PE=4	405270	112425	725562	124126	1041998	947063	276093	1110573	255448	298263	669797	681450	254730	1043458	2278955	173274
Q3T0K2 TCPG_BOVIN 2	2	127,37	0,7507		1,14566	0,06085			0547	T-complex protein 1 subunit gamma OS=Bos taurus OX=9913 GN=CCT3 PE	12852	49613	46812	7944	103303	10267	92556	195586	112663	44908	22673	1661	132550	48493	76782	15433
A0A3Q1MC55 A0A3Q1MC5 4	4	317,01	0,75082	0,66797	1,17303	0,06084			4715	Syntaxin-binding protein 6 OS=Bos taurus OX=9913 GN=STXBP6 PE=4 SV=1	898737	378094	870236	357293	554817	367962	945136	950522	750802	238498	292588	409719	1261925	970287	1342408	374475
Q95JH2 PLCA_BOVIN 3	3	134,63	0,75164	0,66797	1,27871	0,06076		HL :	1984	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha OS=Bos taurus OX=9	32281	7424	175389	15180	135311	119693	107986	212738	58527	31593	22437	29951	73183	277078	316517	56529
E1BG08 E1BG08_BOVIN 2 F1MHS5 F1MHS5 BOVIN 3	2	95,33 234.37	0,75427 0,75464	0,66797 0.66797	1,08181	0,06053			4973 7118	Axin interactor, dorsalization associated OS=Bos taurus OX=9913 GN=AID/ Protein S100-A9 OS=Bos taurus OX=9913 GN=S100A9 PE=3 SV=3	335265 95719	219468 329894	290038 56048	584964 273302	316049 326210	472295 78600	424045 3763616	327124 66630	101570 32165	375082 1473632	321318 49705	555172 129427	431167 594652	149282 77419	405268 144371	406677 3816944
F1N0D61F1N0D6 BOVIN 6	6	413.49	0.7576	.,	1,14067	0.06023			33568	Tyrosine-protein kinase OS=Bos taurus OX=9913 GN=JAK1 PE=3 SV=3	345805	410670	973148	411862	761699	360243	212914	847670	576231	103895	292857	482999	414311	413118	839758	435585
A0A3Q1M010 A0A3Q1M01 9	9	516,36	0,76552	0,6718	1,04563	0,05955			5605	UTPglucose-1-phosphate uridylyltransferase OS=Bos taurus OX=9913 GN	1967407	3428961	1537530	1815702	4667790	1876143	3147189	3601117	4364206	2227383	1887651	1739748	4647910	2595357	2850601	924373
Q3MHP2 RB11B_BOVIN;A0 5	4	231,94	0,77121		1,13081	0,05907				Ras-related protein Rab-11B OS=Bos taurus OX=9913 GN=RAB11B PE=2 SV	5866819	2411930	3296956	2980753	2581130	1950005	5663562	3386956	3053292	1765824	1918744	2950261	5734073	4564128	6312325	3377686
Q32LK2 CYTM1_BOVIN 2	2	165,73	0,77186		1,27737	0,05902		HL :		Cysteine-rich and transmembrane domain-containing protein 1 OS=Bos tau	745966	596290	1014398	437476	716191	702802	1211465	985286	648065	92395	239607	435114	1577150	1999004	1554338	760863
Q5E971 TMEDA_BOVIN 3 A0A3Q1LYE8 A0A3Q1LYE8 5	5	186,74 482,35	0,77429 0,77453		1,29887 1.03086	0,05882			4812 7242	Transmembrane emp24 domain-containing protein 10 OS=Bos taurus OX= LipocIn cvtosolic FA-bd dom domain-containing protein OS=Bos taurus C	389517 878264	356946 755166	456692 3721792	562043 5434605	591518 742951	623211 1467700	813363 3555265	1248525 5246344	488259 312923	375417 960248	273610 2745754	451960 4143844	1309976 3346542	754179 4212368	1724621 3018859	476981 3240637
A0A301MFD01A0A301MFC 10	10	402,33	0,77435		1.08385	0.05832			6039	Maior vault protein OS=Bos taurus OX=9913 GN=MVP PE=4 SV=1	1087311	843209	539989	1650592	966535	482857	469073	2093440	991610	1178480	608388	767034	995445	4212308	1056009	1849049
A0A3Q1LI93 A0A3Q1LI93_E 11		636,79	.,	.,	1,21074	0,05824		LL 1	62954	CD109 molecule OS=Bos taurus OX=9913 GN=CD109 PE=4 SV=1	5497286	1030915	510277	5139430	1405373	506746	377130	285264	1941227	1637747	1026893	4571880	1133364	216783	214511	385552
F1N720 F1N720_BOVIN;Q9 10	10	923,33		0,67563						Toll-like receptor 2 OS=Bos taurus OX=9913 GN=TLR2 PE=3 SV=1	10231176	7437956	13435903	8225782	10640054	8566482	12512239	11717669	13322024	18600191	16383247	16697628	8798905	5961913	6647430	16290932
A0A3Q1LK11 A0A3Q1LK11_2	2	121,28	.,	0,67563		0,05785		HL ·		Casein kinase I isoform alpha OS=Bos taurus OX=9913 GN=CSNK1A1 PE=1	189037	89348	86673	89112	290968	292211	186957	140908	105554	73244	33407	84632	200760	487745	205573	85597
F1MDQ6 F1MDQ6_BOVIN;I 16 O3T0Y8IVAMP8 BOVIN 3		1126,66	-,		1,04522 1.22839	0,05783				cGMP-dependent protein kinase OS=Bos taurus OX=9913 GN=PRKG2 PE=3 Vesicle-associated membrane protein 8 OS=Bos taurus OX=9913 GN=VAM	14783733	14896016	13844379	6596546	15660105	14892698	11487872	15653823	16583144	4294769	6516778	10050128	23634977	17362543	22107666	5834750 582443
Q3T0Y8 VAMP8_BOVIN 3 Q2LGB5 TOLIP BOVIN 3	3	193,6 270,18	0,79294 0.79371		,	0,05738				Vesicle-associated membrane protein 8 OS=Bos taurus OX=9913 GN=VAM Toll-interacting protein OS=Bos taurus OX=9913 GN=TOLLIP PE=2 SV=1	696088 2802123	493938 927170	682223 1949392	350797 392757	207654 1260292	1077192 1565586	1311602 2719967	837703 1255319	632410 1129835	135028 1349735	157111 1390484	355600 587485	1010926 1956725	1160648 2013235	1079847 2396382	582443 855009
A0A3Q1LP69 A0A3Q1LP69 2	-	73,89	0,79451	.,	1,23928	-,				Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1	2202123	24309	53445	33644	75277	90899	25720	1255519	42601	11525	22713	20956	113875	164260	213709	103564
Q3T149 HSPB1_BOVIN 6	6	460,91	0,79502		1,16668					Heat shock protein beta-1 OS=Bos taurus OX=9913 GN=HSPB1 PE=2 SV=1	2982691	941779	1610890	1217468	1308290	953899	2366542	4869469	1915783	1081269	1615285	912368	2081756	5122952	5966438	1823526
Q3ZBU9 UBXN4_BOVIN 3		178,13			1,06823	.,				UBX domain-containing protein 4 OS=Bos taurus OX=9913 GN=UBXN4 PE=	486329	565002	1113148	461454	504571	588447	441503	596105	613685	669395	732427	652448	234533	844509	662449	666564
E1BB46 E1BB46_BOVIN 3		129,6	-,	0,67723		.,				SH3 domain binding protein 4 OS=Bos taurus OX=9913 GN=SH3BP4 PE=4 5	170351	270293	246117	27952	229751	162236	231067	299481	427775	129112	216608	193153	229876	261504	217716	44908
A0A3Q1MJK1 A0A3Q1MJK1 2 Q3T169 RS3 BOVIN;A0A3Q 3		87,17		0,67723						Serpin B6 OS=Bos taurus OX=9913 GN=SERPINB6 PE=3 SV=1	533035	305280	157589	126143	436072	224771	230524	417142	555080	333569	112195	338362	262094	409362 680762	343965	140064
Q3T169 RS3_BOVIN;A0A3Q 3 G3N2D8 G3N2D8 BOVIN 2		133,49 286.01		0,67772 0.67772		0,05686				40S ribosomal protein S3 OS=Bos taurus OX=9913 GN=RPS3 PE=2 SV=1 Uncharacterized protein OS=Bos taurus OX=9913 GN=GGT1 PE=1 SV=2	268741 23237319	261369 24964240	116118 17968802	99180 13598227	436882 11086771	211501 9296874	555799 14002471	1035364 9806931	271881 13727045	141365 27342802	19112 20406826	36144 11300138	1147617 9955868	680762 8991048	1018943 5079687	122978 26496231
A0A3S5ZPW7 A0A3S5ZPW7 32	-	3065,59		0,68028		0,05629				Xanthine dehydrogenase/oxidase OS=Bos taurus OX=9913 GN=XDH PE=4 \$ 2				3182385413 1									1335881001			821708249
A0A3Q1MDW8 A0A3Q1ME 2	2	68,01	0,81104	0,68028	1,01327	0,05612	LL	HL :	3763	Phospholipid-transporting ATPase OS=Bos taurus OX=9913 GN=ATP11B PE	42241	38338	75867	52345	82550	145043	17764	93438	66470	188562	47713	187026	25884	54996	67216	35430
A0A3Q1LIW3 A0A3Q1LIW3 2		127,4	- , -	0,68028		0,05604				AP-2 complex subunit alpha OS=Bos taurus OX=9913 GN=AP2A2 PE=3 SV=	11397	22050	5294	0	73971	150757	0	35580	12208	14447	23661	0	19720	46122	61575	3036
Q2TBH2 Q2TBH2_BOVIN 7	6	571,75	0,81257			0,05602				RAS related OS=Bos taurus OX=9913 GN=RRAS PE=1 SV=1	12041277	5615964	7398919	3539345	4849853	2617451	10634895	9036721	4834688	4582285	4300828	3842957	9939178	10420144	10959600	6649535
A0A3Q1LXZ2 A0A3Q1LXZ2_ 17 F1MGR1 F1MGR1_BOVIN 6		1126,51 236,61		0,68028 0,68028		0,05587 0.0558				Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC521568 PE=4 SV Sodium/nucleoside cotransporter OS=Bos taurus OX=9913 GN=SLC28A3 P	636015 55066071	1157454 72995644	228280 124281671	566393 36590295	7201655 70145107	246780 61291653	70527 48294567	105086 68826645	136340 89889042	907416 57815418	379761 80335095	668263 61231348	5438518 52722908	1764562 94254495	192289 66208662	108242 43233342
F1N422 F1N422 BOVIN;Q2 2	-	236,61 95,4		0,68028		.,				Ubiquitin carboxyl-terminal hydrolase MINDY-1 OS=Bos taurus OX=9913 G	215530	439433	164183	177553	162690	223868	48294567 146514	169952	211046	105829	96587	270547	310948	205125	257931	43233342 71500
	-	,-	2,22250	,,	,	.,		•													/					

			116,57			1,24076	0,05558	LL	HL	22938	60S ribosomal protein L28 OS=Bos taurus OX=9913 GN=RPL28 PE=4 SV=1	8937	18182	14399	5956	80567	23316	152985	165286	83630	4548	7199	4869	133367	134032	150070	18806
A4FV54 RAB8A_BOVIN;A0A		-	637,52	-,	-,	1,17785	0,05554	LL	HL	23669	Ras-related protein Rab-8A OS=Bos taurus OX=9913 GN=RAB8A PE=2 SV=1	1490281	907426	1271873	333318	994427	1022840	1588174	2020224	938181	250822	594694	282298	1471683	3388392	2640053	1199162
F1MSQ2 F1MSQ2_BOVIN;A		2	91,04	.,	0,68028	1,05969	0,05553	HL	LL	56740	Receptor protein serine/threonine kinase OS=Bos taurus OX=9913 GN=AC	169023	186168	99195	55660	78266	26293	125870	118622	123760	131741	84480	32835	94223	37115	61710	119890
Q08DI5 RAP2C_BOVIN;A0A	-		345,03		0,68028	1,04255	0,05552	LL	HL	20731	Ras-related protein Rap-2c OS=Bos taurus OX=9913 GN=RAP2C PE=2 SV=1	770145	250712	133633	180723	237494	143674	441792	512193	185701	135390	177824	98861	589205	585319	475241	200393
A0A3Q1NHI6 A0A3Q1NHI6			276,05	.,		1,22051	0,05546	LL	HL	55258	Protein FAM114A2 OS=Bos taurus OX=9913 GN=FAM114A1 PE=4 SV=1	385053	633316	645274	1072746	476738	884263	331244	369591	377278	2182461	750876	808763	144027	690262	410456	655837
A0A3Q1M7E0 A0A3Q1M7E	-	2	81,8	-,	-,	1,28064	0,05532	HL	LL	63777	24-dehydrocholesterol reductase OS=Bos taurus OX=9913 GN=DHCR24 PE	807266	315761	126758	49241	310788	61224	516800	160040	290376	197820	171211	114973	173262	294184	274404	180272
P20000 ALDH2_BOVIN	5	5	268,42	0,82403	0,68028	1,03049	0,05529	HL	LL	56617	Aldehyde dehydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=ALD	213332	478263	240601	512626	2267689	221503	1206959	1265348	345277	814012	221667	821377	1356782	388755	1383149	1721024
A0A3Q1LQ52 A0A3Q1LQ52	2	2	107,1	-,	0,68042	1,0557	0,0552	LL	HL	26217	SEA domain-containing protein OS=Bos taurus OX=9913 PE=4 SV=1	292622	141514	720866	992525	316867	796311	274160	266025	177304	1076566	811060	563645	257698	568999	151494	947055
A0A3Q1M1I0 A0A3Q1M1I0	4	3	173,45	-,	0,68439	1,14292	0,05473	HL	LL	40626	Calcium-binding protein 39 OS=Bos taurus OX=9913 GN=CAB39 PE=4 SV=1	684473	246652	452742	235328	221095	104893	787744	374600	246067	178320	173100	164042	395802	446636	553261	215646
A0A452DIP2 A0A452DIP2_E			132,06			1,0131	0,05473	LL	HL	54619	UDP-glucose 4-epimerase OS=Bos taurus OX=9913 GN=GALE PE=3 SV=1	320420	372030	221721	370036	539211	319069	468201	296443	472684	895673	623137	368712	713483	310971	289607	209266
F6QJJ8 F6QJJ8_BOVIN	2	2	90,21	0,83356	0,68439	1,17622	0,05472	LL	HL	26046	Progesterone receptor membrane component 2 OS=Bos taurus OX=9913	34917	3755	110523	11905	41522	43927	28922	56056	5679	44316	11914	14508	26410	83826	114449	60648
A0A3Q1LKB7 A0A3Q1LKB7	4	2	180,45	0,83508	0,68489	1,09729	0,05463	LL	HL	21628	HRas proto-oncogene, GTPase OS=Bos taurus OX=9913 GN=HRAS PE=4 SV	410253	189053	359557	166697	570103	292610	401637	437495	261525	257619	143754	188979	501192	623364	530861	206110
A0A3Q1MIB0 A0A3Q1MIB0	3	3	248,28	0,83738	0,68603	1,03632	0,0545	LL	HL	180725	IQ motif containing GTPase activating protein 1 OS=Bos taurus OX=9913 G	131747	186543	93591	519818	480190	166164	288076	479448	425475	804512	355905	253022	215985	139587	130530	363143
A0A3Q1LPA4 A0A3Q1LPA4	2	2	63,56	0,8431	0,68942	1,22637	0,05419	LL	HL	93089	Ras GTPase-activating protein 3 OS=Bos taurus OX=9913 GN=RASA3 PE=4	27329	44426	18150	7423	17708	28970	65589	8335	18117	898	7723	15079	88563	17498	56153	8502
Q95M18 ENPL_BOVIN	8	7	585,57	0,84335	0,68942	1,1232	0,05417	HL	LL	92369	Endoplasmin OS=Bos taurus OX=9913 GN=HSP90B1 PE=2 SV=1	324611	554279	649159	357148	981346	403395	471066	1319702	1049491	250192	257521	235952	771545	611369	967063	249244
Q3B7M5 LASP1_BOVIN	4	4	243,19	0,85142	0,69225	1,11134	0,05375	LL	HL	29658	LIM and SH3 domain protein 1 OS=Bos taurus OX=9913 GN=LASP1 PE=2 S ¹	119759	111410	264082	81575	273862	150272	231530	326495	155931	45056	70018	93527	176529	386139	581560	128711
A0A3Q1LZU8 A0A3Q1LZU8	4	4	191,12	0,85431	0,69311	1,0603	0,0536	HL	LL	106854	Glucosidase II alpha subunit OS=Bos taurus OX=9913 GN=GANAB PE=1 SV=	139449	186525	83304	230058	203364	78014	153500	323274	263977	224245	362232	151625	249835	161510	102580	61475
Q58DQ3 RL6_BOVIN;G3N2I	5	5	262,74	0,8603	0,69664	1,05324	0,05331	LL	HL	32670	60S ribosomal protein L6 OS=Bos taurus OX=9913 GN=RPL6 PE=2 SV=3	387265	335045	406913	331498	999404	369817	687478	1096756	816912	279599	91580	212189	1330441	651008	1078816	506048
A0A140T841 A0A140T841_	4	4	373,14	0,86052	0,69664	1,27774	0,0533	LL	HL	21467	Prostamide/prostaglandin F synthase OS=Bos taurus OX=9913 GN=PRXL2E	6248782	2637485	3800557	1846621	2124678	3839946	6912701	4065851	2409100	488719	989879	1963505	7099213	8246535	9887084	3101203
A0A3Q1LXR2 A0A3Q1LXR2	5	3	353,68	0,86283	0,69776	1,04341	0,05319	LL	HL	23476	Ras-related C3 botulinum toxin substrate 1 OS=Bos taurus OX=9913 GN=R.	9740900	2437959	3411918	3591959	2734789	3567453	9582643	4841092	2526178	1834414	1728057	1748809	7436962	7686816	9057722	2291821
A0A3Q1MTL6 A0A3Q1MTL	2	2	90,93	0,86462	0,69817	1,35656	0,0531	HL	LL	54654	T-complex protein 1 subunit theta OS=Bos taurus OX=9913 GN=CCT8 PE=1	21417	23113	58958	5414	60276	45169	26916	64857	24490	5589	10221	2528	39776	78643	66439	8069
A5D7A4 A5D7A4_BOVIN	4	4	163,86	0,86519	0,69817	1,02855	0,05308	HL	LL	25040	RIT1 protein OS=Bos taurus OX=9913 GN=RIT1 PE=2 SV=1	1109904	645398	1326735	256724	537245	765463	2125604	954201	586207	219290	783076	409312	1162747	1449375	1427861	451956
A0A3Q1LMG1 A0A3Q1LMG	3	3	188,6	0,87822	0,70519	1,16063	0,05251	HL	LL	39508	Fructose-bisphosphate aldolase OS=Bos taurus OX=9913 GN=ALDOA PE=1	295743	506708	78493	191423	467996	130242	460598	304904	415221	192709	73116	249471	402306	203777	246143	293013
Q3SZA1 RHOF_BOVIN	5	5	372,32	0,8806	0,70519	1,15967	0,05241	LL	HL	23825	Rho-related GTP-binding protein RhoF OS=Bos taurus OX=9913 GN=RHOF	3375029	1583328	2845201	1265063	1674675	1679069	2320999	3660585	1680545	1058245	1135924	959840	3317892	3968358	5341940	1731751
Q2KJ25 PSD12_BOVIN	2	2	93,12	0,88279	0,70519	1,20444	0,05232	HL	LL	53019	26S proteasome non-ATPase regulatory subunit 12 OS=Bos taurus OX=991	0	0	5989	8137	37584	8671	0	40453	3648	11323	0	469	0	25161	36834	2716
A0A3Q1M739 A0A3Q1M73	3	3	118,54	0,88408	0,70519	1,05789	0,05227	HL	LL	67779	Tyrosine-protein phosphatase non-receptor type OS=Bos taurus OX=9913	56719	92241	121019	45654	132961	79947	40000	188034	99206	117571	31737	94746	33462	52228	155068	70073
A0A3Q1M9J5 A0A3Q1M9J5	6	6	419,89	0,88504	0,70519	1,11895	0,05223	HL	LL	140481	Phospholipid-transporting ATPase OS=Bos taurus OX=9913 GN=ATP8B1 PE	454764	277805	525850	1319248	521579	416568	239745	663339	456912	475349	410222	764338	405337	513167	453319	377330
F1MZY2 F1MZY2 BOVIN;AC	6	6	218,15	0,88515	0,70519	1,08233	0,05223	LL	HL	76703	Glutaminefructose-6-phosphate transaminase 1 OS=Bos taurus OX=9913	55455	117881	185983	59506	341457	239019	40198	391702	311519	51673	37635	67627	133122	286250	403260	92120
A0A452DID1 A0A452DID1	3	3	273,13	0,88629	0,70536	1,13476	0,05218	LL	HL	24628	Translationally-controlled tumor protein OS=Bos taurus OX=9913 GN=TPT	431286	311146	486583	238400	427007	512377	481505	597364	246037	162577	409937	396252	359634	475353	1069283	445596
F1MYV9 F1MYV9 BOVIN	2	2	104,27	0,88825	0,70571	1,10315	0,05211	LL	HL	57891	Oxidative stress responsive kinase 1 OS=Bos taurus OX=9913 GN=OXSR1 P	111537	219305	76397	140033	162147	47550	200694	110520	338761	118404	75929	38196	176839	266903	184882	18453
A0A3Q1LJQ7 A0A3Q1LJQ7_	2	2	86,67	0,8946	0,70748	1,17773	0,05187	HL	LL	51288	Adenylyl cyclase-associated protein OS=Bos taurus OX=9913 PE=3 SV=1	70516	144102	52609	480607	207999	262939	268729	229411	368043	564526	98333	254781	172199	130410	157418	476481
A0A3Q1LQ87 A0A3Q1LQ87	3	3	142.5	0.89576	0.70765	1.67341	0.05183	LL	HL	19061	40S ribosomal protein S16 OS=Bos taurus OX=9913 GN=RPS16 PE=3 SV=1	20396	32932	49158	37092	144561	64666	84890	393074	164076	2945	9204	24551	439754	323666	446472	107181
	6	5	481,07	0,90207	0,70985	1,14577	0,05161	LL	HL	23011	RAB35 protein OS=Bos taurus OX=9913 GN=RAB35 PE=2 SV=1	5413842	3558884	5514725	1795402	3570426	3573476	5403875	6933327	4616260	2162631	2974771	1946661	5908627	10062452	8601597	2822409
Q3T0U2 RL14 BOVIN; G8JK			144,5	0,90215	0,70985	1,20481	0,05161	LL	HL	23421	60S ribosomal protein L14 OS=Bos taurus OX=9913 GN=RPL14 PE=2 SV=3	29627	73115	143426	163139	279116	179708	148641	347918	159993	45466	44637	81970	294250	298108	528606	187002
E1B7R4 E1B7R4 BOVIN	3	3	185.83	0.90502	0.71106	1.82774	0.05152	HL	LL	165948	Eukaryotic translation initiation factor 3 subunit A OS=Bos taurus OX=9913	13353	37585	9630	3629	130891	744	16844	166066	47155	26765	5240	5735	79087	3255	41888	3273
A0A3Q1NNJ3 A0A3Q1NNJ3	2	2	150.21	0.9077	0.71185	1.16084	0.05143	LL	HL	20498	Flavin reductase (NADPH) OS=Bos taurus OX=9913 GN=BLVRB PE=1 SV=1	450904	448480	711736	252787	442653	319550	637190	611359	437625	117079	270789	197254	660097	797974	902811	542319
A0A3Q1MRR6 A0A3Q1MRF	2	2	85.42	0.90957	0.71257	1.02747	0.05138		HL	77769	Protein kinase C delta type OS=Bos taurus OX=9913 GN=PRKCD PE=3 SV=1	79148	85209	117088	24109	254761	170066	74863	160431	99234	130910	31966	47749	184726	229141	230753	46307
F1ML75 F1ML75 BOVIN	3	3	211.43	- ,	., .	1.00355	0.05112		HL	65789	Interleukin 1 receptor type 1 OS=Bos taurus OX=9913 GN=IL1R1 PE=4 SV=	745598	215630	380301	58361	397289	106366	388639	705519	243777	100494	155919	313782	338021	722993	670409	80680
	2		269.91		.,	1.02424	0.05101	HL	LL	34162	Sulfotransferase 1A1 OS=Bos taurus OX=9913 GN=SULT1A1 PE=1 SV=2	1533717	1018439	430070	575273	647941	1286626	2074483	1710008	677953	758940	452774	594304	1411249	1474204	1704938	870575
O3T0001YKT6 BOVIN	9	9	528.37	0.92474	0 71796	1 18641	0.05095		HL	22452	Synaptobrevin homolog YKT6 OS=Bos taurus OX=9913 GN=YKT6 PE=2 SV=	12283736	6914050	8486935	2737061	6564642	5951974	15605423	11402113	7171128	2789022	2900256	5536297	14788419	19778834	19812737	5599113
F1MZK41F1MZK4_BOVIN:A(4	4	246.15	- , -	.,	1.09908	0.05093	н	11	48013	Basic leucine zipper and W2 domains 1 OS=Bos taurus OX=9913 GN=BZW1	73525	120406	139277	55345	149227	186162	20106	163075	95241	111784	25890	41632	86311	147336	140319	35156
F1MDN4 F1MDN4 BOVIN			134.9		-,	1.09843	0.05092	11	HL	34379	60S acidic ribosomal protein PO OS=Bos taurus OX=9913 GN=RPLPO PE=3 :	108239	139643	48168	39881	433943	59372	209528	456019	206837	242329	21019	25863	361377	267095	336399	154890
			182.97	.,	.,	1.00589	0.05077	н	11	46063	Adipocyte plasma membrane-associated protein OS=Bos taurus OX=9913	112246	175274	419612	152248	602221	287990	88349	427553	183186	174469	165899	189745	173762	602271	481100	113073
09N287 DJC12 BOVIN	2		161.32	-,	-,	1.09966	0.05076	11	HL	23254	DnaJ homolog subfamily C member 12 OS=Bos taurus OX=9913 GN=DNAJ	662692	553009	779233	227975	614119	679631	828853	644000	477730	188142	402774	285491	995415	1025403	949184	695447
			122.39			1.35574	0.05072	11	HL	203727	PATJ crumbs cell polarity complex component OS=Bos taurus OX=9913 GN	8516	11964	110349	159947	201602	274898	27756	158115	25447	325898	258921	203180	875	104909	153394	49248
	-	2	94.78	-,	0,71903	1.00339	0.05071	11	HL	40579	Par-6 family cell polarity regulator beta OS=Bos taurus OX=9913 GN=PARD	170169	140383	150835	192186	137603	129066	113725	136947	80876	70440	113171	181484	85039	189993	289262	198635
A0A3011MB51A0A3011MB		2	130.5	-,	.,	1,13623	0.0507	н	LL	103369	AP complex subunit beta OS=Bos taurus OX=9913 GN=AP1B1 PE=3 SV=1	62092	36397	48798	302245	323514	133054	51818	244846	168320	413274	278892	265141	94452	58850	60009	248070
	-	2	79.1	-,	-,	1,14725	0.05052	ш	LL	10/92	40S ribosomal protein S18 OS=Bos taurus OX=9913 GN=RPS18 PE=1 SV=1	31679	12721	56223	18204	104270	33152	648219	268813	113430	129843	6947	7645	238990	160521	232795	73269
	-	-	864.97	-,	0,72369	1 02996	0,05035	LIL LIL	LL	102524	Aminopeptidase OS=Bos taurus OX=9913 GN=NPEPPS PE=1 SV=2	4816886	5507986	2825800	8542255	7511997	3697718	6106691	3707258	6574516	4420679	6006347	11217777	4166073	4446127	4233477	3924586
A0A301LN741A0A301LN74		3	136.89		0,72569	1.08804	0,05045	11	HL	84604	Synaptotagmin like 4 OS=Bos taurus OX=9913 GN=SYTL4 PE=4 SV=1	10655	38783	89265	45748	122660	93096	19573	55534	44339	16748	20518	40239	132745	70810	51770	15721
A0A301M059 A0A301M0		5	392.15	.,	0,72663	1.00557	0,05032		HL	61055	Solute carrier family 3 member 2 OS=Bos taurus OX=9913 GN=SLC3A2 PE=	4051631	4702129	1951235	3290180	2666505	2383447	3078058	2818978	4462594	4360721	4194046	2815376	3472651	1458738	1699089	2141884
A0A3Q1MIQ357A0A3Q1MIQ A0A3Q1M124 A0A3Q1M12	2		76.71			1.02037	0,05033		HL	82169	Calpain-1 catalytic subunit OS=Bos taurus OX=9913 GN=CAPN1 PE=3 SV=1	133907	85921	133620	21600	91739	98255	129835	105240	118952	77205	65897	25149	157103	137812	46779	97201
A0A452DHW7 A0A452DHW			262.01	-,	.,	1,67573	0,05032	LL	LL	29203	Beta-casein OS=Bos taurus OX=9913 GN=CSN2 PE=1 SV=1	97534	2007771	79096	162031	2264924	89589	6989242	57704	56368	2815256	78481	79623	2827077	114269	247073	4475751
Q5E9F1 Q5E9F1 BOVIN	2	2	240.48	.,	.,	1.30732	0.05032	11	HL	27994	B-cell receptor-associated protein 31 OS=Bos taurus OX=9913 GN=BCAP31	451198	265452	488671	163354	471846	772829	623397	848786	432012	73672	321817	181032	967323	1081594	1110385	356075
A0A3O1LHD8 A0A3O1LHD8	5	5	240,48		-,	1,01691	0.05024	HI	LL	81760	Ribosomal protein S6 kinase OS=Bos taurus OX=9913 GN=RPS6KA3 PE=3 S	104229	129253	239472	236689	545320	274318	101932	436799	443996	148753	641194	153347	304185	156054	317987	84606
A6QNL01A6QNL0 BOVIN			315.71	.,	.,	1.07412	0,05025		LL	20207	Monocyte differentiation antigen CD14 OS=Bos taurus OX=9913 GN=CD14	4638270	2979343	6350325	3721216	6554719	8128909	5892880	4351173	3200357	11837650	3958086	10175430	5392445	2534943	4535977	11061551
A0A3Q1M4Y8 A0A3Q1M4Y	4		195.25		-,	2.32315	0.05017	11	HL	3303/ 49150	Phenylalanine-4-hydroxylase OS=Bos taurus OX=9913 GN=PAH PE=4 SV=1	4638270	116136	0350325	2837	20018	0120303	326201	4351173	23644	399	000000	8512	1071624	2334343	22813	5804
F1MMK71F1MMK7 BOVIN			195,25		., .	1 00203	0,05017		LL	33238	GTP-binding protein OS=Bos taurus OX=9913 GN=RRAD PE=3 SV=1	549201	473271	713822	231671	723886	339077	675273	504653	603745	258749	312838	430740	776321	419746	614270	364542
	-	-	1783.41	-,	-,	1,15392	0,05013		LL	191247	Clathrin heavy chain OS=Bos taurus OX=9913 GN=CLTC PE=1 SV=3	2806312	3248922	3618902	5775701	9470983	3353409	3663002	12686089	8860684	7115658	4150534	3881072	6817825	4203970	5626705	4036194
P080371B4GT1 BOVIN	20 .		444 46	-,	.,	1 18155	0,05012		LL	191247	Beta-1.4-galactosvitransferase 1 OS=Bos taurus OX=9913 GN=B4GALT1 PE	1588869	1739075	607706	3690883	2645132	1457021	1384375	6897257	2430393	3505470	1317051	1752733	2110383	4203970	2077978	1497001
A0A301MB571A0A301MB5	4	<i>,</i>	246.41	0,57257	0,72992	1,16135	0,05012	11	HL	23548	Uncharacterized protein OS=Bos taurus OX=9913 GN=RAB6A PE=4 SV=1	2901290	1415275	1712767	1294217	1159246	595167	2614049	2189353	1936809	1483855	761848	697729	2468594	3073542	2999000	1038071
A0A3Q1MBS7 A0A3Q1MBS A0A3Q11 M20 A0A3Q11 M2		4 2	147.8	-,	-,	1,05345	0.05012	11	HL	23348	Histone H4 OS=Bos taurus OX=9913 GN=LOC112445649 PE=3 SV=1	131312	605724	272461	368495	472734	300120	4393523	540515	80707	558267	58462	342889	2315805	518000	570771	3480476
A0A3Q1LM20 A0A3Q1LM2 A0A3O11U21 A0A3O11U21			147,8	-,	-,	1,05345	0,0501		LL	1499/	Histone H4 US=B0s taurus UX=9913 GN=LUC112445649 PE=3 SV=1 SEC24 homolog C, COPII coat complex component OS=Bos taurus OX=991	131312	245809	272461 203069	353024	4/2/34 361434	300120	4393523	540515 250280	273763	558267	58462	342889 452856	2315805	212566	288921	3480476 154633
A0A3Q1L021 A0A3Q1L021 A0A3Q1LW84 A0A3Q1LW8			197,16 95.22	-,	-,	1,03315	0,05007	пс Ш	LL	64814	SEC24 homolog C, COPII coat complex component OS=Bos taurus OX=991 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alph	1/8148 35635	245809 89712	203069 71568	353024 18492	361434 124681	368/21 178177	43636	42439	2/3/63 85785	568317 80000	80296	452856 63561	214831 47493	212566 89545	288921 81122	16317
GSESS4IGSESS4 BOVIN:G3		2 2	95,22		-,	1,21//3	0,05007	HL II	HL	64814 29196	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpr PNPLA domain-containing protein OS=Bos taurus OX=9913 PE=4 SV=2	35635 4793513	89712 6228737	/1568	18492 1015592	124681 2941278	1/81// 7128657	43636	42439	85785 3264784	1058100	80296	63561 2174398	47493	89545 18757204	81122 7503241	16317
Q5E9F9 PRS7_BOVIN;G3	-	-	150,14 202.78	0,98035	-,	1,10037	0,05006		LL	29196 48603	26S proteasome regulatory subunit 7 OS=Bos taurus OX=9913 PE=4 SV=2		50048	15400107 15709	1015592 33818	2941278 169754	26723	4638224 19832	1755639	3264784 96385	1058100 186655	9801	2174398 6149	3010860 126389	24696	62067	3507820
QSE9F9 PRS7_BOVIN F1N632 F1N632_BOVIN	-			0,98412		1,03432	-,	HL		48603		3600	50048 113448	15709	33818 98704	258141	26723	19832 54090	178531 318902	96385	281946	9801 44904	6149 72910	126389	24696 123894	165928	64108
	-	-	147,51	-,	0,73284	1,03722	0,05003	HL	LL	60314	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase 48 kDa sul	51961															64108 37425
P53619 COPD_BOVIN A0A3011 WM0 A0A3011 WI	-		242,92	-,	-,	1,06155	0,05001	LL	HL	5/238	Coatomer subunit delta OS=Bos taurus OX=9913 GN=ARCN1 PE=1 SV=1	35966 195070	74370 43918	119247 159602	44273 21279	234543 103915	83092 56065	66364	419635 153791	209732 86511	145015 9402	24489 14464	23190 41777	223152 237571	172022 283158	246187 299011	37425 28058
	-	2	105,6	-,	-,	-/	0,05001	LL	HL	20239	RAB22A, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB2							272525									
A0A3S5ZPF7 A0A3S5ZPF7_E	3	3	166,28	-,	0,73284	1,2209	0,05	HL	LL	47946	Phosphoserine aminotransferase OS=Bos taurus OX=9913 GN=PSAT1 PE=1	80313	46529	156080	116223	524678	181109	52626	706548	169052	123403	52925	150437	241532	288585	478508	17079
F1MD34 F1MD34_BOVIN	/	/	407,22	-,	0,73284	1,06926	0,05	LL	HL	110052	Family with sequence similarity 129 member B OS=Bos taurus OX=9913 GI	871954	1100561	1254262	986809	1226313	1632583	638203	1219310	1163000	2900082	1520525	1442623	729229	747887	705079	1047508
Q5E9A3 PCBP1_BOVIN;A0A		3	193,51	0,99733	.,	1,01026	0,05	LL	HL	37474	Poly(rC)-binding protein 1 OS=Bos taurus OX=9913 GN=PCBP1 PE=2 SV=1	997824	909816	1230730	932879	1399949	1434999	1245714	1358635	737544	902494	1062392	991519	1439026	1381778	1204509	1037876
Q3MHG1 SPTC1 BOVIN																									0.04570	20005	
		4	223,7	0,99873	-,	1,0697	0,05	LL	HL		Serine palmitoyltransferase 1 OS=Bos taurus OX=9913 GN=SPTLC1 PE=2 S	107179	125574	142391	24067	172365	232817	63842	222425	203438	131112	134511	23838	116656	261579	200954	29690
F1N3B0 F1N3B0_BOVIN;A0			,.	0,99873 0,99975	-,	1,0697 1,0023	0,05 0,05		HL HL		Serine palmitoyltransferase 1 OS=Bos taurus OX=9913 GN=SPTLC1 PE=2 S Nicotinate phosphoribosyltransferase OS=Bos taurus OX=9913 GN=NAPRT	107179 33144	125574 12172	142391 45777	24067 250927	172365 82458	232817 42776	63842 0	222425 31851	203438 56365	131112 109542	134511 238539	23838 130442	116656 0	261579 51928	200954 42123	29690 12311

iO_BP	<pre>_Enrichment_GO_BP_of_15prot_contributing_to_HL_gr Name</pre>		Term frequency w	Term frequency P-	value (fdr) Query with no gene
0:0010873	positive regulation of cholesterol esterification	Any process that increases the frequency, rate or extent of cholest APOA1 APOA4 APOE	23.08 3/13	37.50 3/8	6,0673E-06
0:0034433			23.08 3/13	25.00 3/12 30.00 3/10	6,0673E-06
iO:0034372 iO:0034370			23.08 3/13 23.08 3/13	30.00 3/10	6,0673E-06 6,0673E-06
0:0034434			23.08 3/13	25.00 3/12	6,0673E-06
0:0010872			23.08 3/13	33.33 3/9	6,0673E-06
O:0034435 O:0043691			23.08 3/13 23.08 3/13	25.00 3/12 27.27 3/11	6,0673E-06 6,0673E-06
0:0033700			23.08 3/13		7,00849E-06
O:0045940			23.08 3/13		2,13232E-05
O:0065005 O:0034369			23.08 3/13 23.08 3/13		2,27971E-05 2,60387E-05
D:0034369 D:0034368			23.08 3/13		2,60387E-05
0:1903494			15.38 2/13		2,69778E-05
0:1903496			15.38 2/13		2,69778E-05
D:0034367 D:0071827			23.08 3/13 23.08 3/13		2,77849E-05 5,79248E-05
):1902995			15.38 2/13		5,95205E-05
D:1902994			15.38 2/13		5,95205E-05
0:0071825			23.08 3/13		5,95205E-05
0:0010033 0:0090207		Any process that results in a change in state or activity of a cell or a APOA1 APOA4 APOE BSI Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE	69.23 9/13 23.08 3/13	1	5,95205E-05 5,95205E-05
0:0032374			23.08 3/13		0,000115493
0:0033344			23.08 3/13	6.98 3/43	0,000115493
0:0032371					0,000115493
0:0120009			23.08 3/13		0,000127189
):0097006):0032489			23.08 3/13 15.38 2/13	6.25 3/48 33.33 2/6	0,000139447 0,00021647
0:0046889			23.08 3/13		0,000230753
0:0051385			15.38 2/13	28.57 2/7	0,000282751
0:0042632			23.08 3/13		0,000304784
0:0055092 0:0034380			23.08 3/13 15.38 2/13		0,000309204 0,000335406
):0034380):0051129	• • • • •	I ne non-covalent aggregation and arrangement of proteins and lip APOA1 APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOA4 APOE CLI			0,000335406
0:0019218	regulation of steroid metabolic process		23.08 3/13	4.23 3/71	0,000352439
0:0051006	positive regulation of lipoprotein lipase activity	Any process that activates or increases the activity of the enzyme li APOA1 APOA4	15.38 2/13	22.22 2/9	0,000392726
D:2001140			15.38 2/13		0,000392726
0:0010898 0:0061365			15.38 2/13 15.38 2/13		0,000422255 0,000422255
D:20011385			15.38 2/13		0,000422255
0:0030301	cholesterol transport	The directed movement of cholesterol, cholest-5-en-3-beta-ol, intc APOA1 APOA4 APOE	23.08 3/13	3.80 3/79	0,000422255
0:0042221		Any process that results in a change in state or activity of a cell or a APOA1 APOA4 APOE BSI			0,000422255
D:1905907 D:0006641			15.38 2/13 23.08 3/13		0,000422255 0,000448668
D:0006641 D:0032368			23.08 3/13 23.08 3/13		0,000448668
0:0032488					0,000482255
0:0034375			15.38 2/13		0,000543077
0:0032570			15.38 2/13		0,000543077
D:1905906 D:0098869			15.38 2/13 23.08 3/13		0,000543077 0,000555547
D:0098889 D:0015918			23.08 3/13		0,000552399
D:0010896			15.38 2/13		0,000582178
D:0051004			15.38 2/13		0,000582178
0:0008203			23.08 3/13		0,000582178
O:0015914 O:1902652			23.08 3/13 23.08 3/13	3.03 3/99 2.97 3/101	0,000609081 0,00063511
0:0016125			23.08 3/13		0,000661667
0:1902903		Any process that modulates the frequency, rate or extent of suprar APOA1 APOE CLU CSN15	30.77 4/13		0,000665794
0:0045834			23.08 3/13		0,000665794
0:1990748			23.08 3/13		0,000665794
O:1905952 O:0097237			23.08 3/13 23.08 3/13		0,000740408 0,000740408
0:0034377					0,000760008
D:0006869		The directed movement of lipids into, out of or within a cell, or bet APOA1 APOA4 APOE LBI			0,000760008
D:0006639			23.08 3/13		0,000765313
D:0006638 D:1990000			23.08 3/13		0,000773799
):0031331		The generation of amyloid fibrils, insoluble fibrous protein aggrega APOE CLU Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE CLI	15.38 2/13 30 77 4/13		0,000793252 0,000793252
D:0010875			15.38 2/13		0,000793252
0:0098754			23.08 3/13	2.54 3/118	0,000808629
0:0055088			23.08 3/13		0,000838202
0046890			23.08 3/13		0,000911385
0:0045723 0:0010876		Any process that activates or increases the frequency, rate or exter APOA1 APOA4 Any process in which a lipid is transported to, or maintained in, a sI APOA1 APOA4 APOE LBI	15.38 2/13 30.77 4/13		0,001020122 0,001020122
D:0060416			15.38 2/13		0,001020122
0:0042157	lipoprotein metabolic process	The chemical reactions and pathways involving any conjugated, wa APOA1 APOA4 APOE	23.08 3/13	2.24 3/134	0,00108753
0:0090208			15.38 2/13		0,001096015
0:0002385 0:0055090			15.38 2/13 15.38 2/13		0,001145662 0,001145662
D:0055090 D:0070328		// ····· · · · · · · · · · · · · · · ·	15.38 2/13		0,001145662
):1902904			23.08 3/13	2.16 3/139	0,001145662
0:0009896		Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE CLI			0,001208571
0:0015748			23.08 3/13		0,001208571
D:0050996 D:0050821			15.38 2/13 23.08 3/13		0,001209518 0,001280069
0:0002376		Any process involved in the development or functioning of the imm APOA1 APOA4 APOE CLI			0,001338684
0:0009636	response to toxic substance	Any process that results in a change in state or activity of a cell or a APOA4 APOE CSN1S1	23.08 3/13	1.99 3/151	0,00135265
0:0002251			15.38 2/13	8.00 2/25	0,00135265
):0010874):0032376			15.38 2/13 15.38 2/13	8.00 2/25 7.69 2/26	0,00135265 0,001432643
0:0032378			15.38 2/13		0,001432643
0:0019433			15.38 2/13		0,001529878
0:0045923	positive regulation of fatty acid metabolic process	Any process that activates or increases the frequency, rate or exter APOA1 APOA4	15.38 2/13		0,001873565
0:0033993		Any process that results in a change in state or activity of a cell or a APOA4 CSN1S1 CSN1S2			0,001891867
):0032355):0030258			15.38 2/13 23.08 3/13		0,002089795 0,002308728
0030258			15.38 2/13		0,002493052
:1902653	secondary alcohol biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOE	15.38 2/13	5.56 2/36	0,002493052
0:0042304			15.38 2/13		0,002493052
0006695			15.38 2/13		0,002493052
D:0046464 D:0015850			15.38 2/13 23.08 3/13		0,002493052 0,002571093
D:0015850 D:0016126			23.08 3/13 15.38 2/13		0,002872222
0:0070887		Any process that results in a change in state or activity of a cell (in 1 APOA1 APOA4 APOE BSI			0,002882097
D:0031960	response to corticosteroid	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2	15.38 2/13	4.88 2/41	0,003115623
0:0043113			15.38 2/13	4.76 2/42	0,00323936
	regulation of inflammatory response		23.08 3/13		0,003251371 0,003333248
D:0050727	positivo rogulation of linear anti-it				1110133333/46
D:0050727 D:0060193			15.38 2/13 23.08 3/13		
D:0050727 D:0060193 D:0008202	steroid metabolic process	The chemical reactions and pathways involving steroids, compound APOA1 APOA4 APOE	15.38 2/13 23.08 3/13 23.08 3/13	1.31 3/229	0,003686906 0,003747571
D:0050727	steroid metabolic process regulation of protein stability	The chemical reactions and pathways involving steroids, compound APOA1 APOA4 APOE Any process that affects the structure and integrity of a protein, alt APOA1 CLU CSN151	23.08 3/13	1.31 3/229 1.30 3/231	0,003686906

GO:0019216 GO:0031329	regulation of lipid metabolic process regulation of cellular catabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE CL	23.08 3/13 30.77 4/13	1.22 3/246 0.65 4/613	0,004346252 0,004476717
GO:0060191	regulation of lipase activity	Any process that modulates the frequency, rate or extent of lipase APOA1 APOA4	15.38 2/13	3.85 2/52	0,004503354
GO:0032370 GO:0046503	positive regulation of lipid transport glycerolipid catabolic process	Any process that activates or increases the frequency, rate or exter APOA1 APOE The chemical reactions and pathways resulting in the breakdown o APOA1 APOA4	15.38 2/13 15.38 2/13	3.85 2/52 3.70 2/54	0,004503354 0,004815256
GO:0097435	supramolecular fiber organization	A process that is carried out at the cellular level which results in the APOA1 APOE CLU CSN1		0.63 4/636	0,004972967
GO:0006066 GO:1903000	alcohol metabolic process	The chemical reactions and pathways involving alcohols, any of a cl APOA1 APOA4 APOE Any process that modulates the frequency, rate or extent of lipid tr APOE	23.08 3/13 7.69 1/13	1.13 3/266 100.00 1/1	0,004986179 0,004986179
GO:1905000 GO:1905853	regulation of heparan sulfate binding	Any process that modulates the frequency, rate or extent of hepar, APOE	7.69 1/13	100.00 1/1	0,004986179
GO:1905855	positive regulation of heparan sulfate binding	Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	100.00 1/1	0,004986179
GO:1905858 GO:0060265	regulation of heparan sulfate proteoglycan binding positive regulation of respiratory burst involved in infla	Any process that modulates the frequency, rate or extent of hepar; APOE a Any process that increases the rate, frequency or extent of a phase LBP	7.69 1/13 7.69 1/13	100.00 1/1 100.00 1/1	0,004986179 0,004986179
GO:0090731	cellular response to very-low-density lipoprotein partie	c Any process that results in a change in state or activity of a cell (in 1 APOE	7.69 1/13	100.00 1/1	0,004986179
GO:0045919 GO:1903002	positive regulation of cytolysis	Any process that activates or increases the frequency, rate or exter LBP n Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13 7.69 1/13	100.00 1/1 100.00 1/1	0,004986179 0,004986179
GO:1905890		Any process that includes of increases the nequency, rate of externa of enterna of enterna of enterna of enterna of the second s	7.69 1/13	100.00 1/1	0,004986179
GO:0006952	defense response	Reactions, triggered in response to the presence of a foreign body APOA1 APOA4 APOE CS		0.43 5/1172	0,004986179
GO:0042268 GO:0150201	regulation of cytolysis positive regulation of transport across blood-brain bar	Any process that modulates the frequency, rate or extent of the ru LBP r Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13 7.69 1/13	100.00 1/1 100.00 1/1	0,004986179 0,004986179
GO:0150200	regulation of transport across blood-brain barrier	Any process that modulates the frequency, rate or extent of transp APOE	7.69 1/13	100.00 1/1	0,004986179
GO:0032805		Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13 7.69 1/13	100.00 1/1	0,004986179
GO:1905860 GO:0071831	intermediate-density lipoprotein particle clearance	n Any process that activates or increases the frequency, rate or exter APOE The process in which a intermediate-density lipoprotein particle is APOE	7.69 1/13	100.00 1/1 100.00 1/1	0,004986179 0,004986179
GO:0016042	lipid catabolic process	The chemical reactions and pathways resulting in the breakdown o APOA1 APOA4 APOE	23.08 3/13	1.06 3/284	0,00549518
GO:0051241 GO:0045807	negative regulation of multicellular organismal process positive regulation of endocytosis	s Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOA4 APOE LB Any process that activates or increases the frequency, rate or exter APOE CLU	130.77 4/13 15.38 2/13	0.58 4/686 3.12 2/64	0,005703479 0,005737915
GO:0016192	vesicle-mediated transport	A cellular transport process in which transported substances are m APOA1 APOE CD5L CLU		0.39 5/1276	0,006401248
GO:0019217 GO:0019915	regulation of fatty acid metabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 The accumulation and maintenance in cells or tissues of lipids, com APOA1 APOE	15.38 2/13 15.38 2/13	2.90 2/69 2.90 2/69	0,006524187 0,006524187
GO:0019915 GO:0006955	lipid storage immune response	Any immune system process that functions in the calibrated responder APOA1 APOA APOA1 APOA1 APOA		0.39 5/1288	0,006540511
GO:1905954	positive regulation of lipid localization	Any process that activates or increases the frequency, rate or exter APOA1 APOE	15.38 2/13	2.82 2/71	0,006809794
GO:0009894 GO:0035023	regulation of catabolic process regulation of Rho protein signal transduction	Any process that modulates the frequency, rate, or extent of the cl APOA1 APOA4 APOE CL Any process that modulates the frequency, rate or extent of Rho pi APOA1 APOE	130.77 4/13	0.55 4/732 2.63 2/76	0,006923904 0,007689011
GO:1901654	response to ketone	A response that results in a state of tolerance to ketone. CSN1S1 CSN1S2	15.38 2/13	2.60 2/77	0,007837493
GO:0034444	regulation of plasma lipoprotein oxidation	Any process that modulates the frequency, rate or extent of lipopri APOA4	7.69 1/13	50.00 1/2	0,008421342
GO:1903365 GO:2000822	regulation of fear response regulation of behavioral fear response	Any process that modulates the frequency, rate or extent of fear re APOE Any process that modulates the frequency, rate or extent of behav APOE	7.69 1/13 7.69 1/13	50.00 1/2 50.00 1/2	0,008421342 0,008421342
GO:0002434	immune complex clearance	A process directed at removing immune complexes from the body. CLU	7.69 1/13	50.00 1/2	0,008421342
GO:0050896 GO:0034445	response to stimulus	Any process that results in a change in state or activity of a cell or a APOA1 APOA4 APOE BS Any process that stops, prevents, or reduces the frequency, rate or APOA4	84.62 11/13 7.69 1/13	0.14 11/7978 50.00 1/2	0,008421342 0,008421342
GO:0034445 GO:0006982	negative regulation of plasma lipoprotein oxidation response to lipid hydroperoxide	Any process that isobs, prevents, or reduces the frequency, rate of APOA4 Any process that results in a change in state or activity of a cell or a APOA4	7.69 1/13	50.00 1/2	0,008421342
GO:0046486	glycerolipid metabolic process	The chemical reactions and pathways involving glycerolipids, any li APOA1 APOA4 APOE	23.08 3/13	0.86 3/347	0,008421342
GO:0002415 GO:0015920	immunoglobulin transcytosis in epithelial cells mediate lipopolysaccharide transport	e The process of transporting polymeric IgA and polymeric IgM immι PIGR The directed movement of lipopolysaccharides into, out of or withi LBP	7.69 1/13 7.69 1/13	50.00 1/2 50.00 1/2	0,008421342 0,008421342
GO:0010877	lipid transport involved in lipid storage	The directed movement of lipids into cells that is part of their accu APOE	7.69 1/13	50.00 1/2	0,008421342
GO:0002414	immunoglobulin transcytosis in epithelial cells	The process of transporting immunoglobulin, via transcytosis, from PIGR	7.69 1/13	50.00 1/2	0,008421342
GO:0097114 GO:1902952	NMDA glutamate receptor clustering positive regulation of dendritic spine maintenance	The receptor clustering process in which N-methyl-D-aspartate (NN APOE Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13 7.69 1/13	50.00 1/2 50.00 1/2	0,008421342 0,008421342
GO:0062013	positive regulation of small molecule metabolic proces	Any process that activates or increases the frequency, rate or exter APOA1 APOA4	15.38 2/13	2.33 2/86	0,008854576
GO:0097305 GO:0098542	response to alcohol defense response to other organism	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2 Reactions triggered in response to the presence of another organis APOA4 APOE CSN1S2 LE	15.38 2/13	2.30 2/87 0.49 4/812	0,009004036 0,009009757
GO:0098542 GO:0043534	blood vessel endothelial cell migration	The orderly movement of an endothelial cell into the extracellular (APOA) APOE	15.38 2/13	2.22 2/90	0,009512196
GO:0050728	negative regulation of inflammatory response	Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE	15.38 2/13	2.20 2/91	0,00966384
GO:0031347 GO:0042158	regulation of defense response lipoprotein biosynthetic process	Any process that modulates the frequency, rate or extent of a defe APOA1 APOE LBP The chemical reactions and pathways resulting in the formation of APOA1 APOE	23.08 3/13 15.38 2/13	0.80 3/376 2.08 2/96	0,010133212 0,010550927
GO:1990266	neutrophil migration	The movement of a neutrophil within or between different tissues GP2 LBP	15.38 2/13	2.08 2/96	0,010550927
GO:0060627 GO:0010565	regulation of vesicle-mediated transport regulation of cellular ketone metabolic process	Any process that modulates the rate, frequency, or extent of vesicl APOA1 APOE CLU Any process that modulates the chemical reactions and pathways i APOA1 APOA4	23.08 3/13 15.38 2/13	0.78 3/385 2.04 2/98	0,01065243 0,010860945
GO:0010585 GO:0061771	response to caloric restriction	A change in state or activity of a cell or an organism (in terms of mcAPOE	7.69 1/13	33.33 1/3	0,010860945
GO:0071830	triglyceride-rich lipoprotein particle clearance	The process in which a triglyceride-rich lipoprotein particle is remo APOE	7.69 1/13	33.33 1/3	0,011551973
GO:1901615 GO:0034382	organic hydroxy compound metabolic process chylomicron remnant clearance	The chemical reactions and pathways involving organic hydroxy col APOA1 APOA4 APOE The process in which a chylomicron remnant is removed from the I APOE	23.08 3/13 7.69 1/13	0.75 3/398 33.33 1/3	0,011551973 0,011551973
GO:0034441	plasma lipoprotein particle oxidation	The modification of a lipid or protein within a plasma lipoprotein p: APOA4	7.69 1/13	33.33 1/3	0,011551973
GO:0051716	cellular response to stimulus	Any process that results in a change in state or activity of a cell (in 1 APOA1 APOA4 APOE BS		0.15 10/6878	0,012172433
GO:0080134 GO:0046165	regulation of response to stress alcohol biosynthetic process	Any process that modulates the frequency, rate or extent of a resp APOA1 APOE CLU LBP The chemical reactions and pathways resulting in the formation of APOA1 APOE	30.77 4/13 15.38 2/13	0.44 4/909 1.83 2/109	0,012591759 0,012797411
GO:1903364		s Any process that activates or increases the frequency, rate or exter APOE CLU	15.38 2/13	1.75 2/114	0,013748188
GO:0001935 GO:0007266	endothelial cell proliferation Rho protein signal transduction	The multiplication or reproduction of endothelial cells, resulting in APOA1 APOE A series of molecular signals within the cell that are mediated by a APOA1 APOE	15.38 2/13 15.38 2/13	1.75 2/114 1.75 2/114	0,013748188 0,013748188
GO:0007200	brainstem development	The progression of the brainstem from its formation to the mature CNTFR	7.69 1/13	25.00 1/4	0,013826807
GO:0032802		c The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13	25.00 1/4	0,013826807
GO:0097530 GO:0045541	granulocyte migration negative regulation of cholesterol biosynthetic process	The movement of a granulocyte within or between different tissue GP2 LBP s Any process that stops, prevents, or reduces the frequency, rate or APOE	15.38 2/13 7.69 1/13	1.69 2/118 25.00 1/4	0,013826807 0,013826807
GO:1900223	positive regulation of amyloid-beta clearance	Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	25.00 1/4	0,013826807
GO:0090206 GO:0032799	negative regulation of cholesterol metabolic process	Any process that decreases the rate, frequency, or extent of choles APOE o The chemical reactions and pathways involving low-density lipopro APOE	7.69 1/13 7.69 1/13	25.00 1/4 25.00 1/4	0,013826807 0,013826807
GO:0032733 GO:0010903		r Any process that decreases the rate, frequency or extent of very-lo APOA1	7.69 1/13	25.00 1/4	0,013826807
GO:0060264		Any process that modulates the rate, frequency or extent of a phas LBP	7.69 1/13	25.00 1/4	0,013826807
GO:0044283 GO:0006694	small molecule biosynthetic process steroid biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4 APOE The chemical reactions and pathways resulting in the formation of APOA1 APOE	23.08 3/13 15.38 2/13	0.69 3/437 1.72 2/116	0,013826807 0,013826807
GO:0106119	negative regulation of sterol biosynthetic process	Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	25.00 1/4	0,013826807
GO:2000646 GO:0032803	positive regulation of receptor catabolic process	Any process that activates or increases the frequency, rate or exter APOE (Any process that modulates the frequency, rate or extent of the ch APOE	7.69 1/13 7.69 1/13	25.00 1/4 25.00 1/4	0,013826807 0,013826807
GO:0002252	immune effector process	Any process of the immune system that executes a component of a APOA1 CLU LBP	23.08 3/13	0.66 3/454	0,014705774
GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4	15.38 2/13	1.61 2/124	0,014907769
GO:0006897 GO:0006954	endocytosis inflammatory response	A vesicle-mediated transport process in which cells take up extern: APOE CD5L CLU The immediate defensive reaction (by vertebrate tissue) to infectic APOA1 APOE LBP	23.08 3/13 23.08 3/13	0.64 3/466 0.64 3/472	0,015675041 0,016031837
GO:0045088	regulation of innate immune response	Any process that modulates the frequency, rate or extent of the ini APOE LBP	15.38 2/13	1.54 2/130	0,016031837
GO:0030100 GO:0097688	regulation of endocytosis glutamate receptor clustering	Any process that modulates the frequency, rate or extent of endoc APOE CLU The neurotransmitter-gated ion channel clustering process in whic APOE	15.38 2/13 7.69 1/13	1.54 2/130 20.00 1/5	0,016031837 0,016203623
GO:0037088 GO:0010901		Any process that modulates the rate, frequency or extent of very-k APOA1	7.69 1/13	20.00 1/5	0,016203623
GO:1990379	lipid transport across blood-brain barrier	The directed movement of lipid molecules passing through the blo APOE	7.69 1/13	20.00 1/5	0,016203623
GO:0034447 GO:0097113	very-low-density lipoprotein particle clearance AMPA glutamate receptor clustering	The process in which a very-low-density lipoprotein particle is rem APOE The glutamate receptor clustering process in which alpha-amino-3- APOE	7.69 1/13 7.69 1/13	20.00 1/5 20.00 1/5	0,016203623 0,016203623
GO:0002536	respiratory burst involved in inflammatory response	A phase of elevated metabolic activity, during which oxygen consul LBP	7.69 1/13	20.00 1/5	0,016203623
GO:0060354		Any process that decreases the rate, frequency or extent of cell ad APOA1	7.69 1/13	20.00 1/5	0,016203623
GO:1901700 GO:0051128	response to oxygen-containing compound regulation of cellular component organization	Any process that results in a change in state or activity of a cell or a APOA4 CSN1S1 CSN1S2 Any process that modulates the frequency, rate or extent of a proc APOA1 APOA4 APOE CL		0.39 4/1028 0.29 5/1732	0,016724838 0,016729878
GO:0051707	response to other organism	Any process that results in a change in state or activity of a cell or a APOA4 APOE CSN1S2 LE	3 30.77 4/13	0.38 4/1066	0,018390714
GO:0002232 GO:1902950	leukocyte chemotaxis involved in inflammatory respon regulation of dendritic spine maintenance	h: The movement of an immune cell in response to an external stimul LBP Any process that modulates the frequency, rate or extent of dendri APOE	7.69 1/13 7.69 1/13	16.67 1/6 16.67 1/6	0,018390714 0,018390714
GO:1902950 GO:0034115	regulation of denaritic spine maintenance negative regulation of heterotypic cell-cell adhesion	Any process that modulates the frequency, rate or extent of denar APOE Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	16.67 1/6 16.67 1/6	0,018390714 0,018390714
GO:0031348	negative regulation of defense response	Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE	15.38 2/13	1.37 2/146	0,018390714
GO:0060267 GO:0090209	positive regulation of respiratory burst negative regulation of triglyceride metabolic process	Any process that increases the rate frequency or extent of a phase LBP Any process that decreases the frequency, rate or extent of the cht APOE	7.69 1/13 7.69 1/13	16.67 1/6 16.67 1/6	0,018390714 0,018390714
GO:0070587	regulation of cell-cell adhesion involved in gastrulation	Any process that modulates the frequency, rate, or extent of attack APOA1	7.69 1/13	16.67 1/6	0,018390714
GO:0043207 GO:1900272	response to external biotic stimulus	Any process that results in a change in state or activity of a cell or a APOA4 APOE CSN1S2 LE	3 30.77 4/13 7.69 1/13	0.37 4/1068 16.67 1/6	0,018390714 0,018390714
GO:1900272 GO:0002682	regulation of long-term synaptic potentiation regulation of immune system process	Any process that stops, prevents or reduces the frequency, rate or APOE Any process that modulates the frequency, rate, or extent of an im APOA1 APOE LBP PIGR		16.67 1/6 0.37 4/1077	0,018390714 0,018724267
GO:0008610	lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4 APOE	23.08 3/13	0.57 3/525	0,019577955
GO:0048545 GO:0072330	response to steroid hormone monocarboxylic acid biosynthetic process	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2 The chemical reactions and pathways resulting in the formation of APOA1 APOA4	15.38 2/13 15.38 2/13	1.32 2/152 1.31 2/153	0,019628779 0,01963209
GO:0061136	regulation of proteasomal protein catabolic process	Any process that modulates the rate, frequency, or extent of the cl APOE CLU	15.38 2/13	1.31 2/153	0,01963209
GO:0009607 GO:1904729	response to biotic stimulus regulation of intestinal lipid absorption	Any process that results in a change in state or activity of a cell or a APOA4 APOE CSN152 LE Any process that modulates the frequency, rate or extent of intesti APOA1	30.77 4/13 7.69 1/13	0.36 4/1098 14.29 1/7	0,01963209 0,020249368
00.1504/29	reparation of intestinal lipit absorption	, any process that modulates the nequency, rate or extent of Intesti APOAL	,.0,1/15	17.23 1/1	0,020243308

GO:0070391	response to lipoteichoic acid regulation of receptor catabolic process	Any process that results in a change in state or activity of an organi LBP Any process that modulates the frequency, rate or extent of recept APOE	7.69 1/13	14.29 1/7	0,020249368
GO:2000644 GO:0070586	cell-cell adhesion involved in gastrulation	The attachment of one cell to another cell affecting gastrulation. APOA1	7.69 1/13 7.69 1/13	14.29 1/7 14.29 1/7	0,020249368 0,020249368
GO:0070120		A series of molecular signals initiated by the binding of a ciliary neu CNTFR	7.69 1/13	14.29 1/7	0,020249368
GO:0030300	regulation of intestinal cholesterol absorption	Any process that modulates the frequency, rate or extent of absor; APOA1	7.69 1/13	14.29 1/7	0,020249368
GO:0071223	cellular response to lipoteichoic acid	Any process that results in a change in state or activity of a cell (in I LBP	7.69 1/13	14.29 1/7	0,020249368
GO:0046578	regulation of Ras protein signal transduction	Any process that modulates the frequency, rate or extent of Ras pr APOA1 APOE	15.38 2/13	1.25 2/160	0,020677805
GO:0045087	innate immune response	Innate immune responses are defense responses mediated by gerr APOA4 APOE LB		0.54 3/558	0,021945498
GO:0097529	myeloid leukocyte migration	The movement of a myeloid leukocyte within or between different GP2 LBP	15.38 2/13	1.20 2/166	0,022026717
GO:0044093 GO:0043542	positive regulation of molecular function endothelial cell migration	Any process that activates or increases the rate or extent of a mole APOA1 APOA4 A The orderly movement of an endothelial cell into the extracellular I APOA1 APOE	15.38 2/13	0.35 4/1149 1.18 2/169	0,022040865 0,02261672
GO:0009967	positive regulation of signal transduction	Any process that activates or increases the frequency, rate or exter APOA1 APOE CL		0.34 4/1161	0,022685293
GO:0042180	cellular ketone metabolic process	The chemical reactions and pathways involving any of a class of org APOA1 APOA4	15.38 2/13	1.18 2/170	0,022687777
GO:0006950	response to stress	Any process that results in a change in state or activity of a cell or a APOA1 APOA4 A	APOE CLI 46.15 6/13	0.21 6/2809	0,022750495
GO:0044419		Any process evolved to enable an interaction with an organism of a APOA4 APOE CS		0.34 4/1167	0,022822023
GO:0006898	receptor-mediated endocytosis	An endocytosis process in which cell surface receptors ensure spec APOE CLU	15.38 2/13	1.16 2/173	0,023098847
GO:0051050 GO:1903050	positive regulation of transport	Any process that activates or increases the frequency, rate or exter APOA1 APOE CL	U 23.08 3/13 15.38 2/13	0.52 3/576 1.15 2/174	0,023098847 0,023254174
GO:0055089	fatty acid homeostasis	Any process that modulates the frequency, rate or extent of protec APOE CLU Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	11.11 1/9	0,023234174
GO:0035376	sterol import	The directed movement of a sterol into a cell or organelle. Sterols ¿ APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0001818	negative regulation of cytokine production	Any process that stops, prevents, or reduces the rate of productior APOA1 LBP	15.38 2/13	1.10 2/181	0,023392718
GO:0032490	detection of molecule of bacterial origin	The series of events in which a stimulus from a molecule of bacteri LBP	7.69 1/13	11.11 1/9	0,023392718
GO:0070508	cholesterol import	The directed movement of cholesterol into a cell or organelle. APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0034384	high-density lipoprotein particle clearance	The process in which a high-density lipoprotein particle is removed APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0016127 GO:1901617	sterol catabolic process organic hydroxy compound biosynthetic process	The chemical reactions and pathways resulting in the breakdown o APOE The chemical reactions and pathways resulting in the formation of APOA1 APOE	7.69 1/13 15.38 2/13	11.11 1/9 1.14 2/175	0,023392718 0,023392718
GO:0045732	positive regulation of protein catabolic process	The chemical reactions and pathways resulting in the formation of APOA1 APOE Any process that activates or increases the frequency, rate or exter APOE CLU	15.38 2/13	1.11 2/180	0,023392718
GO:0051049	regulation of transport	Any process that modulates the frequency, rate or extent of the dii APOA1 APOA4 A		0.33 4/1201	0,023392718
GO:0002679	respiratory burst involved in defense response	A phase of elevated metabolic activity, during which oxygen consul LBP	7.69 1/13	11.11 1/9	0,023392718
GO:0001967	suckling behavior	Specific behavior of a newborn or infant mammal that results in the CNTFR	7.69 1/13	11.11 1/9	0,023392718
GO:1904478	regulation of intestinal absorption	Any process that modulates the frequency, rate or extent of intesti APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0006707	cholesterol catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0016477 GO:0006810	cell migration transport	The controlled self-propelled movement of a cell from one site to a APOA1 APOE GF The directed movement of substances (such as macromolecules, si APOA1 APOA4 A		0.33 4/1202 0.18 7/3886	0,023392718 0,023392718
GO:0060353	regulation of cell adhesion molecule production	Any process that modulates the rate, frequency or extent of cell ad APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0072578	neurotransmitter-gated ion channel clustering	The receptor clustering process in which neurotransmitter-gated ic APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0034374	low-density lipoprotein particle remodeling	The acquisition, loss or modification of a protein or lipid within a lo APOE	7.69 1/13	10.00 1/10	0,024955793
GO:0009605	response to external stimulus	Any process that results in a change in state or activity of a cell or a APOA1 APOA4 A	APOE CSI 38.46 5/13	0.25 5/2004	0,024955793
GO:0044242	cellular lipid catabolic process	The chemical reactions and pathways resulting in the breakdown o APOA1 APOA4	15.38 2/13	1.06 2/188	0,024955793
GO:0034145		Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	10.00 1/10	0,024955793
GO:1900221 GO:0106118	regulation of amyloid-beta clearance regulation of sterol biosynthetic process	Any process that modulates the frequency, rate or extent of amylo APOE Any process that modulates the frequency, rate or extent of a ster(APOE	7.69 1/13 7.69 1/13	10.00 1/10 10.00 1/10	0,024955793 0,024955793
GO:0045540	regulation of cholesterol biosynthetic process	Any process that modulates the frequency, rate of extent of a steri Ar De	7.69 1/13	10.00 1/10	0,024955793
GO:0050776	regulation of immune response	Any process that modulates the frequency, rate or extent of the im APOE LBP PIGR	23.08 3/13	0.49 3/616	0,02507701
GO:0061024	membrane organization	A process which results in the assembly, arrangement of constitue APOA1 APOA4 A		0.48 3/620	0,025437538
GO:0051056		Any process that modulates the frequency, rate or extent of small (APOA1 APOE	15.38 2/13	1.04 2/193	0,025523705
GO:0032879	regulation of localization	Any process that modulates the frequency, rate or extent of any pr APOA1 APOA4 A		0.24 5/2055	0,0261192
GO:0044794	positive regulation by host of viral process	A process in which a host organism activates or increases the frequ APOE	7.69 1/13	9.09 1/11	0,0261192
GO:0002523 GO:0033194	response to hydroperoxide	The movement of a leukocyte within or between different tissues a LBP Any process that results in a change in state or activity of a cell or a APOA4	7.69 1/13 7.69 1/13	9.09 1/11 9.09 1/11	0,0261192 0,0261192
GO:1902931	negative regulation of alcohol biosynthetic process	Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	9.09 1/11	0,0261192
GO:0051234	establishment of localization	Any process that localizes a substance or cellular component. This APOA1 APOA4 A		0.17 7/4033	0,0261192
GO:1903362	regulation of cellular protein catabolic process	Any process that modulates the frequency, rate or extent of cellula APOE CLU	15.38 2/13	1.02 2/196	0,0261192
GO:0097062	dendritic spine maintenance	The organization process that preserves a dendritic spine in a stabl APOE	7.69 1/13	9.09 1/11	0,0261192
GO:0030299	intestinal cholesterol absorption	Uptake of cholesterol into the blood by absorption from the small i APOA1	7.69 1/13	9.09 1/11	0,0261192
GO:0060263	regulation of respiratory burst	Any process that modulates the rate frequency or extent of a phasi LBP The modification of peptidyl-methionine. APOA1	7.69 1/13	9.09 1/11	0,0261192
GO:0018206 GO:0032101	peptidyl-methionine modification regulation of response to external stimulus	The modification of peptidyl-methionine. APOA1 Any process that modulates the frequency, rate or extent of a resp APOA1 APOE LB	7.69 1/13 P 23.08 3/13	9.09 1/11 0.47 3/642	0,0261192 0,026741073
GO:0010647	positive regulation of cell communication	Any process that increases the frequency, rate or extent of a resp Al OAT ALOE LE Any process that increases the frequency, rate or extent of cell con APOA1 APOE CL		0.31 4/1286	0,027281672
GO:0060352	cell adhesion molecule production	The appearance of a cell adhesion molecule due to biosynthesis or APOA1	7.69 1/13	8.33 1/12	0,027681859
GO:0051044		Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	8.33 1/12	0,027681859
GO:0043117	positive regulation of vascular permeability	Any process that increases the extent to which blood vessels can b APOE	7.69 1/13	8.33 1/12	0,027681859
GO:1902430	negative regulation of amyloid-beta formation	Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	8.33 1/12	0,027681859
GO:0023056 GO:0038093	positive regulation of signaling Fc receptor signaling pathway	Any process that activates, maintains or increases the frequency, ri APOA1 APOE CL	U LBP 30.77 4/13 7.69 1/13	0.31 4/1293 8.33 1/12	0,027681859 0,027681859
GO:0038093 GO:0010243	response to organonitrogen compound	A series of molecular signals initiated by the binding of the Fc porti PIGR Any process that results in a change in state or activity of a cell or a APOE CSN1S1 C		0.46 3/658	0,027842254
GO:0010245	cellular response to cytokine stimulus	Any process that results in a change in state of activity of a cell (in 1 APOA1 BSPRY C		0.45 3/660	0,027980979
GO:0002831	regulation of response to biotic stimulus	Any process that modulates the frequency, rate, or extent of a rest APOE LBP	15.38 2/13	0.95 2/211	0,028067229
GO:0035641	locomotory exploration behavior	The specific movement from place to place of an organism in respc APOE	7.69 1/13	7.69 1/13	0,029182936
GO:0044241	lipid digestion	The whole of the physical, chemical, and biochemical processes cal APOA1	7.69 1/13	7.69 1/13	0,029182936
GO:0018158	protein oxidation	The modification of a protein amino acid by oxidation. APOA1	7.69 1/13	7.69 1/13	0,029182936
GO:0098856 GO:0010544	intestinal lipid absorption negative regulation of platelet activation	Any process in which lipids are taken up from the contents of the ir APOA1 Any process that decreases the rate or frequency of platelet actival APOE	7.69 1/13 7.69 1/13	7.69 1/13 7.69 1/13	0,029182936 0,029182936
GO:0010232	vascular transport	The directed movement of substances, into, out of or within a cell, APOE	7.69 1/13	7.14 1/14	0,030604986
GO:0150104	transport across blood-brain barrier	The directed movement of substances (e.g. macromolecules, small APOE	7.69 1/13	7.14 1/14	0,030604986
GO:0055091	phospholipid homeostasis	Any process involved in the maintenance of an internal steady stat APOA1	7.69 1/13	7.14 1/14	0,030604986
GO:0048870	cell motility	Any process involved in the controlled self-propelled movement of APOA1 APOE GF		0.30 4/1350	0,030604986
GO:0032691	negative regulation of interleukin-1 beta production	Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	7.14 1/14	0,030604986
GO:0051000 GO:0051674	positive regulation of nitric-oxide synthase activity localization of cell	Any process that activates or increases the activity of the enzyme r APOE Any process in which a cell is transported to, and/or maintained in, APOA1 APOE GF	7.69 1/13 2 LBP 30.77 4/13	7.14 1/14 0.30 4/1350	0,030604986 0,030604986
GO:0045056	transcytosis	The directed movement of endocytosed material through the cell a PIGR	7.69 1/13	7.14 1/14	0,030604986
GO:0051179	localization	Any process in which a cell, a substance, or a cellular entity, such a APOA1 APOA4 A		0.15 8/5413	0,030904237
GO:0043434	response to peptide hormone	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2	15.38 2/13	0.87 2/229	0,031271859
GO:0010804		Any process that decreases the rate or extent of the tumor necrosi APOA1	7.69 1/13	6.67 1/15	0,032055113
GO:0002281	macrophage activation involved in immune response	A change in morphology and behavior of a macrophage resulting fr LBP	7.69 1/13	6.67 1/15	0,032055113
GO:0043032 GO:0030325	positive regulation of macrophage activation adrenal gland development	Any process that stimulates, induces or increases the rate of macrc LBP The process whose specific outcome is the progression of the adre APOA1	7.69 1/13 7.69 1/13	6.67 1/15 6.67 1/15	0,032055113 0,032055113
GO:1902992		Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	6.67 1/15	0,032055113
GO:0034097	response to cytokine	Any process that results in a change in state or activity of a cell or a APOA1 BSPRY C		0.42 3/713	0,032140446
GO:0010631	epithelial cell migration	The orderly movement of an epithelial cell from one site to anothe APOA1 APOE	15.38 2/13	0.85 2/235	0,032140446
GO:0090132	epithelium migration	The process in which the population of cells that make up an epith APOA1 APOE	15.38 2/13	0.84 2/237	0,032564831
GO:0046394	carboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4	15.38 2/13	0.84 2/239	0,032990424
GO:0007263	nitric oxide mediated signal transduction	Any intracellular signal transduction in which the signal is passed o APOE Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	6.25 1/16	0,033065378
GO:0002719 GO:0002227	innate immune response in mucosa	Any process of the innate immune response that takes place in the APOA1	7.69 1/13 7.69 1/13	6.25 1/16 6.25 1/16	0,033065378 0,033065378
GO:0002227 GO:0016053	organic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4	15.38 2/13	0.83 2/242	0,033065378
GO:0008283	cell population proliferation	The multiplication or reproduction of cells, resulting in the expansi APOA1 APOE CL		0.28 4/1409	0,033065378
GO:0019430	removal of superoxide radicals	Any process, acting at the cellular level, involved in removing super APOA4	7.69 1/13	6.25 1/16	0,033065378
GO:0006656	phosphatidylcholine biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1	7.69 1/13	6.25 1/16	0,033065378
GO:0090130	tissue migration	The process in which the population of cells that make up a tissue I APOA1 APOE A corios of molecular simple initiated by activation of a recentor on APOA1 APOE	15.38 2/13	0.82 2/243	0,033226039
GO:0007166 GO:1902533	cell surface receptor signaling pathway positive regulation of intracellular signal transduction	A series of molecular signals initiated by activation of a receptor or APOA1 APOE CN Any process that activates or increases the frequency, rate or exter APOA1 APOE CL		0.22 5/2259 0.40 3/741	0,033649856 0,034146314
GO:1902533 GO:0042159	lipoprotein catabolic process	Any process that activates or increases the frequency, rate or exter APOAL APOE CL The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13	0.40 3/741 5.88 1/17	0,034146314 0,034146314
GO:1901698	response to nitrogen compound	Any process that results in a change in state or activity of a cell or a APOE CSN1S1 C		0.40 3/741	0,034146314
GO:0071450	cellular response to oxygen radical	Any process that results in a change in state or activity of a cell (in 1 APOA4	7.69 1/13	5.88 1/17	0,034146314
GO:0071451	cellular response to superoxide	Any process that results in a change in state or activity of a cell (in 1 APOA4	7.69 1/13	5.88 1/17	0,034146314
GO:0051043		Any process that modulates the frequency, rate or extent of the pr APOE	7.69 1/13	5.88 1/17	0,034146314
GO:0090023	positive regulation of neutrophil chemotaxis	Any process that increases the frequency, rate, or extent of neutro LBP	7.69 1/13	5.88 1/17	0,034146314
GO:0002697 GO:0034114	regulation of immune effector process regulation of heterotypic cell-cell adhesion	Any process that modulates the frequency, rate, or extent of an im APOA1 LBP Any process that modulates the frequency, rate, or extent of heter APOA1	15.38 2/13 7.69 1/13	0.79 2/252 5.56 1/18	0,034669907 0,035718919
GO:0034114 GO:0032692	negative regulation of interleukin-1 production	Any process that modulates the frequency, rate, or extent of neter APOA1 Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	5.56 1/18	0,035718919
GO:0098581	detection of external biotic stimulus	The series of events in which an external biotic stimulus is detected LBP	7.69 1/13	5.56 1/18	0,035718919
GO:0044087	regulation of cellular component biogenesis	Any process that modulates the frequency, rate or extent of cellula APOA1 APOE CL		0.39 3/762	0,035871075
GO:0051130	positive regulation of cellular component organization	Any process that activates or increases the frequency, rate or exter APOA1 APOE CL	U 23.08 3/13	0.39 3/763	0,035893842
GO:0051235	maintenance of location	Any process in which a cell, substance or cellular entity, such as a p APOA1 APOE	15.38 2/13	0.76 2/262	0,036585695

GO:0006650	glycerophospholipid metabolic process	The chemical reactions and pathways involving glycerophospholipi APOA1 APOA4 Self-propelled movement of a cell or organism from one location tr APOA1 APOE GP2 LB	15.38 2/13	0.76 2/262	0,036585695
GO:0040011 GO:0000303	locomotion response to superoxide	Any process that results in a change in state or activity of a cell or a APOA4	9 30.77 4/13 7.69 1/13	0.27 4/1476 5.26 1/19	0,036726162 0,036825582
GO:0035640	exploration behavior	The specific behavior of an organism in response to a novel enviror APOE	7.69 1/13	5.26 1/19	0.036825582
GO:0034143	regulation of toll-like receptor 4 signaling pathway	Any process that modulates the frequency, rate, or extent of toll-lil LBP	7.69 1/13	5.26 1/19	0,036825582
GO:0032102	negative regulation of response to external stimulus	Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE	15.38 2/13	0.75 2/266	0,037119143
GO:0000305	response to oxygen radical	Any process that results in a change in state or activity of a cell or a APOA4	7.69 1/13	5.00 1/20	0,037669754
GO:0033036	macromolecule localization	Any process in which a macromolecule is transported to, or mainta APOA1 APOA4 APOE		0.21 5/2363	0,037669754
GO:0045939	negative regulation of steroid metabolic process	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	5.00 1/20	0,037669754
GO:0010894 GO:0008211	negative regulation of steroid biosynthetic process glucocorticoid metabolic process	Any process that decreases the frequency, rate or extent of the cht APOE The chemical reactions and pathways involving glucocorticoids, ho APOA1	7.69 1/13 7.69 1/13	5.00 1/20 5.00 1/20	0,037669754 0,037669754
GO:0060999	positive regulation of dendritic spine development	Any process that increases the rate, frequency, or extent of dendri APOE	7.69 1/13	5.00 1/20	0,037669754
GO:0071624	positive regulation of granulocyte chemotaxis	Any process that increases the rate, frequency or extent of granulc LBP	7.69 1/13	5.00 1/20	0,037669754
GO:0006706	steroid catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13	5.00 1/20	0,037669754
GO:0090181	regulation of cholesterol metabolic process	Any process that modulates the rate, frequency, or extent of chole APOE	7.69 1/13	5.00 1/20	0,037669754
GO:0042742	defense response to bacterium	Reactions triggered in response to the presence of a bacterium tha CSN1S2 LBP	15.38 2/13	0.73 2/273	0,03791638
GO:1901652 GO:0006979	response to peptide response to oxidative stress	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2	15.38 2/13	0.73 2/274	0,038075223 0,038128387
GO:0006979 GO:0045862	positive regulation of proteolysis	Any process that results in a change in state or activity of a cell or a APOA4 APOE Any process that activates or increases the frequency, rate or exter APOE CLU	15.38 2/13 15.38 2/13	0.73 2/275 0.73 2/275	0,038128387 0,038128387
GO:0007265	Ras protein signal transduction	A series of molecular signals within the cell that are mediated by a APOA1 APOE	15.38 2/13	0.72 2/276	0,038286961
GO:1902230		Any process that stops, prevents or reduces the frequency, rate or CLU	7.69 1/13	4.76 1/21	0,038783126
GO:0055094	response to lipoprotein particle	Any process that results in a change in state or activity of a cell or a APOE	7.69 1/13	4.76 1/21	0,038783126
GO:1900271	regulation of long-term synaptic potentiation	Any process that modulates the frequency, rate or extent of long-ti APOE	7.69 1/13	4.55 1/22	0,03985352
GO:0048519	negative regulation of biological process	Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOA4 APOE	CLI 53.85 7/13	0.15 7/4543	0,03985352
GO:0050999	regulation of nitric-oxide synthase activity	Any process that modulates the activity of the enzyme nitric-oxide APOE	7.69 1/13	4.55 1/22	0,03985352
GO:0071402	cellular response to lipoprotein particle stimulus	Any process that results in a change in state or activity of a cell (in 1 APOE	7.69 1/13	4.55 1/22	0,03985352
GO:0051788	response to misfolded protein	Any process that results in a change in state or activity of a cell or a CLU	7.69 1/13	4.55 1/22	0,03985352
GO:0032801 GO:0002021	receptor catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE The physiological process in which dietary excess is sensed by the (APOE	7.69 1/13 7.69 1/13	4.55 1/22 4.55 1/22	0,03985352 0,03985352
GO:0002021 GO:0050900	response to dietary excess leukocyte migration	The movement of a leukocyte within or between different tissues a GP2 LBP	15.38 2/13	4.55 1/22 0.69 2/289	0,03985352
GO:0019934	cGMP-mediated signaling	Any intracellular signal transduction in which the signal is passed o APOE	7.69 1/13	4.35 1/23	0,041319408
GO:0007616	long-term memory	The memory process that deals with the storage, retrieval and mot APOE	7.69 1/13	4.35 1/23	0,041319408
GO:0002701		Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	4.17 1/24	0,042447919
GO:0034123	positive regulation of toll-like receptor signaling pathw	Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	4.17 1/24	0,042447919
GO:1902624	positive regulation of neutrophil migration	Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	4.17 1/24	0,042447919
GO:0043085	positive regulation of catalytic activity	Any process that activates or increases the activity of an enzyme. APOA1 APOA4 APOE	23.08 3/13	0.36 3/845	0,042447919
GO:0019835	cytolysis	The rupture of cell membranes and the loss of cytoplasm. LBP	7.69 1/13	4.17 1/24	0,042447919
GO:0045730	respiratory burst	A phase of elevated metabolic activity, during which oxygen consul LBP	7.69 1/13	4.17 1/24	0,042447919
GO:0044255	cellular lipid metabolic process	The chemical reactions and pathways involving lipids, as carried ou APOA1 APOA4 APOE	23.08 3/13	0.35 3/852	0,043284516
GO:0002764 GO:0090022	immune response-regulating signaling pathway regulation of neutrophil chemotaxis	The cascade of processes by which a signal interacts with a receptc LBP PIGR Any process that modulates the frequency, rate, or extent of neutr LBP	15.38 2/13 7.69 1/13	0.66 2/303 4.00 1/25	0,043321258 0,043381743
GO:0030022	positive regulation of monooxygenase activity	Any process that includates the nequency, rate, or extent of neutricity Any process that activates or increases the activity of a monooxyge APOE	7.69 1/13	4.00 1/25	0,043381743
GO:0001662	behavioral fear response	An acute behavioral change resulting from a perceived external thr APOE	7.69 1/13	4.00 1/25	0,043381743
GO:0034381	plasma lipoprotein particle clearance	The process in which a lipoprotein particle is removed from the blc APOE	7.69 1/13	4.00 1/25	0,043381743
GO:0050892	intestinal absorption	Any process in which nutrients are taken up from the contents of t APOA1	7.69 1/13	4.00 1/25	0,043381743
GO:0042176	regulation of protein catabolic process	Any process that modulates the frequency, rate or extent of the ch APOE CLU	15.38 2/13	0.65 2/310	0,043860115
GO:0042311	vasodilation	An increase in the internal diameter of blood vessels, especially art APOE	7.69 1/13	3.85 1/26	0,043860115
GO:0050673	epithelial cell proliferation	The multiplication or reproduction of epithelial cells, resulting in th APOA1 APOE	15.38 2/13	0.65 2/308	0,043860115
GO:0044788	modulation by host of viral process	A process in which a host organism modulates the frequency, rate APOE	7.69 1/13	3.85 1/26	0,043860115
GO:0043537 GO:0048584		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13 9 30.77 4/13	3.85 1/26	0,043860115
GO:0048584 GO:0044058	positive regulation of response to stimulus regulation of digestive system process	Any process that activates, maintains or increases the rate of a resi APOA1 APOE CLU LB Any process that modulates the frequency, rate or extent of a dige APOA1	7.69 1/13	0.25 4/1617 3.85 1/26	0,043860115 0,043860115
GO:1902003	regulation of amyloid-beta formation	Any process that modulates the frequency, rate of extent of a tige APOAT Any process that modulates the frequency, rate or extent of amylo APOE	7.69 1/13	3.85 1/20	0,043860115
GO:0002209	behavioral defense response	A behavioral response seeking to protect an organism from an a pc APOE	7.69 1/13	3.85 1/26	0,043860115
GO:0006953	acute-phase response	An acute inflammatory response that involves non-antibody protei LBP	7.69 1/13	3.85 1/26	0,043860115
GO:0097242	amyloid-beta clearance	The process in which amyloid-beta is removed from extracellular b APOE	7.69 1/13	3.85 1/26	0,043860115
GO:1902930	regulation of alcohol biosynthetic process	Any process that modulates the frequency, rate or extent of alcohc APOE	7.69 1/13	3.70 1/27	0,044858905
GO:0006631	fatty acid metabolic process	The chemical reactions and pathways involving fatty acids, aliphatic APOA1 APOA4	15.38 2/13	0.63 2/316	0,044858905
GO:0009595	detection of biotic stimulus	The series of events in which a biotic stimulus, one caused or prod LBP	7.69 1/13	3.70 1/27	0,044858905
GO:0042744	hydrogen peroxide catabolic process	The chemical reactions and pathways resulting in the breakdown o APOA4	7.69 1/13	3.70 1/27	0,044858905
GO:0001941 GO:0043114	postsynaptic membrane organization	A process which results in the assembly, arrangement of constitue APOE	7.69 1/13	3.70 1/27	0,044858905
GO:0043114 GO:0048662	regulation of vascular permeability	Any process that modulates the extent to which blood vessels can APOE	7.69 1/13 7.69 1/13	3.70 1/27	0,044858905
GO:0048662 GO:0060998	regulation of dendritic spine development	Any process that stops, prevents or reduces the rate or extent of sI APOE Any process that modulates the rate, frequency, or extent of dendi APOE	7.69 1/13	3.57 1/28 3.57 1/28	0,046277957 0,046277957
GO:0048878	chemical homeostasis	Any biological process involved in the maintenance of an internal s APOA1 APOA4 APOE	23.08 3/13	0.33 3/900	0,046920218
GO:0043254	regulation of protein-containing complex assembly	Any process that modulates the frequency, rate or extent of protei APOE CLU	15.38 2/13	0.61 2/330	0,047334955
GO:0035025	positive regulation of Rho protein signal transduction	Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	3.45 1/29	0,047334955
GO:0019068	virion assembly	A late phase of the viral life cycle during which all the components APOE	7.69 1/13	3.45 1/29	0,047334955
GO:1902229	regulation of intrinsic apoptotic signaling pathway in re	Any process that modulates the frequency, rate or extent of intrins CLU	7.69 1/13	3.45 1/29	0,047334955
GO:0010543	regulation of platelet activation	Any process that modulates the rate or frequency of platelet activa APOE	7.69 1/13	3.33 1/30 0.60 2/335	0,04836565
GO:0044057 GO:0050795	regulation of system process regulation of behavior	Any process that modulates the frequency, rate or extent of a syst APOA1 APOE Any process that modulates the frequency, rate or extent of behav APOE	15.38 2/13 7.69 1/13	3.33 1/30	0,04836565 0,04836565
GO:0042596	fear response	The response of an organism to a perceived external threat. APOE	7.69 1/13	3.33 1/30	0,04836565
GO:1902991		Any process that modulates the frequency, rate or extent of amylo APOE	7.69 1/13	3.33 1/30	0,04836565
GO:0001667	ameboidal-type cell migration	Cell migration that is accomplished by extension and retraction of a APOA1 APOE	15.38 2/13	0.59 2/337	0,04851473
GO:0006644	phospholipid metabolic process	The chemical reactions and pathways involving phospholipids, any APOA1 APOA4	15.38 2/13	0.59 2/338	0,048669334
GO:0006928	movement of cell or subcellular component	The directed, self-propelled movement of a cell or subcellular com APOA1 APOE GP2 LB		0.23 4/1707	0,049543195
GO:1900026		Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	3.12 1/32	0,05106943
GO:0048260		Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13	3.03 1/33	0,052031715
GO:0001580 GO:0010803		The series of events required for a bitter taste stimulus to be receiv PIGR Any process that modulates the rate or extent of the tumor necros APOA1	7.69 1/13 7.69 1/13	3.03 1/33 3.03 1/33	0,052031715 0,052031715
GO:0010803 GO:0030195	negative regulation of blood coagulation	Any process that modulates the rate of extent of the tumor neuros APOAT Any process that stops, prevents, or reduces the frequency, rate of APOE	7.69 1/13	3.03 1/33	0,052031715
GO:0034205	amyloid-beta formation	The generation of amyloid-beta by cleavage of the amyloid precurs APOE	7.69 1/13	3.03 1/33	0,052031715
GO:1901575	organic substance catabolic process	The chemical reactions and pathways resulting in the breakdown o APOA1 APOA4 APOE		0.23 4/1742	0,052168958
GO:1900047	negative regulation of hemostasis	Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	2.94 1/34	0,053093937
GO:0001937	negative regulation of endothelial cell proliferation	Any process that stops, prevents, or reduces the rate or extent of ε APOE	7.69 1/13	2.94 1/34	0,053093937
GO:0034142	toll-like receptor 4 signaling pathway	Any series of molecular signals generated as a consequence of binc LBP	7.69 1/13	2.94 1/34	0,053093937
GO:0009968	negative regulation of signal transduction	Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE CLU	23.08 3/13	0.31 3/964	0,053290293
GO:1902622 GO:0032768	regulation of neutrophil migration regulation of monooxygenase activity	Any process that modulates the frequency, rate or extent of neutrc LBP Any process that modulates the activity of a monooxygenase. APOE	7.69 1/13 7.69 1/13	2.86 1/35 2.86 1/35	0,054011214 0,054011214
GO:0062208		Any process that incoductes the activity of a monocoxygenese. A for	7.69 1/13	2.86 1/35	0,054011214
GO:0043030	regulation of macrophage activation	Any process that modulates the frequency or rate of macrophage a LBP	7.69 1/13	2.86 1/35	0,054011214
GO:0050819	negative regulation of coagulation	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	2.78 1/36	0,055283676
GO:0050913	sensory perception of bitter taste	The series of events required to receive a bitter taste stimulus, con PIGR	7.69 1/13	2.78 1/36	0,055283676
GO:0006509	membrane protein ectodomain proteolysis	The proteolytic cleavage of transmembrane proteins and release o APOE	7.69 1/13	2.70 1/37	0,056672733
GO:0007264	small GTPase mediated signal transduction	Any series of molecular signals in which a small monomeric GTPase APOA1 APOE	15.38 2/13	0.53 2/378	0,057276578
GO:0044248	cellular catabolic process	The chemical reactions and pathways resulting in the breakdown o APOA1 APOA4 APOE The series of events involved in the percention of tests in which as PIGP		0.22 4/1814	0,057824709
GO:0050912 GO:0048523	detection of chemical stimulus involved in sensory per negative regulation of cellular process	The series of events involved in the perception of taste in which a § PIGR Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOA4 APOE	7.69 1/13 CU 46 15 6/13	2.63 1/38 0.16 6/3856	0,057824709 0,05853875
GO:0048523 GO:0034113	heterotypic cell-cell adhesion	The attachment of a cell to a cell of a different type via adhesion m APOA1 APOA1	7.69 1/13	2.56 1/39	0,05853875
GO:0050709	negative regulation of protein secretion	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	2.50 1/39	0,059929432
GO:0051055	negative regulation of lipid biosynthetic process	Any process that stops, prevents, or reduces the frequency, rate of APOE	7.69 1/13	2.50 1/40	0,059929432
GO:0010648	negative regulation of cell communication	Any process that decreases the frequency, rate or extent of cell coi APOA1 APOE CLU	23.08 3/13	0.29 3/1021	0,059929432
GO:0050435	amyloid-beta metabolic process	The chemical reactions and pathways involving amyloid-beta, a gly APOE	7.69 1/13	2.50 1/40	0,059929432
GO:0023057	negative regulation of signaling	Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE CLU	23.08 3/13	0.29 3/1023	0,059929432
GO:0071310	cellular response to organic substance	Any process that results in a change in state or activity of a cell (in 1 APOA1 BSPRY CNTFF		0.22 4/1848	0,060402842
GO:0046164	alcohol catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13	2.44 1/41	0,060647805
GO:0010596	negative regulation of endothelial cell migration	Any process that decreases the rate, frequency, or extent of the or APOE The chemical reactions and pathways involving bydrogen peroxide APOA4	7.69 1/13	2.44 1/41	0,060647805
GO:0042743 GO:0032720	hydrogen peroxide metabolic process	The chemical reactions and pathways involving hydrogen peroxide APOA4 Any process that stops, prevents, or reduces the frequency, rate, o LBP	7.69 1/13 7.69 1/13	2.44 1/41 2.44 1/41	0,060647805 0,060647805
GO:0032720 GO:0071622	regulation of granulocyte chemotaxis	Any process that stops, prevents, or reduces the frequency, rate, or LBP Any process that modulates the rate, frequency or extent of granul LBP	7.69 1/13	2.38 1/42	0,061430492
GO:0071022 GO:0043407	negative regulation of MAP kinase activity	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	2.38 1/42	0,061430492
GO:1903556	J		7.69 1/13		0,061430492
00.1909990	negative regulation of tumor necrosis factor superfami	Any process that stops, prevents or reduces the frequency, rate or LBP	7.05 1/15	2.38 1/42	0,001430492
GO:0042981	negative regulation of tumor necrosis factor superfami regulation of apoptotic process	Any process that stops, prevents or reduces the frequency, rate or LBP Any process that modulates the occurrence or rate of cell death by APOE CLU CNTFR	23.08 3/13	0.29 3/1039	0,061430492

GO:0010629	negative regulation of gene expression	Any process that decreases the frequency, rate or extent of gene e APOA1 APOE LBP	23.08 3/13	0.29 3/1043	0,061528017
GO:0051353 GO:0042987	positive regulation of oxidoreductase activity amyloid precursor protein catabolic process	Any process that activates or increases the frequency, rate or exter APOE The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13 7.69 1/13	2.33 1/43 2.33 1/43	0,062330041 0,062330041
GO:0042587 GO:0051180	vitamin transport	The directed movement of vitamins into, out of or within a cell, or APOA1	7.69 1/13	2.33 1/43	0,062330041
GO:0019221	cytokine-mediated signaling pathway	A series of molecular signals initiated by the binding of a cytokine t APOA1 CNTFR	15.38 2/13	0.49 2/408	0,062596225
GO:0043954	cellular component maintenance	The organization process that preserves a cellular component in a : APOE	7.69 1/13	2.27 1/44	0,063077938
GO:0032757	positive regulation of interleukin-8 production	Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	2.27 1/44	0,063077938
GO:0031663	lipopolysaccharide-mediated signaling pathway	A series of molecular signals initiated by the binding of a lipopolysa LBP	7.69 1/13	2.27 1/44	0,063077938
GO:1900024		Any process that modulates the frequency, rate or extent of substr APOA1	7.69 1/13	2.27 1/44	0,063077938
GO:0043067 GO:1902532	regulation of programmed cell death	Any process that modulates the frequency, rate or extent of progra APOE CLU CNTFR Any process that stops, prevents or reduces the frequency, rate or APOE CLU	23.08 3/13 15.38 2/13	0.28 3/1065 0.48 2/415	0,063716124 0,063774319
GO:0050919	negative regulation of intracential signal transduction	The directed movement of a motile cell or organism towards a low APOA1	7.69 1/13	2.22 1/45	0,064080681
GO:0009719	response to endogenous stimulus	Any process that results in a change in state or activity of a cell or a APOE CSN1S1 CSN1S2		0.28 3/1076	0,064885454
GO:0051345	positive regulation of hydrolase activity	Any process that activates or increases the frequency, rate or exter APOA1 APOA4	15.38 2/13	0.48 2/420	0,064885454
GO:0007610	behavior	The internally coordinated responses (actions or inactions) of anim APOE CNTFR	15.38 2/13	0.48 2/421	0,064937264
GO:0097061	dendritic spine organization	A process that is carried out at the cellular level which results in the APOE	7.69 1/13	2.13 1/47	0,066324433
GO:0033619	membrane protein proteolysis	The proteolytic cleavage of a transmembrane protein leading to th APOE	7.69 1/13	2.08 1/48	0,0670086
GO:0050766	positive regulation of phagocytosis	Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	2.08 1/48	0,0670086
GO:0006801 GO:0051239	superoxide metabolic process regulation of multicellular organismal process	The chemical reactions and pathways involving superoxide, the sur APOA4 Any process that modulates the frequency, rate or extent of a mult APOA1 APOA4 APOE	7.69 1/13	2.08 1/48 0.21 4/1943	0,0670086 0,0670086
GO:0031239 GO:0030193	regulation of blood coagulation	Any process that modulates the frequency, rate or extent of a mult APOA1 APOA4 APOE Any process that modulates the frequency, rate or extent of blood APOE	7.69 1/13	2.08 1/48	0,0670086
GO:0061045	negative regulation of wound healing	Any process that modulates the nequency, rate of extent of blood. All of Any process that decreases the rate, frequency, or extent of the se APOE	7.69 1/13	2.03 1/43	0.0682418
GO:0046579		Any process that activates or increases the frequency, or extent of the Service APOA1	7.69 1/13	2.00 1/50	0,068332543
GO:0048844	artery morphogenesis	The process in which the anatomical structures of arterial blood ve APOE	7.69 1/13	2.00 1/50	0,068332543
GO:0065008	regulation of biological quality	Any process that modulates a qualitative or quantitative trait of a b APOA1 APOA4 APOE	CLI 38.46 5/13	0.17 5/2959	0,068332543
GO:0001960		Any process that stops, prevents, or reduces the frequency, rate or APOA1	7.69 1/13	2.00 1/50	0,068332543
GO:0033555	multicellular organismal response to stress	Any process that results in a change in state or activity of a multice APOE	7.69 1/13	2.00 1/50	0,068332543
GO:0010770		Any process that increases the frequency, rate or extent of cell mo APOA1	7.69 1/13	2.00 1/50	0,068332543
GO:0050810 GO:1900046	regulation of steroid biosynthetic process regulation of hemostasis	Any process that modulates the frequency, rate or extent of the ch APOE Any process that modulates the frequency, rate or extent of hemo: APOE	7.69 1/13 7.69 1/13	2.00 1/50 2.00 1/50	0,068332543 0,068332543
GO:0071702	organic substance transport	The directed movement of organic substances into, out of or within APOA1 APOA4 APOE		0.20 4/1968	0,068332543
GO:2001244		Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13	1.96 1/51	0,068973218
GO:0019935	cyclic-nucleotide-mediated signaling	Any intracellular signal transduction in which the signal is passed o APOE	7.69 1/13	1.96 1/51	0,068973218
GO:0106027	neuron projection organization	A process that is carried out at the cellular level which results in the APOE	7.69 1/13	1.96 1/51	0,068973218
GO:0099175	regulation of postsynapse organization	Any process that modulates the physical form of a postsynapse. APOE	7.69 1/13	1.96 1/51	0,068973218
GO:0060761	negative regulation of response to cytokine stimulus	Any process that decreases the rate, frequency, or extent of a resp APOA1	7.69 1/13	1.96 1/51	0,068973218
GO:0048583	regulation of response to stimulus	Any process that modulates the frequency, rate or extent of a resp APOA1 APOE CLU LBF		0.17 5/2982	0,069120741
GO:0006629	lipid metabolic process	The chemical reactions and pathways involving lipids, compounds : APOA1 APOA4 APOE	23.08 3/13	0.27 3/1124	0,069125283
GO:0050818 GO:0032233	regulation of coagulation positive regulation of actin filament bundle assembly	Any process that modulates the frequency, rate or extent of coagu APOE Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13 7.69 1/13	1.92 1/52 1.89 1/53	0,069880346 0,070917637
GO:0032233 GO:0010633	negative regulation of actin mament bundle assembly	Any process that stops, prevents, or reduces the frequency, rate or APOA1	7.69 1/13	1.89 1/53	0,070917637
GO:0060996	dendritic spine development	The process whose specific outcome is the progression of the denc APOE	7.69 1/13	1.85 1/54	0,070954481
GO:0032611	interleukin-1 beta production	The appearance of interleukin-1 beta due to biosynthesis or secret APOA1	7.69 1/13	1.85 1/54	0,070954481
GO:0032651	regulation of interleukin-1 beta production	Any process that modulates the frequency, rate, or extent of interl APOA1	7.69 1/13	1.85 1/54	0,070954481
GO:0010941	regulation of cell death	Any process that modulates the rate or frequency of cell death. Cel APOE CLU CNTFR	23.08 3/13	0.26 3/1142	0,070954481
GO:0042982	amyloid precursor protein metabolic process	The chemical reactions and pathways involving amyloid precursor APOE	7.69 1/13	1.85 1/54	0,070954481
GO:0051057		Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	1.85 1/54	0,070954481
GO:0032722	positive regulation of chemokine production	Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	1.85 1/54	0,070954481
GO:0051851 GO:0002532	modulation by host of symbiont process	The process in which an organism effects a change in the structure APOE The synthesis or release of any molecular mediator of the inflamm. LBP	7.69 1/13 7.69 1/13	1.85 1/54 1.85 1/54	0,070954481 0,070954481
GO:0010498	proteasomal protein catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE CLU	15.38 2/13	0.43 2/464	0,072181144
GO:0009893	positive regulation of metabolic process	Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE		0.16 5/3040	0,072184268
GO:0042127	regulation of cell population proliferation	Any process that modulates the frequency, rate or extent of cell pr APOE CLU CNTFR	23.08 3/13	0.26 3/1156	0,072184268
GO:0032787	monocarboxylic acid metabolic process	The chemical reactions and pathways involving monocarboxylic aci APOA1 APOA4	15.38 2/13	0.43 2/470	0,073467859
GO:0072657	protein localization to membrane	A process in which a protein is transported to, or maintained in, a s APOE PIGR	15.38 2/13	0.42 2/473	0,073752568
GO:0034121	regulation of toll-like receptor signaling pathway	Any process that modulates the frequency, rate, or extent of toll-lil LBP	7.69 1/13	1.75 1/57	0,073752568
GO:0060291	long-term synaptic potentiation	A process that modulates synaptic plasticity such that synapses are APOE	7.69 1/13	1.75 1/57	0,073752568
GO:0050865	regulation of cell activation	Any process that modulates the frequency, rate or extent of cell ac APOE LBP	15.38 2/13	0.42 2/472	0,073752568
GO:0002526 GO:1901616	acute inflammatory response organic hydroxy compound catabolic process	Inflammation which comprises a rapid, short-lived, relatively unifoi LBP The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13 7.69 1/13	1.72 1/58 1.72 1/58	0,074650289 0,074650289
GO:1901616 GO:0015909	long-chain fatty acid transport	The directed movement of long-chain fatty acids into, out of or wit APOE	7.69 1/13	1.69 1/59	0,074650289
GO:0032677	regulation of interleukin-8 production	Any process that modulates the frequency, rate, or extent of interly LBP	7.69 1/13	1.69 1/59	0,075189028
GO:0031638	zymogen activation	The proteolytic processing of an inactive enzyme to an active form. CD5L	7.69 1/13	1.69 1/59	0,075189028
GO:0050909	sensory perception of taste	The series of events required for an organism to receive a gustator PIGR	7.69 1/13	1.69 1/59	0,075189028
GO:0032637	interleukin-8 production	The appearance of interleukin-8 due to biosynthesis or secretion fc LBP	7.69 1/13	1.69 1/59	0,075189028
GO:0042116	macrophage activation	A change in morphology and behavior of a macrophage resulting fr LBP	7.69 1/13	1.67 1/60	0,076294813
GO:0009725	response to hormone	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2	15.38 2/13	0.41 2/488	0,076744769
GO:0014070	response to organic cyclic compound negative regulation of response to wounding	Any process that results in a change in state or activity of a cell or a CSN1S1 CSN1S2	15.38 2/13	0.40 2/495	0,077874217
GO:1903035 GO:0032760		Any process that stops, prevents or reduces the frequency, rate or APOE Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13 7.69 1/13	1.61 1/62 1.61 1/62	0,077874217 0,077874217
GO:0002367	cytokine production involved in immune response	The appearance of a cytokine due to biosynthesis or secretion follc APOA1	7.69 1/13	1.61 1/62	0,077874217
GO:0061077	chaperone-mediated protein folding	The process of inhibiting aggregation and assisting in the covalent - CLU	7.69 1/13	1.61 1/62	0,077874217
GO:0002718	regulation of cytokine production involved in immune r	Any process that modulates the frequency, rate, or extent of cytok APOA1	7.69 1/13	1.61 1/62	0,077874217
GO:0009056	catabolic process	The chemical reactions and pathways resulting in the breakdown o APOA1 APOA4 APOE	CLI 30.77 4/13	0.19 4/2106	0,078066328
GO:0048259	regulation of receptor-mediated endocytosis	Any process that modulates the frequency, rate or extent of recept CLU	7.69 1/13	1.59 1/63	0,078100545
GO:0032652	regulation of interleukin-1 production	Any process that modulates the frequency, rate, or extent of interl APOA1	7.69 1/13	1.59 1/63	0,078100545
GO:0010769 GO:0032612	interleukin-1 production	Any process that modulates the frequency, rate or extent of cell m APOA1 The appearance of interleukin-1 due to biosynthesis or secretion fc APOA1	7.69 1/13 7.69 1/13	1.59 1/63 1.59 1/63	0,078100545 0,078100545
GO:0007631	feeding behavior	Behavior associated with the intake of food. CNTFR	7.69 1/13	1.59 1/63	0,078100545
GO:0006935	chemotaxis	The directed movement of a motile cell or organism, or the directe APOA1 LBP	15.38 2/13	0.40 2/503	0,079137945
GO:1903557	positive regulation of tumor necrosis factor superfamily	Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	1.54 1/65	0,079789134
GO:0002275	myeloid cell activation involved in immune response	A change in the morphology or behavior of a myeloid cell resulting LBP	7.69 1/13	1.54 1/65	0,079789134
GO:2001021		Any process that stops, prevents or reduces the frequency, rate or CLU	7.69 1/13	1.54 1/65	0,079789134
GO:0042330 GO:0048585	taxis	The directed movement of a motile cell or organism in response to APOA1 LBP Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE CLU	15.38 2/13 23.08 3/13	0.40 2/506	0,079789134
GO:0048585 GO:0022600	negative regulation of response to stimulus digestive system process	Any process that stops, prevents, or reduces the requercy, rate of APOA1 APOE CLO A physical, chemical, or biochemical process carried out by living or APOA1	7.69 1/13	0.24 3/1236 1.52 1/66	0,080494961 0,080694822
GO:0022000	response to bacterium	Any process that results in a change in state or activity of a cell or a CSN1S2 LBP	15.38 2/13	0.39 2/514	0,081254242
GO:0001817	regulation of cytokine production	Any process that modulates the frequency, rate, or extent of produ APOA1 LBP	15.38 2/13	0.39 2/515	0,081295375
GO:0050829	defense response to Gram-negative bacterium	Reactions triggered in response to the presence of a Gram-negativ LBP	7.69 1/13	1.49 1/67	0,081295375
GO:0050764	regulation of phagocytosis	Any process that modulates the frequency, rate or extent of phago APOA1	7.69 1/13	1.49 1/67	0,081295375
GO:0043535	regulation of blood vessel endothelial cell migration	Any process that modulates the frequency, rate or extent of the mi APOE	7.69 1/13	1.47 1/68	0,082184286
GO:0051492	regulation of stress fiber assembly	Any process that modulates the frequency, rate or extent of the as APOA1	7.69 1/13	1.47 1/68	0,082184286
GO:0032602 GO:0001816	chemokine production cytokine production	The appearance of a chemokine due to biosynthesis or secretion fc LBP The appearance of a cytokine due to biosynthesis or secretion follc APOA1 LBP	7.69 1/13 15.38 2/13	1.45 1/69 0.38 2/522	0,082320393 0,082320393
GO:0001818 GO:0062014		Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	1.45 1/69	0,082320393
GO:0062014 GO:0060840	artery development	The progression of the artery over time, from its initial formation ti APOE	7.69 1/13	1.45 1/69	0,082320393
GO:0032642	regulation of chemokine production	Any process that modulates the frequency, rate, or extent of chem LBP	7.69 1/13	1.45 1/69	0,082320393
GO:0030168	platelet activation	A series of progressive, overlapping events triggered by exposure c APOE	7.69 1/13	1.45 1/69	0,082320393
GO:0007613	memory	The activities involved in the mental information processing system APOE	7.69 1/13	1.45 1/69	0,082320393
GO:0032755	positive regulation of interleukin-6 production	Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	1.43 1/70	0,08318993
GO:0051341	regulation of oxidoreductase activity	Any process that modulates the frequency, rate or extent of oxidor APOE The collular process in which a signal is convoyed to trigger a charge APOA1 APOE CLUCAN	7.69 1/13	1.43 1/70	0,08318993
GO:0007165 GO:1902531	signal transduction	The cellular process in which a signal is conveyed to trigger a chang APOA1 APOE CLU CN Any process that modulates the frequency, rate or extent of intract APOA1 APOE CLU	FF 53.85 7/13 23.08 3/13	0.12 7/5642 0.24 3/1270	0,08325862 0,083444285
GO:1902531 GO:0015908	regulation of intracellular signal transduction fatty acid transport	Any process that modulates the frequency, rate or extent of intraci APOA1 APOE CLU The directed movement of fatty acids into, out of or within a cell, o APOE	23.08 3/13 7.69 1/13	0.24 3/12/0 1.41 1/71	0,083444285 0,08345751
GO:0015908 GO:0048660	regulation of smooth muscle cell proliferation	Any process that modulates the frequency, rate or extent of smoot APOE	7.69 1/13	1.41 1/71	0,08345751
GO:0045833	negative regulation of lipid metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of smoot AFOE	7.69 1/13	1.41 1/71	0,08345751
GO:0051702		An interaction between two organisms living together in more or le APOE	7.69 1/13	1.41 1/71	0,08345751
GO:0032436	positive regulation of proteasomal ubiquitin-dependen	Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13	1.39 1/72	0,08445835
GO:1901264	carbohydrate derivative transport	The directed movement of a carbohydrate derivative into, out of o LBP	7.69 1/13	1.37 1/73	0,085154604
GO:0048659	smooth muscle cell proliferation	The multiplication or reproduction of smooth muscle cells, resultin APOE	7.69 1/13	1.37 1/73	0,085154604
GO:0032092		Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	1.37 1/73	0,085154604
	positive regulation of protein binding	Any process in which a substance or collular optity, such as a party ADOS DICD	15 20 3/13		0.095336353
GO:0051668 GO:0033209	localization within membrane	Any process in which a substance or cellular entity, such as a prote APOE PIGR A series of molecular signals initiated by the binding of a tumor net APOA1	15.38 2/13 7.69 1/13	0.37 2/541	0,085236353 0.085842875
GO:0051668 GO:0033209 GO:0110020		Any process in which a substance or cellular entity, such as a prote APOE PIGR A series of molecular signals initiated by the binding of a tumor ne APOA1 Any process that modulates the frequency, rate or extent of the as APOA1	15.38 2/13 7.69 1/13 7.69 1/13		0,085236353 0,085842875 0,085842875
GO:0033209	localization within membrane tumor necrosis factor-mediated signaling pathway	A series of molecular signals initiated by the binding of a tumor net APOA1	7.69 1/13	0.37 2/541 1.35 1/74	0,085842875

GO:0010976		Any process that increases the rate, frequency or extent of neuron APOE	7.69 1/13	1.33 1/75	0,086674025
GO:0043086 GO:0002690		Any process that stops or reduces the activity of an enzyme. APOA1 APOE Any process that activates or increases the frequency, rate, or exte LBP	15.38 2/13 7.69 1/13	0.36 2/555 1.30 1/77	0,088470115 0,088470115
GO:0002030		Any process that activates or increases the frequency, rate, or exter LBP	7.69 1/13	1.30 1/77	0,088470115
GO:0048522		Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE CI		0.13 6/4480	0,08855188
GO:0002698		Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	1.28 1/78	0,088975658
GO:0050729		Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	1.28 1/78	0,088975658
GO:0030593		The directed movement of a neutrophil cell, the most numerous pc LBP	7.69 1/13	1.28 1/78	0,088975658
GO:0007173 GO:0030038		A series of molecular signals initiated by binding of a ligand to the t PIGR Assembly of actin filament bundles in which the filaments are loost APOA1	7.69 1/13 7.69 1/13	1.27 1/79 1.25 1/80	0,089934828 0,09027069
GO:0030038 GO:0051224		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	1.25 1/80	0,09027069
GO:2000060		Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13	1.25 1/80	0,09027069
GO:0062207	regulation of pattern recognition receptor signaling pat	Any process that modulates the rate, frequency or extent of a patti LBP	7.69 1/13	1.25 1/80	0,09027069
GO:0043149		The aggregation, arrangement and bonding together of a set of cor APOA1	7.69 1/13	1.25 1/80	0,09027069
GO:0009966		Any process that modulates the frequency, rate or extent of signal APOA1 APOE CLU LBP	30.77 4/13	0.18 4/2282	0,091127281
GO:0012501		A process which begins when a cell receives an internal or external APOE CLU CNTFR	23.08 3/13	0.22 3/1343	0,091432903
GO:2001243 GO:0032231		Any process that stops, prevents or reduces the frequency, rate or CLU Any process that modulates the frequency, rate or extent of the as APOA1	7.69 1/13 7.69 1/13	1.22 1/82 1.20 1/83	0,092002344 0,092469774
GO:0032231		Any biological process involved in the maintenance of an internal s APOA1 APOA4 APOE	23.08 3/13	0.22 3/1352	0,092469774
GO:1904950		Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	1.20 1/83	0,092469774
GO:0007586		The whole of the physical, chemical, and biochemical processes car APOA1	7.69 1/13	1.20 1/83	0,092469774
GO:0071901		Any process that decreases the rate, frequency, or extent of protei APOE	7.69 1/13	1.19 1/84	0,093242151
GO:1990830		Any process that results in a change in state or activity of a cell (in 1 BSPRY	7.69 1/13	1.19 1/84	0,093242151
GO:0010977 GO:1990823		Any process that decreases the rate, frequency or extent of neuror APOE	7.69 1/13 7.69 1/13	1.18 1/85	0,094008716 0,094008716
GO:0038127		Any process that results in a change in state or activity of a cell or a BSPRY A series of molecular signals initiated by binding of a ligand to a me PIGR	7.69 1/13	1.18 1/85 1.16 1/86	0,094927738
GO:1903531		Any process that stops, prevents or reduces the frequency, rate or APOE	7.69 1/13	1.15 1/87	0,095843053
GO:0007229		A series of molecular signals initiated by the binding of extracellula APOA1	7.69 1/13	1.14 1/88	0,09675468
GO:0050830		Reactions triggered in response to the presence of a Gram-positive LBP	7.69 1/13	1.12 1/89	0,097662638
GO:0035296	•	Any process that modulates the diameter of a tube. APOE	7.69 1/13	1.11 1/90	0,098078989
GO:0061041		Any process that modulates the rate, frequency, or extent of the sc APOE	7.69 1/13	1.11 1/90	0,098078989
GO:0010811 GO:0097746		Any process that increases the frequency, rate or extent of cell-sub APOA1 Any process that modulates the diameter of blood vessels. APOE	7.69 1/13 7.69 1/13	1.11 1/90 1.11 1/90	0,098078989 0,098078989
GO:0035150		Ensuring that a tube is of the correct length and diameter. Tube siz APOE	7.69 1/13	1.10 1/91	0,098813226
GO:0008630		A series of molecular signals in which an intracellular signal is conv CLU	7.69 1/13	1.10 1/91	0,098813226
GO:0034446	substrate adhesion-dependent cell spreading	The morphogenetic process that results in flattening of a cell as a c APOA1	7.69 1/13	1.09 1/92	0,099705469
GO:1901800		Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13	1.08 1/93	0,100594155
GO:0030162	• • •	Any process that modulates the frequency, rate or extent of the hy APOE CLU	15.38 2/13	0.32 2/620	0,101345243
GO:0002224		Any series of molecular signals generated as a consequence of binc LBP	7.69 1/13	1.06 1/94	0,101345243
GO:0034614 GO:0008219		Any process that results in a change in state or activity of a cell (in 1 APOA4 Any biological process that results in permanent cessation of all vit APOE CLU CNTFR	7.69 1/13 23.08 3/13	1.05 1/95 0.21 3/1432	0,102193945 0,102814184
GO:0050806		Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	1.03 1/97	0,103944398
GO:0071621		The movement of a granulocyte in response to an external stimulu LBP	7.69 1/13	1.02 1/98	0,104814427
GO:0023052	signaling	The entirety of a process in which information is transmitted withir APOA1 APOE CLU CNTF	F 53.85 7/13	0.12 7/6020	0,104815771
GO:0035270		Progression of the endocrine system over time, from its formation APOA1	7.69 1/13	1.01 1/99	0,105339557
GO:0051048		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	1.01 1/99	0,105339557
GO:1903052 GO:0065009		Any process that activates or increases the frequency, rate or exter CLU Any process that modulates the frequency, rate or extent of a mole APOA1 APOA4 APOE CL	7.69 1/13	1.00 1/100 0.16 4/2439	0,10593642 0,10593642
GO:0003003 GO:0002688		Any process that modulates the frequency, rate of extent of a mole APOAT APOAT APOE C	7.69 1/13	1.00 1/100	0,10593642
GO:0001959		Any process that modulates the frequency, rate or extent of the cy APOA1	7.69 1/13	0.99 1/101	0,106202928
GO:0050680	negative regulation of epithelial cell proliferation	Any process that stops, prevents or reduces the rate or extent of e APOE	7.69 1/13	0.99 1/101	0,106202928
GO:0044281		The chemical reactions and pathways involving small molecules, ar APOA1 APOA4 APOE	23.08 3/13	0.21 3/1460	0,106202928
GO:0001936		Any process that modulates the frequency, rate, or extent of endol APOE	7.69 1/13	0.99 1/101	0,106202928
GO:0043066 GO:0007154		Any process that stops, prevents, or reduces the frequency, rate or CLU CNTFR Any process that mediates interactions between a cell and its surrc APOA1 APOE CLU CNTF	15.38 2/13	0.31 2/646 0.12 7/6065	0,106391557 0,106849976
GO:0007154 GO:0002833		Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	0.12 7/6065	0,108849978
GO:0002833		Any process that stops, prevents, or reduces the frequency, rate, or excercising Any process that stops, prevents, or reduces the frequency, rate or CNTFR	7.69 1/13	0.96 1/104	0,108052023
GO:0032640		The appearance of tumor necrosis factor due to biosynthesis or set LBP	7.69 1/13	0.96 1/104	0,108052023
GO:0032680	regulation of tumor necrosis factor production	Any process that modulates the frequency, rate or extent of tumor LBP	7.69 1/13	0.96 1/104	0,108052023
GO:0098609		The attachment of one cell to another cell via adhesion molecules. APOA1 APOA4	15.38 2/13	0.31 2/655	0,108052023
GO:0032635		The appearance of interleukin-6 due to biosynthesis or secretion fc LBP	7.69 1/13	0.94 1/106	0,109545519
GO:0032675 GO:0099173		Any process that modulates the frequency, rate, or extent of interly LBP	7.69 1/13 7.69 1/13	0.94 1/106	0,109545519 0,109545519
GO:0099173 GO:0043069		A process that is carried out at the cellular level which results in the APOE Any process that stops, prevents, or reduces the frequency, rate or CLU CNTFR	15.38 2/13	0.94 1/106 0.30 2/663	0,109545519
GO:0060759		Any process that modulates the rate, frequency, or extent of a rest APOA1	7.69 1/13	0.93 1/107	0,109683911
GO:1903555		Any process that modulates the frequency, rate or extent of tumor LBP	7.69 1/13	0.93 1/107	0,109683911
GO:0071706	tumor necrosis factor superfamily cytokine production	The appearance of any member of the TNF superfamily due to bios LBP	7.69 1/13	0.93 1/107	0,109683911
GO:2001235		Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13	0.93 1/107	0,109683911
GO:0002687		Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	0.92 1/109	0,111493948
GO:0032434 GO:0033002		Any process that modulates the frequency, rate or extent of the br CLU The expansion of a muscle cell population by cell division. APOE	7.69 1/13 7.69 1/13	0.91 1/110 0.91 1/110	0,112134172 0,112134172
GO:0065003		The aggregation, arrangement and bonding together of a set of ma APOA1 APOA4 APOE CI		0.16 4/2520	0,112134172
GO:1903034		Any process that modulates the frequency, rate or extent of response APOE	7.69 1/13	0.89 1/112	0,113752085
GO:0050921		Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	0.88 1/113	0,114379623
GO:0035966		Any process that results in a change in state or activity of a cell or a CLU	7.69 1/13	0.88 1/113	0,114379623
GO:0031345		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.87 1/115	0,116155859
GO:0051603		The hydrolysis of a peptide bond or bonds within a protein as part APOE CLU	15.38 2/13	0.29 2/696	0,117004369
GO:0030334 GO:0002700		Any process that modulates the frequency, rate or extent of cell mi APOE LBP Any process that modulates the frequency, rate, or extent of the pi APOA1	15.38 2/13 7.69 1/13	0.29 2/697 0.85 1/117	0,117118434 0,11721475
GO:0010646		Any process that modulates the frequency, rate or extent of the practice of APOAL APOE CLU LBP	30.77 4/13	0.16 4/2562	0,11721475
GO:0010605	•	Any process that decreases the frequency, rate or extent of the cht APOA1 APOE CLU LBP	30.77 4/13	0.16 4/2563	0,11721475
GO:0023051	regulation of signaling	Any process that modulates the frequency, rate or extent of a sign; APOA1 APOE CLU LBP	30.77 4/13	0.16 4/2573	0,118422427
GO:0031333		Any process that stops, prevents, or reduces the frequency, rate or CLU	7.69 1/13	0.83 1/120	0,119553112
GO:0090090		Any process that decreases the rate, frequency, or extent of the W APOE	7.69 1/13	0.83 1/120	0,119553112
GO:0000302 GO:0048518		Any process that results in a change in state or activity of a cell or a APOA4 Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE CI	7.69 1/13	0.83 1/121 0.12 6/4958	0,120330555 0,120330683
GO:0060548		Any process that decreases the rate or frequency, fate of external OAT AFOAT AFOE C	15.38 2/13	0.28 2/719	0,121959776
GO:0048167		A process that modulates synaptic plasticity, the ability of synapses APOE	7.69 1/13	0.79 1/126	0,123987015
GO:0031328	positive regulation of cellular biosynthetic process	Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE	23.08 3/13	0.19 3/1596	0,123987015
GO:0051017		The assembly of actin filament bundles; actin filaments are on the APOA1	7.69 1/13	0.79 1/126	0,123987015
GO:0051092 GO:0043409		Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13 7.69 1/13	0.79 1/126 0.79 1/127	0,123987015 0,124499498
GO:0043409 GO:0031325		Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE CI		0.15 4/2631	0,124499498
GO:0044257		The chemical reactions and pathways resulting in the breakdown o APOE CLU	15.38 2/13	0.27 2/732	0,124499498
GO:0061572		A process that results in the assembly, arrangement of constituent APOA1	7.69 1/13	0.78 1/128	0,124939733
GO:0010594				0.78 1/128	0,124939733
		Any process that modulates the rate, frequency, or extent of the or APOE	7.69 1/13		
GO:0019752	carboxylic acid metabolic process	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4	15.38 2/13	0.27 2/736	0,125120083
GO:0060538	carboxylic acid metabolic process skeletal muscle organ development	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR	15.38 2/13 7.69 1/13	0.27 2/736 0.78 1/129	0,125130411
GO:0060538 GO:0071222	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in 1 LBP	15.38 2/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129	0,125130411 0,125130411
GO:0060538 GO:0071222 GO:0003018	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129	0,125130411 0,125130411 0,125130411
GO:0060538 GO:0071222	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in 1 LBP	15.38 2/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129	0,125130411 0,125130411
GO:0060538 GO:0071222 GO:0003018 GO:1901215	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in 1 LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or CNTFR	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130	0,125130411 0,125130411 0,125130411 0,125318278
GO:0060538 GO:0071222 GO:0003018 GO:1901215 GO:0009891 GO:2000058 GO:0043112	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic pro- receptor metabolic process	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that accurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE Any process that activates the frequency, rate or exter APOA1 APOA4 APOE Any process that activates the frequency, rate or exter APOA1 APOA4 APOE Any process that activates the frequency, rate or exter APOA1 APOA4 APOE The chemical reactions and pathways involving a receptor molecul APOE	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.19 3/1617 0.77 1/130 0.77 1/130	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278
GO:0060538 GO:0071222 GO:0003018 GO:1901215 GO:0009891 GO:2000058 GO:0043112 GO:2000145	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of biolyuthr-dependent protein catabolic pro- receptor metabolic process regulation of cell motility	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or CNTFR Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE Any process that activates of increases the frequency, rate or exter of Ubiqui CLU The chemical reactions and pathways involving a receptor molecul APOE Any process that modulates the frequency, rate or extern of cell m. APOE LBP	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 7.69 1/13 15.38 2/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.19 3/1617 0.77 1/130 0.77 1/130 0.27 2/742	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,125318278 0,125396873
GO:0060538 GO:0071222 GO:0003018 GO:1901215 GO:0009891 GO:2000058 GO:0043112 GO:2000145 GO:0051099	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic pro- receptor metabolic process regulation of cell motility positive regulation of binding	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that activates or increases the frequency, rate or CNTFR Any process that activates or increases the frequency, rate or extent APOA1 APOA4 APOE Any process that modulates the frequency, rate or extent of ubiqui CLU The chemical reactions and pathways involving a receptor molecul APOE Any process that modulates the frequency, rate or extent of LBP Any process that activates or increases the rate or extent of bindin, APOE	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.19 3/1617 0.77 1/130 0.77 1/130 0.77 1/130 0.77 2/742 0.76 1/131	0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,125318278 0,125318278
GO:0060538 GO:0071222 GO:0003018 GO:1901215 GO:0009891 GO:2000058 GO:0043112 GO:2000145 GO:0051099 GO:0002221	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of heiron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic proce receptor metabolic process regulation of cell motility positive regulation of binding pattern recognition receptor signaling pathway	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in 1BP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that atos, prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that accurs at the level of the vasculature. APOE Any process that accurs frequency, rate or exter of Ubiqui CLU The chemical reactions and pathways involving a receptor molecul. APOE Any process that activates or increases the rate or extent of bindin, APOE Any process that activates or increases the rate or extent of bindin, APOE Any series of molecular signals generated as a consequence of a pa LBP	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.77 1/130 0.19 3/1617 0.77 1/130 0.77 1/130 0.27 2/742 0.76 1/131	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,12530385 0,125503385
GO:0060538 GO:0071222 GO:0003018 GO:1901215 GO:0009891 GO:2000058 GO:0043112 GO:2000145 GO:0051099 GO:0002221 GO:0007596	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic proc receptor metabolic process regulation of cell motility positive regulation of binding pattern recognition receptor signaling pathway blood coagulation	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that atops, prevents or reduces the frequency, rate or CNTFR Any process that attivates or increases the frequency, rate or exten APOA1 APOA4 APOE Any process that attivates or increases the frequency, rate or exten 4POA1 APOA4 APOE Any process that modulates the frequency, rate or extent of Ubiqui CLU The chemical reactions and pathways involving a receptor molecul APOE Any process that attivates or increases the rate or extent of bindin APOE Any process that attivates or increases the rate or extent of bindin APOE Any series of molecular signals generated as a consequence of a pLBP The sequential process in which the multiple coagulation factors of APOE	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.79 3/1617 0.77 1/130 0.77 1/130 0.27 2/742 0.76 1/131 0.76 1/131	0,125130411 0,125130411 0,125334811 0,125318278 0,125318278 0,125318278 0,125318278 0,12530385 0,125503385 0,125503385
GO:0060538 GO:0071222 GO:0003018 GO:1901215 GO:0009891 GO:2000058 GO:0043112 GO:2000145 GO:0051099 GO:0002221	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic pro- receptor metabolic process regulation of cell motility positive regulation of binding pattern recognition receptor signaling pathway blood coagulation oxacaid metabolic process	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in 1BP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that atosta prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that accurs at the level of the vasculature. APOE Any process that accurs are the frequency, rate or exter of UDIQU The chemical reactions and pathways involving a receptor molecul. APOE Any process that activates or increases the rate or extent of bindin, APOE Any process that activates or increases the rate or extent of bindin, APOE Any series of molecular signals generated as a consequence of a pa LBP	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.77 1/130 0.19 3/1617 0.77 1/130 0.77 1/130 0.27 2/742 0.76 1/131	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,12530385 0,125503385
G0:0060538 G0:0071222 G0:0003018 G0:1901215 G0:0008911 G0:00043112 G0:000145 G0:0005109 G0:0002221 G0:0007596 G0:0043423 G0:0007599	carboxylic acid metabolic process skeletal muscle organ development cellular response to lippophysiccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic proc receptor metabolic process regulation of cell motility positive regulation of binding pattern recognition receptor signaling pathway blood coagulation oxoacid metabolic process regulation of neuron apoptotic process hemostasis	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that activates or increases the frequency, rate or CNTFR Any process that activates or increases the frequency, rate or exten APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or exten 4POA1 APOA4 APOE Any process that modulates the frequency, rate or extent of Ubiqui CLU The chemical reactions and pathways involving a receptor molecul APOE Any process that activates or increases the rate or extent of bindin APOE Any process that activates or increases the rate or extent of bindin APOE Any series of molecular signals generated as a consequence of a pLBP The sequential process in which the multiple coagulation factors of APOE The chemical reactions and pathways involving any oxocaid; an ox APOA1 APOA4 Any process that modulates the focurrence or rate of cell death by CNTFR The stopping of bleeding (loss of body fluid) or the arrest of the cin APOE	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 7.69 1/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.19 3/1617 0.77 1/130 0.77 1/130 0.77 1/130 0.77 1/130 0.77 1/130 0.72 1/742 0.76 1/131 0.76 1/131 0.76 1/132 0.76 1/132	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,12530385 0,125503385 0,125503385 0,125503385 0,125535906 0,126053821 0,126785581
G0:0060538 G0:0071222 G0:0003018 G0:1001215 G0:000891 G0:0004312 G0:0004312 G0:000145 G0:0002221 G0:0007596 G0:0043436 G0:0043523 G0:0043933	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of neuron death positive regulation of biosynthetic process regulation of biosynthetic process regulation of coll motility positive regulation of binding pattern recognition receptor signaling pathway blood coagulation soxacid metabolic process regulation of neuron apoptotic process hemostasis protein-containing complex organization	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that tostop, arevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or extern of bioliqui CLU The chemical reactions and pathways involving a receptor molecul APOE Any process that activates or increases the rate or extern of bioling APOE Any process that activates or increases the rate or extent of bioling APOE Any series of molecular signals generated as a consequence of a pt LBP The sequential process in which the multiple coagulation factors ol APOE Any process that modulates the frequency and yo xoacid; an ox APOA1 APOA4 APOA4 ANy process that modulates the frequency and yo xoacid; and XAPOA4 APOA7 The chemical reactions and pathways involving any xoacid; and XAPOA4 APOA7 Any process that modulates the occurrence or rate of cell death by CNTFR The stopping of bleeding (loss of body fluid) or the arrest of the cin APOE Any process in which macromolecules aggregate, disaggregate, or APOA1 APOA4 APOA4 APOA 4POA APOA process of the cin APOE	15.38 2/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 15.38 2/13 7.69 1/13 1.50.77 4/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.77 1/130 0.77 1/130 0.77 1/130 0.77 1/130 0.77 2/742 0.76 1/131 0.76 1/131 0.76 1/131 0.76 1/131 0.76 1/132 0.77 1/130 0.77 1/130 0.77 1/130 0.76 1/131 0.76 1/131 0.76 1/132 0.75 1/133 0.15 4/2678	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,12550385 0,12550385 0,125503385 0,125503385 0,125535906 0,126053821 0,126053821 0,127309365
G0:0060538 G0:0071222 G0:0003018 G0:1901215 G0:0009891 G0:000058 G0:0043112 G0:2000145 G0:0051099 G0:0002221 G0:0007596 G0:0043436 G0:0043523 G0:0043523 G0:0007599 G0:0043933	carboxylic acid metabolic process skeletal muscle organ development cellular response to lipopolysaccharide vascular process in circulatory system negative regulation of hiosynthetic process regulation of biosynthetic process regulation of biosynthetic process regulation of cell motility positive regulation of binding pattern recognition receptor signaling pathway blood coagulation oxoacid metabolic process regulation of neuron apoptotic process hemostasis protein-containing complex organization coagulation	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in 1LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or CNTFR Any process that atobase or increases the frequency, rate or exten APOA1 APOA4 APOE Any process that atobase or increases the frequency, rate or exten 4POA1 APOA4 APOE Any process that atobase or increases the requency, rate or exten 4POA1 APOA4 APOE Any process that modulates the frequency, rate or extent of biqui CLU The chemical reactions and pathways involving a receptor molecul. APOE Any process that atobase generated as a consequence of a pt LBP The sequential process in which the multiple coagulation factors of APOE The chemical reactions and pathways involving any oxoacid; an ox APOA1 APOA4 Any process that modulates the occurrence or rate of cell death by CNTFR The stopping of bleeding (loss of body fluid) or the arrest of the cin APOE Any process in which macromolecules aggregate, disaggregate, or APOA1 APOA4 APOE CI The process in which a fluid solution, or part of it, changes into a sx APOE	15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 23.08 3/13 7.69 1/13 15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 3.0.77 4/13 7.69 1/13	$\begin{array}{c} 0.22\ 2/736\\ 0.78\ 1/129\\ 0.78\ 1/129\\ 0.78\ 1/129\\ 0.71\ 1/130\\ 0.71\ 1/130\\ 0.71\ 1/130\\ 0.77\ 1/130\\ 0.27\ 2/742\\ 0.76\ 1/131\\ 0.76\ 1/131\\ 0.76\ 1/131\\ 0.75\ 1/131\\ 0.75\ 1/132\\ 0.75\ 1/132\\ 0.75\ 1/132\\ 0.75\ 1/134\end{array}$	0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,125318278 0,125318278 0,125503385 0,125503385 0,125503385 0,125503385 0,125503385 0,126785581 0,126785581 0,127309365
G0:0060538 G0:0071222 G0:0003018 G0:1001215 G0:000891 G0:0004312 G0:0004312 G0:000145 G0:0002221 G0:0007596 G0:0043436 G0:0043523 G0:0043933	carboxylic acid metabolic process skeletal muscle organ development cellular response to lippophysiccharide vascular process in circulatory system negative regulation of houron death positive regulation of biosynthetic process regulation of ubiquitin-dependent protein catabolic proc receptor metabolic process regulation of cell motility positive regulation of binding pattern recognition receptor signaling pathway blood coagulation oxoacid metabolic process regulation of neuron apoptotic process regulation of neuron apoptotic process protein-containing complex organization coagulation negative regulation of protein localization	The chemical reactions and pathways involving carboxylic acids, an APOA1 APOA4 The progression of a skeletal muscle organ over time from its initia CNTFR Any process that results in a change in state or activity of a cell (in LBP A circulatory process that occurs at the level of the vasculature. APOE Any process that stops, prevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that tostop, arevents or reduces the frequency, rate or exter APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or exter APOA1 APOA4 APOE Any process that activates or increases the frequency, rate or extern of bioliqui CLU The chemical reactions and pathways involving a receptor molecul APOE Any process that activates or increases the rate or extern of bioling APOE Any process that activates or increases the rate or extent of bioling APOE Any series of molecular signals generated as a consequence of a pt LBP The sequential process in which the multiple coagulation factors ol APOE Any process that modulates the frequency and yo xoacid; an ox APOA1 APOA4 APOA4 ANy process that modulates the frequency and yo xoacid; and XAPOA4 APOA7 The chemical reactions and pathways involving any xoacid; and XAPOA4 APOA7 Any process that modulates the occurrence or rate of cell death by CNTFR The stopping of bleeding (loss of body fluid) or the arrest of the cin APOE Any process in which macromolecules aggregate, disaggregate, or APOA1 APOA4 APOA4 APOA 4POA APOA process of the cin APOE	15.38 2/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13 15.38 2/13 7.69 1/13 1.50.77 4/13	0.27 2/736 0.78 1/129 0.78 1/129 0.78 1/129 0.77 1/130 0.77 1/130 0.77 1/130 0.77 1/130 0.77 1/130 0.77 2/742 0.76 1/131 0.76 1/131 0.76 1/131 0.76 1/131 0.76 1/132 0.77 1/130 0.77 1/130 0.77 1/130 0.76 1/131 0.76 1/131 0.76 1/132 0.75 1/133 0.15 4/2678	0,125130411 0,125130411 0,125130411 0,125318278 0,125318278 0,125318278 0,125318278 0,12550385 0,12550385 0,125503385 0,125503385 0,125503385 0,1256053821 0,126053821 0,126053821

GO:0022408					
		Any process that stops, prevents or reduces the rate or extent of cr APOA1	7.69 1/13	0.73 1/137	0,129497658
GO:0019538 GO:0009892		The chemical reactions and pathways involving a protein. Includes APOA1 APOA4 APOE BS Any process that stops, prevents, or reduces the frequency, rate or APOA1 APOE CLU LBP		0.12 6/5108 0.15 4/2707	0,130185757 0.130364418
GO:2001242		Any process that modulates the frequency, rate or extent of intrins CLU	7.69 1/13	0.72 1/139	0,130364418
GO:0050807		Any process that modulates the physical form of a synapse, the jun APOE	7.69 1/13	0.72 1/139	0,130364418
GO:0043405	regulation of MAP kinase activity	Any process that modulates the frequency, rate or extent of MAP k APOE	7.69 1/13	0.72 1/139	0,130364418
GO:0040012		Any process that modulates the frequency, rate or extent of locom APOE LBP	15.38 2/13	0.26 2/773	0,131292122
GO:0006082 GO:0007369		The chemical reactions and pathways involving organic acids, any a APOA1 APOA4 A complex and coordinated series of cellular movements that occu APOA1	15.38 2/13 7.69 1/13	0.26 2/774 0.71 1/141	0,131395627 0,131593151
GO:0006508		The hydrolysis of proteins into smaller polypeptides and/or amino APOE CD5L CLU	23.08 3/13	0.18 3/1674	0,131834103
GO:1902905		Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	0.70 1/142	0,132108189
GO:0002440		The synthesis or release of any molecular mediator of the immune APOA1	7.69 1/13	0.70 1/143	0,13280921
GO:0034249 GO:0050803		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13 7.69 1/13	0.69 1/144 0.69 1/144	0,133317515 0,133317515
GO:0050803 GO:0051270		Any process that modulates the physical form or the activity of a sy APOE Any process that modulates the frequency, rate or extent of the mi APOE LBP	15.38 2/13	0.25 2/788	0.134158391
GO:0030178		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.68 1/146	0,134705499
GO:0019637		The chemical reactions and pathways involving organophosphates, APOA1 APOA4	15.38 2/13	0.25 2/793	0,134822032
GO:0001775		A change in the morphology or behavior of a cell resulting from ext APOE LBP	15.38 2/13	0.25 2/793	0,134822032
GO:0050866 GO:0070374		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.68 1/147 0.68 1/147	0,134822032
GO:0070374 GO:0002274		Any process that activates or increases the frequency, rate or exter APOE A change in the morphology or behavior of a myeloid leukocyte res LBP	7.69 1/13 7.69 1/13	0.67 1/149	0,134822032 0,136190891
GO:0043393		Any process that modulates the frequency, rate or extent of protei APOE	7.69 1/13	0.67 1/149	0,136190891
GO:0071356	cellular response to tumor necrosis factor	Any process that results in a change in state or activity of a cell (in 1 APOA1	7.69 1/13	0.66 1/151	0,137743424
GO:0007626		The specific movement from place to place of an organism in respc APOE	7.69 1/13	0.65 1/153	0,138899335
GO:0050708 GO:1901701		Any process that modulates the frequency, rate or extent of the co APOE Any process that results in a change in state or activity of a cell (in 1 APOA4 LBP	7.69 1/13 15.38 2/13	0.65 1/153 0.25 2/811	0,138899335 0,138899335
GO:0044092		Any process that results in a change in state or activity of a cert (in FAPOA4 EBP Any process that stops or reduces the rate or extent of a molecular APOA1 APOE	15.38 2/13	0.25 2/811	0.140029785
GO:0016358		The process whose specific outcome is the progression of the denc APOE	7.69 1/13	0.65 1/155	0,140043497
GO:0010810		Any process that modulates the frequency, rate or extent of cell-su APOA1	7.69 1/13	0.65 1/155	0,140043497
GO:0051336		Any process that modulates the frequency, rate or extent of hydrol APOA1 APOA4	15.38 2/13	0.24 2/819	0,140320408
GO:0046474 GO:0031032		The chemical reactions and pathways resulting in the formation of APOA1 A process that is carried out at the cellular level which results in the APOA1	7.69 1/13 7.69 1/13	0.64 1/156 0.64 1/157	0,140513436 0,141176059
GO:0006469		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.63 1/158	0,141639878
GO:0051495		Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	0.63 1/158	0,141639878
GO:0071216		Any process that results in a change in state or activity of a cell (in 1 LBP	7.69 1/13	0.63 1/159	0,142100623
GO:0031349		Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	0.63 1/159	0,142100623
GO:0007611 GO:0051248		The acquisition and processing of information and/or the storage a APOE Any process that stops, prevents, or reduces the frequency, rate or APOE CLU	7.69 1/13 15.38 2/13	0.62 1/161 0.24 2/839	0,143604767 0,144590764
GO:0007186		A series of molecular signals that proceeds with an activated recep APOA1 APOE GNB2	23.08 3/13	0.17 3/1776	0,145417166
GO:0051402		Any apoptotic process in a neuron, the basic cellular unit of nervou CNTFR	7.69 1/13	0.61 1/164	0,145548879
GO:0072593		The chemical reactions and pathways involving a reactive oxygen s APOA4	7.69 1/13	0.60 1/167	0,147877068
GO:0030163 GO:0002685		The chemical reactions and pathways resulting in the breakdown o APOE CLU	15.38 2/13 7.69 1/13	0.23 2/855 0.59 1/169	0,148478489
GO:002685 GO:0034612		Any process that modulates the frequency, rate, or extent of leuko LBP Any process that results in a change in state or activity of a cell or a APOA1	7.69 1/13	0.59 1/169	0,148743611 0,148743611
GO:0002699		Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	0.59 1/169	0,148743611
GO:0033673		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.58 1/172	0,150983994
GO:0001932		Any process that modulates the frequency, rate or extent of additic APOA1 APOE	15.38 2/13	0.23 2/867	0,150983994
GO:2001234 GO:0010632		Any process that stops, prevents or reduces the frequency, rate or CLU	7.69 1/13 7.69 1/13	0.57 1/174 0.57 1/176	0,152295279 0,153746068
GO:0051651		Any process that modulates the frequency, rate or extent of epithe APOE Any process in which a substance or cellular entity, such as a prote APOE	7.69 1/13	0.56 1/177	0,154364585
GO:0050920		Any process that modulates the frequency, rate or extent of the dii LBP	7.69 1/13	0.56 1/178	0,154980931
GO:1901214		Any process that modulates the frequency, rate or extent of neuro CNTFR	7.69 1/13	0.56 1/179	0,155385135
GO:0006457		The process of assisting in the covalent and noncovalent assembly CLU	7.69 1/13	0.56 1/179	0,155385135
GO:0017038 GO:0044403		The targeting and directed movement of proteins into a cell or org; APOE A process carried out by gene products in an organism that enable APOE	7.69 1/13 7.69 1/13	0.55 1/181 0.55 1/182	0,156817033 0,157424785
GO:0030595		The movement of a leukocyte in response to an external stimulus. LBP	7.69 1/13	0.55 1/182	0,158030411
GO:0002768		A series of molecular signals initiated by the binding of an extracell PIGR	7.69 1/13	0.54 1/184	0,158421274
GO:2001020		Any process that modulates the frequency, rate or extent of respor CLU	7.69 1/13	0.54 1/184	0,158421274
GO:0008654		The chemical reactions and pathways resulting in the formation of APOA1	7.69 1/13	0.54 1/185	0,158601739
GO:0050790 GO:0098742		Any process that modulates the activity of an enzyme. APOA1 APOA4 APOE The attachment of one cell to another cell via adhesion molecules (APOA1	23.08 3/13 7.69 1/13	0.16 3/1868 0.54 1/185	0,158601739 0,158601739
GO:0006909		A vesicle-mediated transport process that results in the engulfmen APOA1	7.69 1/13	0.53 1/188	0,160384562
GO:0034599		Any process that results in a change in state or activity of a cell (in 1 APOA4	7.69 1/13	0.53 1/188	0,160384562
GO:0032496		Any process that results in a change in state or activity of an organi LBP	7.69 1/13	0.53 1/188	0,160384562
GO:0032268		Any process that modulates the frequency, rate or extent of the ch APOA1 APOE CLU	23.08 3/13	0.16 3/1884	0,160762609
GO:0050890 GO:0045017		The operation of the mind by which an organism becomes aware c APOE The chemical reactions and pathways resulting in the formation of APOA1	7.69 1/13 7.69 1/13	0.53 1/189 0.53 1/190	0,160762609 0,161351601
GO:0016485		Any protein maturation process achieved by the cleavage of a pept CD5L	7.69 1/13	0.52 1/192	0,16273845
GO:0051348		Any process that stops or reduces the rate of transferase activity, t APOE	7.69 1/13	0.51 1/196	0,165714026
GO:0030336		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.51 1/197	0,166290792
GO:0051094 GO:0002237		Any process that activates or increases the rate or extent of develo APOA1 APOE Any process that results in a change in state or activity of an organi LBP	15.38 2/13 7.69 1/13	0.21 2/946 0.49 1/204	0,16919499 0,171392867
GO:0007548		The establishment of the sex of an organism by physical differentia CNTFR	7.69 1/13	0.49 1/204	0,171956085
GO:0019932		Any intracellular signal transduction in which the signal is passed o APOE	7.69 1/13	0.49 1/206	0 172201240
GO:0010720		Any process that increases the rate, frequency or extent of the pro APOA1		0.49 1/206	0,172291246
GO:2000146	negative regulation of cell motility		7.69 1/13	0.49 1/206	0,172291246
GO:0007162	accentive requilation of call adhesing	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.49 1/206 0.48 1/207	0,172291246 0,17285013
GO:0070372		Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1	7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208	0,172291246 0,17285013 0,173407081
GO:0070372 GO:0031346	regulation of ERK1 and ERK2 cascade	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.49 1/206 0.48 1/207	0,172291246 0,17285013
GO:0031346 GO:0051271	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cellular component movement	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that stotys, prevents, or reduces the frequency, rate or APOE	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/211	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641
GO:0031346 GO:0051271 GO:0070997	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cellular component movement neuron death	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of Signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that tops, prevents, or reduces the frequency, rate or APOE The process of cell death in a neuron. CMTFR	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/211 0.47 1/213	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641 0,176163105
GO:0031346 GO:0051271 GO:0070997 GO:0060828	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that stops, prevents, or reduces the frequency, rate or APOE The process of cell death in a neuron. Any process that modulates the rate, frequency, or extent of the W APOE	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641 0,176163105 0,176163105
GO:0031346 GO:0051271 GO:0070997	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of Signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that tops, prevents, or reduces the frequency, rate or APOE The process of cell death in a neuron. CMTFR	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/211 0.47 1/213	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641 0,176163105
GO:0031346 GO:0051271 GO:0070997 GO:0060828 GO:0051091 GO:0044265 GO:0042325	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor cellular macromolecule catabolic process regulation of phosphorylation	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that stops, prevents, or reduces the frequency, rate or APOE The process of cell death in a neuron. Any process that activates or increases the frequency, or extent of the W APOE Any process that activates or increases the frequency, rate or exter CLU The chemical reactions and pathways resulting in the breakdown or APOE CLU Any process that modulates the frequency, rate or extent of additit APOA1 APOE	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/215 0.20 2/985 0.20 2/986	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641 0,176163105 0,176163105 0,177482151 0,17783505 0,177901885
GO:0031346 GO:0051271 GO:0070997 GO:0060828 GO:0051091 GO:0044265 GO:0042325 GO:0019058	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor cellular macromolecule catabolic process regulation of phosphorylation viral life cycle	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that stops, prevents, or reduces the frequency, rate or APOE The process of cell death in a neuron. CNTFR Any process that activates or increases the frequency, rate or exter CU The concess that activates or increases the frequency, rate or exter CU The concess that activates or increases the frequency, rate or exter CU Any process that activates or increases the frequency, rate or exter CU Any process that undulates the frequency, rate or extent of additi APOA1 APOE A set of processes which all viruses follow to ensure survival; includ APOE	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/215 0.20 2/985 0.20 2/986 0.46 1/217	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641 0,176163105 0,176163105 0,177482151 0,177482151 0,17783505 0,1779301885
GO:0031346 GO:0051271 GO:0070997 GO:0060828 GO:0051091 GO:0044265 GO:0042325 GO:0019058 GO:0019058 GO:0002366	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor cellular macromolecule catabolic process regulation of phosphorylation viral life cycle leukocyte activation involved in immune response	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that activates or increases the frequency, rate or exter APOE The process of cell death in a neuron. CMTFR Any process that modulates the rate, frequency, or exten to f the VA APOE Any process that activates or increases the frequency, or exten to f the VA APOE Any process that activates or increases the frequency, are or exter CLU The chemical reactions and pathways resulting in the breakdown oa APOE CLU Any process that modulates the frequency, rate or extent of additik APOA1 APOE A set of processes which all viruses follow to ensure survival; inclut APOE A change in morphology and behavior of a leukocyte resulting fron LBP	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 15.38 2/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/215 0.20 2/985 0.20 2/985 0.20 2/985 0.46 1/217 0.45 1/222	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,176163105 0,176163105 0,177632151 0,17783505 0,17783505 0,177833911 0,181705455
GO:0031346 GO:0051271 GO:0070997 GO:0060828 GO:0051091 GO:0044265 GO:0042325 GO:0019058 GO:0019058 GO:0002366 GO:0062197	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cell projection component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor cellular macromolecule catabolic process regulation of phosphorylation viral life cycle leukocyte activation involved in immune response cellular response to chemical stress	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that nodulates the frequency, rate or extent of signal APOE The process of cell death in a neuron. Any process that activates or increases the frequency, or extent of the W APOE Any process that activates or increases the frequency, or extent of the W APOE Any process that activates or increases the frequency, are or exter CLU The chemical reactions and pathways resulting in the breakdown on APOE CLU Any process that modulates the frequency, rate or extent of additit APOA1 APOE A set of processes which all viruses follow to ensure survival; incluc APOE A change in morphology and behavior of a leukocyte resulting from LBP Any process that results in a change in state or activity of a cell (In 1APOA4	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 15.38 2/13 15.38 2/13 7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/213 0.20 2/985 0.20 2/985 0.20 2/986 0.46 1/217 0.45 1/222	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,17506641 0,175163105 0,1776163105 0,177482151 0,17748215 0,177901885 0,177901885 0,178339911 0,181705455
GO:0031346 GO:0051271 GO:0070997 GO:0060828 GO:0051091 GO:0044265 GO:0042325 GO:0019058 GO:0019058 GO:0002366	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor cellular macromolecule catabolic process regulation of phosphorylation viral life cycle leukocyte activation involved in immune response cellular response to chemical stress muscle organ development	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that stops, prevents, or reduces the frequency, rate or APOA1 Any process that modulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE The process of cell death in a neuron. CMTFR Any process that modulates the rate, frequency, or exten to fthe VA APOE Any process that activates or increases the frequency, or exten to fthe VA APOE Any process that activates or increases the frequency, or exten to fthe VA APOE Any process that activates or increases the frequency, are or exter CLU The chemical reactions and pathways resulting in the breakdown oa APOE CLU Any process that modulates the frequency, rate or extent of additik APOA1 APOE A set of processes which all viruses follow to ensure survival; inclux APOE A change in morphology and behavior of a leukocyte resulting fron LBP	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 15.38 2/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/215 0.20 2/985 0.20 2/985 0.20 2/985 0.46 1/217 0.45 1/222	0,172291246 0,17285013 0,173407081 0,17506641 0,17506641 0,176163105 0,176163105 0,177632151 0,17783505 0,17783505 0,177833911 0,181705455
G0:0031346 G0:0051271 G0:0070997 G0:0060828 G0:0051091 G0:0042255 G0:0019058 G0:0019058 G0:0002366 G0:0007517 G0:0007371 G0:0007371	regulation of ERK1 and ERK2 cascade positive regulation of cell projection organization negative regulation of cell projection organization negative regulation of cellular component movement neuron death regulation of canonical Wnt signaling pathway positive regulation of DNA-binding transcription factor cellular macromolecule catabolic process regulation of phosphorylation viral life cycle leukocyte activation involved in immune response cellular response to chemical stress muscle organ development ERK1 and ERK2 cascade cell activation involved in immune response	Any process that stops, prevents, or reduces the frequency, rate or APOE Any process that tops, prevents, or reduces the frequency, rate or APOA1 Any process that nodulates the frequency, rate or extent of signal APOE Any process that activates or increases the frequency, rate or exter APOE Any process that stops, prevents, or reduces the frequency, rate or APOE The process of cell death in a neuron. CNTFR Any process that activates or increases the frequency, rate or exter CIU The chemical reactions and pathways resulting in the breakdown o APOE CLU Any process that activates or increases the frequency, rate or exter CLU The chemical reactions and pathways resulting in the breakdown o APOE CLU Any process that troubulates the frequency, rate or extent of additi. APOA1 APOE A star of processes which all viruses follow to ensure survival; inclu APOE A change in morphology and behavior of a leukocyte resulting from LBP Any process that results in a change in state or activity of a cell (in 14 POA4 The process whose specific outcome is the progression of the mus CNTFR An intracellular protein kinase cascade containing at least ERX1 or 1APOE A change in the morphology or behavior of a cell resulting from ex JLBP	7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 15.38 2/13 15.38 2/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13 7.69 1/13	0.49 1/206 0.48 1/207 0.48 1/208 0.47 1/211 0.47 1/211 0.47 1/211 0.47 1/213 0.47 1/213 0.47 1/213 0.47 1/215 0.20 2/985 0.46 1/217 0.45 1/222 0.45 1/224 0.45 1/224	0.172291246 0.17285013 0.173407081 0.17506641 0.17506641 0.17506641 0.176163105 0.177482151 0.177783505 0.17793833911 0.181705455 0.182529035 0.182529035
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GO:0009593	detection of chemical stimulus	The series of events in which a chemical stimulus is received by a c LBP PIGR	15.38 2/13	0.18 2/1107	0,206436292
GO:0051098 GO:0031589	regulation of binding cell-substrate adhesion	Any process that modulates the frequency, rate or extent of bindin APOE The attachment of a cell to the underlying substrate via adhesion n APOA1	7.69 1/13 7.69 1/13	0.37 1/267 0.37 1/268	0,207900797 0,208359481
GO:0031385	regulation of Wnt signaling pathway	Any process that modulates the frequency, rate or extent of the ac APOE	7.69 1/13	0.37 1/269	0,208335481
GO:0051051	negative regulation of transport	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.37 1/272	0,209920074
GO:0031326	regulation of cellular biosynthetic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE CL	30.77 4/13	0.12 4/3385	0,209920074
GO:0042326	negative regulation of phosphorylation	Any process that stops, prevents or decreases the rate of addition APOE	7.69 1/13	0.37 1/271	0,209920074
GO:0050794 GO:0009991	regulation of cellular process response to extracellular stimulus	Any process that modulates the frequency, rate or extent of a cellu APOA1 APOA4 APOE CL Any process that results in a change in state or activity of a cell or a APOE	69.23 9/13 7.69 1/13	0.09 9/10398	0,209920074 0,210370081
GO:1901565	organonitrogen compound catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE CLU	15.38 2/13	0.37 1/273 0.18 2/1129	0,210570081
GO:0060326	cell chemotaxis	The directed movement of a motile cell guided by a specific chemic LBP	7.69 1/13	0.36 1/275	0,211266796
GO:0016032	viral process	A multi-organism process in which a virus is a participant. The othe APOE	7.69 1/13	0.36 1/276	0,211712862
GO:0009057	macromolecule catabolic process	The chemical reactions and pathways resulting in the breakdown o APOE CLU	15.38 2/13	0.18 2/1142	0,213766539
GO:0002696	positive regulation of leukocyte activation	Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	0.36 1/280	0,214004591
GO:0051247 GO:0010975	positive regulation of protein metabolic process regulation of neuron projection development	Any process that activates or increases the frequency, rate or exter APOE CLU Any process that modulates the rate, frequency or extent of neuro APOE	15.38 2/13 7.69 1/13	0.17 2/1145 0.36 1/281	0,21413537 0,214181715
GO:0071900		Any process that modulates the rate, frequency, or extent of prote APOE	7.69 1/13	0.35 1/282	0,214618966
GO:0009889	regulation of biosynthetic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE CL		0.12 4/3433	0,215348593
GO:0050867	positive regulation of cell activation	Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	0.35 1/286	0,216616035
GO:2001233 GO:0032103	regulation of apoptotic signaling pathway	Any process that modulates the frequency, rate or extent of apopt CLU	7.69 1/13	0.35 1/286	0,216616035
GO:0032103 GO:0044282	positive regulation of response to external stimulus small molecule catabolic process	Any process that activates, maintains or increases the rate of a resi LBP The chemical reactions and pathways resulting in the breakdown o APOE	7.69 1/13 7.69 1/13	0.35 1/287 0.35 1/289	0,217046107 0,218165997
GO:0002683	negative regulation of immune system process	Any process that stops, prevents, or reduces the frequency, rate, o APOA1	7.69 1/13	0.34 1/294	0,22131033337
GO:0050808	synapse organization	A process that is carried out at the cellular level which results in the APOE	7.69 1/13	0.34 1/296	0,222185296
GO:0032956	regulation of actin cytoskeleton organization	Any process that modulates the frequency, rate or extent of the for APOA1	7.69 1/13	0.34 1/296	0,222185296
GO:0007159	leukocyte cell-cell adhesion	The attachment of a leukocyte to another cell via adhesion molecu APOA4	7.69 1/13	0.34 1/298	0,223017081
GO:0050804 GO:0099177	modulation of chemical synaptic transmission regulation of trans-synaptic signaling	Any process that modulates the frequency or amplitude of synaptic APOE Any process that modulates the frequency, rate or extent of trans-: APOE	7.69 1/13 7.69 1/13	0.34 1/298 0.33 1/299	0,223017081 0,223430852
GO:0031399	regulation of protein modification process	Any process that modulates the frequency, rate or extent of thans- APOE Any process that modulates the frequency, rate or extent of the co APOA1 APOE	15.38 2/13	0.17 2/1192	0,223430832
GO:0010035	response to inorganic substance	Any process that results in a change in state or activity of a cell or a APOA4	7.69 1/13	0.33 1/304	0,226290751
GO:0048732	gland development	The process whose specific outcome is the progression of a gland c APOA1	7.69 1/13	0.33 1/306	0,227373454
GO:0003008	system process	A multicellular organismal process carried out by any of the organs APOA1 APOE PIGR	23.08 3/13	0.13 3/2314	0,228258451
GO:0051606	detection of stimulus	The series of events in which a stimulus is received by a cell or org: LBP PIGR	15.38 2/13	0.16 2/1215	0,230084939
GO:0051223 GO:0051346	regulation of protein transport negative regulation of hydrolase activity	Any process that modulates the frequency, rate or extent of the dii APOE Any process that stops or reduces the rate of hydrolase activity, thi APOA1	7.69 1/13 7.69 1/13	0.32 1/314 0.32 1/317	0,231938893 0,233392136
GO:0006874	cellular calcium ion homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.32 1/317	0,233392136
GO:0008015	blood circulation	The flow of blood through the body of an animal, enabling the tran APOE	7.69 1/13	0.31 1/320	0,235114394
GO:0045936	negative regulation of phosphate metabolic process	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.31 1/321	0,23522024
GO:0010563		Any process that decreases the frequency, rate or extent of the cht APOE	7.69 1/13	0.31 1/321	0,23522024
GO:0032970 GO:0009611	regulation of actin filament-based process response to wounding	Any process that modulates the frequency, rate or extent of any ce APOA1	7.69 1/13 7.69 1/13	0.31 1/324 0.31 1/326	0,236929371 0,237970511
GO:0009611 GO:0055074	calcium ion homeostasis	Any process that results in a change in state or activity of a cell or a APOE Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.30 1/328	0,237970511
GO:0034248	regulation of cellular amide metabolic process	Any process that modulates the frequency, rate or extent of the ch APOE	7.69 1/13	0.30 1/329	0,239383041
GO:0001819	positive regulation of cytokine production	Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	0.30 1/330	0,239757211
GO:0051090		Any process that modulates the frequency, rate or extent of the ac CLU	7.69 1/13	0.30 1/333	0,24144015
GO:0070201	regulation of establishment of protein localization	Any process that modulates the frequency, rate or extent of the di APOE	7.69 1/13	0.30 1/336	0,242957053
GO:0006796 GO:0003013	phosphate-containing compound metabolic process	The chemical reactions and pathways involving the phosphate grou APOA1 APOA4 APOE	23.08 3/13 7.69 1/13	0.12 3/2404 0.29 1/342	0,242957053 0,246154629
GO:0003013 GO:0022607	circulatory system process cellular component assembly	A organ system process carried out by any of the organs or tissues APOE The aggregation, arrangement and bonding together of a cellular c APOA1 APOA4 APOE CL		0.29 1/342 0.11 4/3663	0,246154629
GO:0006793	phosphorus metabolic process	The chemical reactions and pathways involving the nonmetallic ele APOA1 APOA4 APOE	23.08 3/13	0.12 3/2425	0,246523915
GO:0045785	positive regulation of cell adhesion	Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	0.29 1/345	0,247515849
GO:0022407	regulation of cell-cell adhesion	Any process that modulates the frequency, rate or extent of attach APOA1	7.69 1/13	0.29 1/346	0,247870716
GO:0071396	cellular response to lipid	Any process that results in a change in state or activity of a cell (in 1 LBP	7.69 1/13	0.29 1/347	0,24793472
GO:0072503 GO:0043065	cellular divalent inorganic cation homeostasis positive regulation of apoptotic process	Any process involved in the maintenance of an internal steady stat APOE Any process that activates or increases the frequency, rate or exter CLU	7.69 1/13 7.69 1/13	0.29 1/347 0.29 1/349	0,24793472 0,248928016
GO:0032501	multicellular organismal process	Any biological process, occurring at the level of a multicellular orga APOA1 APOA4 APOE CN		0.09 6/6399	0,250398406
GO:0016055	Wnt signaling pathway	The series of molecular signals initiated by binding of a Wnt proteir APOE	7.69 1/13	0.28 1/355	0,252177649
GO:1903530	regulation of secretion by cell	Any process that modulates the frequency, rate or extent of secret APOE	7.69 1/13	0.28 1/357	0,252862676
GO:0198738	cell-cell signaling by wnt	Any process that mediates the transfer of information from one ce APOE	7.69 1/13	0.28 1/357	0,252862676
GO:0043068 GO:0060284	positive regulation of programmed cell death regulation of cell development	Any process that activates or increases the frequency, rate or exter CLU Any process that modulates the rate, frequency or extent of the pr APOA1	7.69 1/13 7.69 1/13	0.28 1/360 0.28 1/361	0,254469765 0,254807102
GO:0080284 GO:0072507	divalent inorganic cation homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.27 1/364	0,256403624
GO:0006468	protein phosphorylation	The process of introducing a phosphate group on to a protein. APOA1 APOE	15.38 2/13	0.15 2/1340	0,258358008
GO:0043410	positive regulation of MAPK cascade	Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	0.27 1/373	0,261451749
GO:0090066	regulation of anatomical structure size	Any process that modulates the size of an anatomical structure. APOE	7.69 1/13	0.26 1/379	0,264888846
GO:0044089		Any process that activates or increases the frequency, rate or exter APOA1	7.69 1/13	0.26 1/382	0,266445924
GO:1901361 GO:0010942	organic cyclic compound catabolic process positive regulation of cell death	The chemical reactions and pathways resulting in the breakdown o APOE Any process that increases the rate or frequency of cell death. Cell CLU	7.69 1/13 7.69 1/13	0.26 1/386 0.26 1/388	0,268614067 0,269230092
GO:0031400	negative regulation of protein modification process	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.26 1/388	0,269230092
GO:0043161		The chemical reactions and pathways resulting in the breakdown o CLU	7.69 1/13	0.26 1/391	0,27076494
GO:0030335		Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	0.25 1/393	0,271680698
GO:0007015	actin filament organization	A process that is carried out at the cellular level which results in the APOA1	7.69 1/13	0.25 1/396	0,272891771
GO:0050778 GO:0010638	positive regulation of immune response positive regulation of organelle organization	Any process that activates or increases the frequency, rate or exter LBP Any process that increases the frequency, rate or extent of a proce APOA1	7.69 1/13 7.69 1/13	0.25 1/396 0.25 1/398	0,272891771 0,273798258
GO:0051046	regulation of secretion	Any process that modulates the frequency, rate or extent of the co APOE	7.69 1/13	0.25 1/400	0,2747012
GO:0044085	cellular component biogenesis	A process that results in the biosynthesis of constituent macromole APOA1 APOA4 APOE CL		0.10 4/3907	0,280759789
GO:0034613	cellular protein localization	Any process in which a protein is transported to, and/or maintaine APOE PIGR	15.38 2/13	0.14 2/1432	0,280980247
GO:2000147	positive regulation of cell motility	Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13	0.24 1/412	0,280998782
GO:0070727 GO:0051272	cellular macromolecule localization positive regulation of cellular component movement	Any process in which a macromolecule is transported to, and/or m APOE PIGR Any process that activates or increases the frequency, rate or exter LBP	15.38 2/13 7.69 1/13	0.14 2/1438 0.24 1/417	0,282093234 0,283353704
GO:0031272 GO:0034645	cellular macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOE	15.38 2/13	0.14 2/1449	0,283333704
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent of a biolc APOA1 APOA4 APOE CL		0.08 9/11175	0,285250534
GO:1905114		Any cell surface receptor signaling pathway that is involved in cell-(APOE	7.69 1/13	0.24 1/424	0,286552791
GO:0040017	positive regulation of locomotion	Any process that activates or increases the frequency, rate or exter LBP	7.69 1/13 15.38 2/13	0.24 1/425	0,286821692
GO:0033554 GO:0120035	cellular response to stress regulation of plasma membrane bounded cell projection	Any process that results in a change in state or activity of a cell (in 1 APOA4 CLU Any process that modulates the frequency, rate or extent of a proc APOE	7.69 1/13	0.14 2/1463 0.23 1/433	0,287441725 0,290888498
GO:0006875	cellular metal ion homeostasis	Any process involved in the maintenance of an internal steady stati APOE	7.69 1/13	0.23 1/435	0,291734768
GO:0051493	regulation of cytoskeleton organization	Any process that modulates the frequency, rate or extent of the for APOA1	7.69 1/13	0.23 1/437	0,292577709
GO:0090407	organophosphate biosynthetic process	The chemical reactions and pathways resulting in the biosynthesis APOA1	7.69 1/13	0.23 1/439	0,293417335
GO:0031344	regulation of cell projection organization	Any process that modulates the frequency, rate or extent of a proc APOE	7.69 1/13	0.23 1/441 0.23 1/444	0,294253657
GO:0002694 GO:0061061	regulation of leukocyte activation muscle structure development	Any process that modulates the frequency, rate, or extent of leuko LBP The progression of a muscle structure over time, from its formatioi CNTFR	7.69 1/13 7.69 1/13	0.22 1/444	0,295667245 0,295916443
GO:0001001 GO:0048514	blood vessel morphogenesis	The process in which the anatomical structures of blood vessels an APOE	7.69 1/13	0.22 1/445	0,29732078
GO:0097190	apoptotic signaling pathway	A series of molecular signals which triggers the apoptotic death of CLU	7.69 1/13	0.22 1/459	0,303315344
GO:0008285	negative regulation of cell population proliferation	Any process that stops, prevents or reduces the rate or extent of cr APOE	7.69 1/13	0.21 1/469	0,308685376
GO:0010604		Any process that increases the frequency, rate or extent of the che APOE CLU LBP	23.08 3/13	0.11 3/2795	0,311072191
GO:1901566 GO:0030003	organonitrogen compound biosynthetic process cellular cation homeostasis	The chemical reactions and pathways resulting in the formation of APOA1 APOE Any process involved in the maintenance of an internal steady stat APOE	15.38 2/13 7.69 1/13	0.13 2/1575 0.20 1/491	0,315851788 0,320051181
GO:0030003 GO:0048468	cell development	The process whose specific outcome is the progression of the cell c APOA1 APOE	15.38 2/13	0.13 2/1592	0,320051181
GO:0048598	embryonic morphogenesis	The process in which anatomical structures are generated and org; APOA1	7.69 1/13	0.20 1/494	0,321015759
GO:0055065	metal ion homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.20 1/495	0,321063025
GO:0045859	regulation of protein kinase activity	Any process that modulates the frequency, rate or extent of protei APOE	7.69 1/13	0.20 1/496	0,321063025
GO:0007169 GO:0016310	transmembrane receptor protein tyrosine kinase signal phosphorylation	A series of molecular signals initiated by the binding of an extracell PIGR The process of introducing a phosphate group into a molecule, usu APOA1 APOE	7.69 1/13 15.38 2/13	0.20 1/496 0.12 2/1608	0,321063025 0,322877391
GO:0010310 GO:0080135	regulation of cellular response to stress	Any process that modulates the frequency, rate or extent of a cellu CLU	7.69 1/13	0.20 1/503	0,32422243
GO:0006873	cellular ion homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.20 1/504	0,324416163
GO:0098916	anterograde trans-synaptic signaling	Cell-cell signaling from pre to post-synapse, across the synaptic cle APOE	7.69 1/13	0.20 1/508	0,325897401
GO:0007268	chemical synaptic transmission	The vesicular release of classical neurotransmitter molecules from APOE	7.69 1/13	0.20 1/508	0,325897401
GO:0001568	blood vessel development	The process whose specific outcome is the progression of a blood \ APOE Cell-cell signaling in either direction across the synaptic cleft. APOE	7.69 1/13	0.19 1/516	0,329544752
GO:0099537 GO:0034330	trans-synaptic signaling cell junction organization	Cell-cell signaling in either direction across the synaptic cleft. APOE A process that is carried out at the cellular level which results in the APOE	7.69 1/13 7.69 1/13	0.19 1/516 0.19 1/522	0,329544752 0,332437581
GO:00343300 GO:0043408	regulation of MAPK cascade	Any process that modulates the frequency, rate or extent of signal APOE	7.69 1/13	0.19 1/524	0,333154883
GO:0099536	synaptic signaling	Cell-cell signaling to, from or within a synapse. APOE	7.69 1/13	0.18 1/541	0,341913202
GO:0001944	vasculature development	The process whose specific outcome is the progression of the vasci APOE	7.69 1/13	0.18 1/544	0,343138517
GO:0032940	secretion by cell	The controlled release of a substance by a cell. APOE	7.69 1/13	0.18 1/545	0,34329622

GO:0010468	regulation of gene expression	Any process that modulates the frequency, rate or extent of gene & APOA1 APOE CLU LBP		0.09 4/4340	0,345279159
GO:0000904	cell morphogenesis involved in differentiation	The change in form (cell shape and size) that occurs when relativel APOA1	7.69 1/13	0.18 1/552	0,346253185
GO:0055080	cation homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.18 1/556	0,347983958
GO:0098771	inorganic ion homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.18 1/565	0,352322678
GO:0030155	regulation of cell adhesion	Any process that modulates the frequency, rate or extent of attach APOA1	7.69 1/13	0.17 1/573	0,356106743
GO:0055082	cellular chemical homeostasis	Any biological process involved in the maintenance of an internal s APOE	7.69 1/13	0.17 1/586	0,362439936
GO:0140352	export from cell	The directed movement of some substance from a cell, into the exi APOE	7.69 1/13	0.17 1/587	0,362562147
GO:0043549 GO:0006511	regulation of kinase activity	Any process that modulates the frequency, rate or extent of kinase APOE The chemical reactions and pathways resulting in the breakdown o CLU	7.69 1/13	0.17 1/588	0,362683779 0,362804833
GO:0006511 GO:0000165	ubiquitin-dependent protein catabolic process MAPK cascade	An intracellular protein kinase cascade containing at least a MAPK, APOE	7.69 1/13 7.69 1/13	0.17 1/589 0.17 1/591	0,362804833 0,363436429
GO:000165 GO:0044267		The chemical reactions and pathways involving a specific protein, r APOA1 APOE BSPRY CLU		0.09 4/4461	0,363436429
GO:0044287 GO:0032880	cellular protein metabolic process regulation of protein localization	Any process that modulates the frequency, rate or extent of any pr APOE	7.69 1/13	0.09 4/4481	0,363621939
GO:0032880 GO:0045597	positive regulation of cell differentiation	Any process that modulates the nequency, rate of extent of any process that activates or increases the frequency, rate or exten APOA1	7.69 1/13	0.17 1/594	0,363791845
GO:0050801	ion homeostasis	Any process involved in the maintenance of an internal steady stati APOE	7.69 1/13	0.17 1/602	0,367454167
GO:0019941	modification-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakdown o CLU	7.69 1/13	0.17 1/603	0,367564965
GO:0030036	actin cytoskeleton organization	A process that is carried out at the cellular level which results in the APOA1	7.69 1/13	0.16 1/611	0,370796073
GO:0043632		The chemical reactions and pathways resulting in the breakdown o CLU	7.69 1/13	0.16 1/611	0,370796073
GO:0065007	biological regulation	Any process that modulates a measurable attribute of any biologic APOA1 APOA4 APOE CL		0.08 9/11905	0,371110441
GO:0050793	regulation of developmental process	Any process that modulates the frequency, rate or extent of develc APOA1 APOE	15.38 2/13	0.11 2/1822	0,37196899
GO:0050877	nervous system process	A organ system process carried out by any of the organs or tissues APOE PIGR	15.38 2/13	0.11 2/1827	0,372955229
GO:0019222	regulation of metabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE CL		0.08 5/5976	0,376657959
GO:0046903	secretion	The controlled release of a substance by a cell or a tissue. APOE	7.69 1/13	0.16 1/645	0,385588701
GO:0035239	tube morphogenesis	The process in which the anatomical structures of a tube are gener APOE	7.69 1/13	0.15 1/646	0,385666206
GO:0008284	positive regulation of cell population proliferation	Any process that activates or increases the rate or extent of cell pri CNTFR	7.69 1/13	0.15 1/651	0,387686058
GO:0036211	protein modification process	The covalent alteration of one or more amino acids occurring in pri APOA1 APOE BSPRY	23.08 3/13	0.09 3/3236	0,388693709
GO:0006464	cellular protein modification process	The covalent alteration of one or more amino acids occurring in pri APOA1 APOE BSPRY	23.08 3/13	0.09 3/3236	0,388693709
GO:0019725	cellular homeostasis	Any process involved in the maintenance of an internal steady stat APOE	7.69 1/13	0.15 1/660	0,390795323
GO:0003006	developmental process involved in reproduction	A developmental process in which a progressive change in the stat CNTFR	7.69 1/13	0.15 1/666	0,393259156
GO:0006974	cellular response to DNA damage stimulus	Any process that results in a change in state or activity of a cell (in 1 CLU	7.69 1/13	0.15 1/668	0,393799491
GO:0022603	regulation of anatomical structure morphogenesis	Any process that modulates the frequency, rate or extent of anator APOA1	7.69 1/13	0.15 1/671	0,394813775
GO:0051172		Any process that stops, prevents, or reduces the frequency, rate or APOE CLU	15.38 2/13	0.10 2/1924	0,395060766
GO:0030029	actin filament-based process	Any cellular process that depends upon or alters the actin cytoskel APOA1	7.69 1/13	0.15 1/675	0,395880714
GO:0051338	regulation of transferase activity	Any process that modulates the frequency, rate or extent of transf APOE	7.69 1/13	0.15 1/676	0,395937736
GO:0002684	positive regulation of immune system process	Any process that activates or increases the frequency, rate, or exte LBP	7.69 1/13	0.15 1/677	0,395994347
GO:0008104	protein localization	Any process in which a protein is transported to, or maintained in, APOE PIGR	15.38 2/13	0.10 2/1967	0,405004369
GO:0031175	neuron projection development	The process whose specific outcome is the progression of a neuror APOE	7.69 1/13	0.14 1/701	0,406393709
GO:0016567	protein ubiquitination	The process in which one or more ubiquitin groups are added to a BSPRY	7.69 1/13	0.14 1/702	0,406431971
GO:0045321	leukocyte activation	A change in morphology and behavior of a leukocyte resulting from LBP	7.69 1/13	0.14 1/713	0,411084482
GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units in a polyp APOA1 APOE BSPRY	23.08 3/13	0.09 3/3413	0,420547459
GO:0080090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE CL		0.08 4/4857	0,42410368
GO:0032446	protein modification by small protein conjugation	A protein modification process in which one or more groups of a sr BSPRY	7.69 1/13	0.13 1/758	0,430150421
GO:0016043 GO:0007167	cellular component organization enzyme linked receptor protein signaling pathway	A process that results in the assembly, arrangement of constituent APOA1 APOA4 APOE CL Any series of molecular signals initiated by the binding of an extrac PIGR	7.69 1/13	0.08 5/6354 0.13 1/778	0,430796145 0,438101381
GO:0009653	anatomical structure morphogenesis	The process in which anatomical structures are generated and org: APOA1 APOE	15.38 2/13	0.09 2/2107	0,438101381
GO:0032269		Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.13 1/792	0,443306075
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOE CLU	23.08 3/13	0.08 3/3552	0,446397462
GO:0035295	tube development	The process whose specific outcome is the progression of a tube or APOE	7.69 1/13	0.12 1/804	0,446649717
GO:0000902	cell morphogenesis	The developmental process in which the size or shape of a cell is gr APOA1	7.69 1/13	0.12 1/802	0,446649717
GO:0072359	circulatory system development	The process whose specific outcome is the progression of the circu APOE	7.69 1/13	0.12 1/804	0,446649717
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOA4 APOE CL		0.08 4/5027	0,450445619
GO:0048731	system development	The process whose specific outcome is the progression of an organ APOA1 APOE CNTFR	23.08 3/13	0.08 3/3612	0,456320018
GO:0048666	neuron development	The process whose specific outcome is the progression of a neuror APOE	7.69 1/13	0.12 1/830	0,456320018
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent macromole APOA1 APOA4 APOE CL		0.08 5/6564	0,460658644
GO:0044249	cellular biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4 APOE CL		0.08 4/5094	0,460658644
GO:0010628	positive regulation of gene expression	Any process that increases the frequency, rate or extent of gene ex LBP	7.69 1/13	0.12 1/857	0,466167228
GO:0009790	embryo development	The process whose specific outcome is the progression of an embr APOA1	7.69 1/13	0.11 1/874	0,472186037
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4 APOE CL	30.77 4/13	0.08 4/5165	0,472186037
GO:0070647	protein modification by small protein conjugation or re	A protein modification process in which one or more groups of a sr BSPRY	7.69 1/13	0.11 1/877	0,472924217
GO:0006518	peptide metabolic process	The chemical reactions and pathways involving peptides, compoun APOE	7.69 1/13	0.11 1/897	0,480520167
GO:0009058	biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOA4 APOE CL	30.77 4/13	0.08 4/5231	0,481937985
GO:0033043	regulation of organelle organization	Any process that modulates the frequency, rate or extent of a proc APOA1	7.69 1/13	0.11 1/903	0,481937985
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromolecules, a APOA1 APOE BSPRY CLU		0.08 4/5305	0,494496024
GO:0007275	multicellular organism development	The biological process whose specific outcome is the progression c APOA1 APOE CNTFR	23.08 3/13	0.08 3/3871	0,503073785
GO:0051641	cellular localization	A cellular localization process whereby a substance or cellular entit APOE PIGR	15.38 2/13	0.08 2/2418	0,507309426
GO:0051173		Any process that activates or increases the frequency, rate or exter APOE CLU	15.38 2/13	0.08 2/2473	0,520095882
GO:0030182	neuron differentiation	The process in which a relatively unspecialized cell acquires special APOE	7.69 1/13	0.10 1/1022	0,524497076
GO:0022414	reproductive process	A biological process that directly contributes to the process of proc CNTFR	7.69 1/13	0.10 1/1021	0,524497076
GO:000003	reproduction	The production of new individuals that contain some portion of gei CNTFR	7.69 1/13	0.10 1/1024	0,524700345
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOE CLU LBP	7 60 4 /42	0.07 4/5552	0,534251272
GO:0050907 GO:0048513	animal organ development	The series of events in which a chemical stimulus is received and cr PIGR	7.69 1/13	0.09 1/1085	0,545578724
GO:0048513 GO:0043603	cellular amide metabolic process	Development of a tissue or tissues that work together to perform a APOA1 CNTFR The chemical reactions and pathways involving an amide, any deriv APOE	15.38 2/13 7.69 1/13	0.09 1/1112	0,549636105 0,553902636
GO:0045595	regulation of cell differentiation	Any process that modulates the frequency, rate or extent of cell dil APOA1	7.69 1/13	0.09 1/1122	0,5557134281
GO:0043393	peptidyl-amino acid modification	The alteration of an amino acid residue in a peptide. APOA1	7.69 1/13	0.09 1/1125	0,55725833
GO:0050906		The series of events involved in sensory perception in which a sens PIGR	7.69 1/13	0.09 1/1133	0,559428443
GO:0007267	cell-cell signaling	Any process that mediates the transfer of information from one ce APOE	7.69 1/13	0.09 1/1138	0,560563984
GO:0048699	generation of neurons	The process in which nerve cells are generated. This includes the p APOE	7.69 1/13	0.09 1/1146	0,562704087
GO:0007606	sensory perception of chemical stimulus	The series of events required for an organism to receive a sensory PIGR	7.69 1/13	0.09 1/1156	0,565495908
GO:0120036	plasma membrane bounded cell projection organizatio	A process that is carried out at the cellular level which results in the APOE	7.69 1/13	0.09 1/1160	0,566264143
GO:0030030	cell projection organization	A process that is carried out at the cellular level which results in the APOE	7.69 1/13	0.08 1/1190	0,575595382
GO:0015031	protein transport	The directed movement of proteins into, out of or within a cell, or APOE	7.69 1/13	0.08 1/1193	0,575997775
GO:0009059	macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formation of APOA1 APOE CLU	23.08 3/13	0.07 3/4337	0,582048203
GO:0048856	anatomical structure development	The biological process whose specific outcome is the progression c APOA1 APOE CNTFR	23.08 3/13	0.07 3/4373	0,588043902
GO:0007010	cytoskeleton organization	A process that is carried out at the cellular level which results in the APOA1	7.69 1/13	0.08 1/1245	0,590303082
GO:0022008	neurogenesis	Generation of cells within the nervous system. APOE	7.69 1/13	0.08 1/1245	0,590303082
GO:0010467	gene expression	The process in which a gene's sequence is converted into a mature APOA1 APOE CD5L CLU		0.07 5/7489	0,592935623
GO:1903506	regulation of nucleic acid-templated transcription	Any process that modulates the frequency, rate or extent of nuclei APOE CLU	15.38 2/13	0.07 2/2881	0,598834421
GO:0006355	regulation of transcription, DNA-templated	Any process that modulates the frequency, rate or extent of cellula APOE CLU	15.38 2/13	0.07 2/2881	0,598834421
GO:0009890	negative regulation of biosynthetic process	Any process that stops, prevents, or reduces the rate of the chemic APOE	7.69 1/13	0.08 1/1277	0,598834421
GO:2001141	regulation of RNA biosynthetic process	Any process that modulates the frequency, rate or extent of RNA b APOE CLU	15.38 2/13	0.07 2/2884	0,598873483
GO:0045184	establishment of protein localization	The directed movement of a protein to a specific location. APOE	7.69 1/13	0.08 1/1286	0,599425856
GO:1902680	positive regulation of RNA biosynthetic process	Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	0.07 1/1360	0,619564812
GO:0045893	positive regulation of transcription, DNA-templated	Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	0.07 1/1358	0,619564812
GO:1903508		Any process that activates or increases the frequency, rate or exter APOE The cellular synthesis of RNA on a template of DNA. APOE CLU	7.69 1/13	0.07 1/1358	0,619564812
GO:0006351 GO:0097659	transcription, DNA-templated nucleic acid-templated transcription	The cellular synthesis of RNA on a template of DNA. APOE CLU The cellular synthesis of RNA on a template of nucleic acid (DNA or APOE CLU	15.38 2/13 15.38 2/13	0.07 2/3019 0.07 2/3019	0,623076713 0,623076713
GO:0097659 GO:0032774	RNA biosynthetic process	The cellular synthesis of RNA on a template of nucleic acid (DNA of APOE CLU The chemical reactions and pathways resulting in the formation of APOE CLU	15.38 2/13	0.07 2/3019 0.07 2/3030	0,623076713
GO:0032774 GO:0030154	cell differentiation	The process in which relatively unspecialized cells, e.g. embryonic (APOA1 APOE	15.38 2/13	0.06 2/3098	0,624671372
GO:0050154 GO:0051171	regulation of nitrogen compound metabolic process	Any process that modulates the frequency, rate or extent of the ch APOA1 APOE CLU	23.08 3/13	0.06 3/4722	0,639275541
GO:0007600	sensory perception	The series of events required for an organism to receive a sensory PIGR	7.69 1/13	0.07 1/1454	0,642140251
GO:0051252	regulation of RNA metabolic process	Any process that modulates the frequency, rate or extent of the ch APOE CLU	15.38 2/13	0.06 2/3134	0,642229693
GO:0051252	positive regulation of RNA metabolic process	Any process that activates or increases the frequency, rate or exter APOE	7.69 1/13	0.07 1/1459	0,642229693
GO:0032502	developmental process	A biological process whose specific outcome is the progression of a APOA1 APOE CNTFR	23.08 3/13	0.06 3/4755	0,642240252
GO:0043170	macromolecule metabolic process	The chemical reactions and pathways involving macromolecules, a APOA1 APOA4 APOE BS		0.06 7/10935	0,642971788
GO:0048869	cellular developmental process	A biological process whose specific outcome is the progression of a APOA1 APOE	15.38 2/13	0.06 2/3162	0,645488616
GO:0010557		Any process that increases the rate, frequency or extent of the che APOE	7.69 1/13	0.07 1/1528	0,657822923
GO:0010556	regulation of macromolecule biosynthetic process	Any process that modulates the rate, frequency or extent of the ch APOE CLU	15.38 2/13	0.06 2/3278	0,665862095
GO:0071705	nitrogen compound transport	The directed movement of nitrogen-containing compounds into, or APOE	7.69 1/13	0.06 1/1587	0,671363035
GO:0045935		Any cellular process that activates or increases the frequency, rate APOE	7.69 1/13	0.06 1/1597	0,673163562
GO:0019219		Any cellular process that modulates the frequency, rate or extent c APOE CLU	15.38 2/13	0.06 2/3342	0,675453838
GO:0034654	nucleobase-containing compound biosynthetic process	The chemical reactions and pathways resulting in the formation of APOE CLU	15.38 2/13	0.06 2/3364	0,678698589
GO:0018130	heterocycle biosynthetic process	The chemical reactions and pathways resulting in the formation of APOE CLU	15.38 2/13	0.06 2/3434	0,690236036
GO:0019438	aromatic compound biosynthetic process	The chemical reactions and pathways resulting in the formation of APOE CLU	15.38 2/13	0.06 2/3441	0,690767929
GO:0007399	nervous system development	The process whose specific outcome is the progression of nervous APOE	7.69 1/13	0.06 1/1710	0,696425723
	organic cyclic compound metabolic process	The chemical reactions and pathways involving organic cyclic comp APOA1 APOA4 APOE CL	30.77 4/13	0.06 4/7066	0,736495369
GO:1901360	organic cyclic compound metabolic process				

GO:0031324	negative regulation of cellular metabolic process	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.05 1/2035	0,761153639
GO:0044271	cellular nitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formation of APOE CLU	15.38 2/13	0.05 2/4213	0,801554622
GO:0071704	organic substance metabolic process	The chemical reactions and pathways involving an organic substan APOA1 APOA4 APOE BS	53.85 7/13	0.06 7/12360	0,813612225
GO:0006807	nitrogen compound metabolic process	The chemical reactions and pathways involving organic or inorgani APOA1 APOA4 APOE BS	46.15 6/13	0.05 6/10926	0,817432796
GO:0044238	primary metabolic process	The chemical reactions and pathways involving those compounds \ APOA1 APOA4 APOE BS	46.15 6/13	0.05 6/11429	0,863735743
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism and cat APOA1 APOA4 APOE BS	53.85 7/13	0.05 7/12915	0,865498758
GO:0006996	organelle organization	A process that is carried out at the cellular level which results in the APOA1	7.69 1/13	0.03 1/3330	0,9128581
GO:0016070	RNA metabolic process	The cellular chemical reactions and pathways involving RNA, ribon APOE CLU	15.38 2/13	0.03 2/5843	0,934248931
GO:0009987	cellular process	Any process that is carried out at the cellular level, but not necessa APOA1 APOA4 APOE BS	84.62 11/13	0.06 11/18706	0,949011927
GO:0090304	nucleic acid metabolic process	Any cellular metabolic process involving nucleic acids. APOE CLU	15.38 2/13	0.03 2/6311	0,953583437
GO:0044237	cellular metabolic process	The chemical reactions and pathways by which individual cells tran APOA1 APOA4 APOE BS	38.46 5/13	0.04 5/11581	0,95708073
GO:0006139	nucleobase-containing compound metabolic process	Any cellular metabolic process involving nucleobases, nucleosides, APOE CLU	15.38 2/13	0.03 2/6721	0,965715164
GO:0046483	heterocycle metabolic process	The chemical reactions and pathways involving heterocyclic compc APOE CLU	15.38 2/13	0.03 2/6828	0,967847786
GO:0006725	cellular aromatic compound metabolic process	The chemical reactions and pathways involving aromatic compoun APOE CLU	15.38 2/13	0.03 2/6891	0,968619603
GO:0034641	cellular nitrogen compound metabolic process	The chemical reactions and pathways involving various organic and APOE CLU	15.38 2/13	0.03 2/7596	0,982311673
GO:0008150	biological_process	A biological process represents a specific objective that the organis APOA1 APOA4 APOE BS	100.00 13/13	0.06 13/20110	1

sPLS_Lipolysi	s_Enrichment_GO_BP_of_15prot_contributing_to_LL_group				
GO_BP	Name	Function Gene Name Any process that activates or increases the frequency, rate or extent of protein lipida RAB3GAP1 RAB3GAP2	Term frequen	cy Term frequen	P-value (fdr) Query with no gene names
GO:1903061	positive regulation of protein lipidation		14.29 2/14	66.67 2/3	0,000232138
	establishment of protein localization to endoplasmic reticulum me	The directed movement of a protein to a specific location in the endoplasmic reticul. RAB3GAP1 RAB3GAP2	14.29 2/14	66.67 2/3	0,000232138
	positive regulation of lipoprotein metabolic process	Any process that activates or increases the frequency, rate or extent of the chemical RAB3GAP1 RAB3GAP2	14.29 2/14	66.67 2/3	0,000232138
GO:1903373 GO:1903059		Any process that activates or increases the frequency, rate or extent of endoplasmic RAB3GAP1 RAB3GAP2 Any process that modulates the frequency, rate or extent of protein lipidation. RAB3GAP1 RAB3GAP2	14.29 2/14 14.29 2/14	50.00 2/4 33.33 2/6	0,000348068
GO:1903371		Any process that modulates the frequency, rate or extent of endoplasmic reticulum t RAB3GAP1 RAB3GAP2 Any process that modulates the frequency, rate or extent of the chemical reactions a RAB3GAP1 RAB3GAP2	14.29 2/14 14.29 2/14	33.33 2/6 20.00 2/10	0,000579652
GO:2000786	positive regulation of autophagosome assembly endoplasmic reticulum tubular network organization	Any process that activates or increases the frequency, rate or extent of autophagic ve RAB3GAP1 RAB3GAP2 A process that is carried out at the cellular level which results in the assembly, arrang RAB3GAP1 RAB3GAP2	14.29 2/14 14.29 2/14	13.33 2/15 13.33 2/15	0,002695373 0.002695373
GO:0044090	positive regulation of vacuole organization	Any process that activates or increases the frequency, rate or extent of a process invc RAB3GAP1 RAB3GAP2	14.29 2/14	11.11 2/18	0,003530572
	positive regulation of organelle organization regulation of autophagosome assembly	Any process that increases the frequency, rate or extent of a process involved in the I ALOX15 RAB3GAP1 RAB3GAP2 SURF4 Any process that modulates the frequency, rate or extent of autophagosome assemb RAB3GAP1 RAB3GAP2	14.29 2/14	1.01 4/398 5.00 2/40	0,006063322 0,014868471
GO:0016239	regulation of vacuole organization	Any process that modulates the frequency, rate or extent of a process involved in the RAB3GAP1 RAB3GAP2	14.29 2/14	4.55 2/44	0,016619188
	positive regulation of macroautophagy	Any process, such as recognition of nutrient depletion, that activates or increases the RAB3GAP1 RAB3GAP2	14.29 2/14	3.57 2/56	0,025002424
GO:0072599	establishment of protein localization to endoplasmic reticulum	The directed movement of a protein to a specific location in the endoplasmic reticult RAB3GAP1 RAB3GAP2	14.29 2/14	3.45 2/58	0,02502797
GO:1901074	regulation of engulfment of apoptotic cell	Any process that modulates the frequency, rate or extent of engulfment of apoptotic ALOX15	7.14 1/14	50.00 1/2	0,031226796
GO:0035963	cellular response to interleukin-13	Any process that results in a change in state or activity of a cell (in terms of movemer ALOX15	7.14 1/14	50.00 1/2	0,031226796
GO:1902117	positive regulation of organelle assembly	Any process that activates or increases the frequency, rate or extent of organelle assi RAB3GAP1 RAB3GAP2	14.29 2/14	2.99 2/67	0,031226796
GO:0070972	protein localization to endoplasmic reticulum	A process in which a protein is transported to, or maintained in, a location within the RAB3GAP1 RAB3GAP2	14.29 2/14	2.56 2/78	0,031226796
GO:0035962	response to interleukin-13	Any process that results in a change in state or activity of a cell or an organism (in ter ALOX15	7.14 1/14	50.00 1/2	0,031226796
GO:1990962	xenobiotic transport across blood-brain barrier endoplasmic reticulum organization	The directed movement of a xenobiotic through the blood-brain barrier. ABCG2 A process that is carried out at the cellular level which results in the assembly. arrane RAB3GAP1 RAB3GAP2	7.14 1/14	50.00 1/2 2.67 2/75	0,031226796
	renal urate salt excretion positive regulation of cellular component organization	The elimination of urate salt or uric acid from peritubular capillaries (or surrounding ABCG2 Any process that activates or increases the frequency, rate or extent of a process inv ALOX15 RAB3GAP1 RAB3GAP2 SURF4	7.14 1/14	50.00 1/2 0.52 4/763	0,031226796 0.032631168
GO:0042158	lipoprotein biosynthetic process regulation of macroautophagy	The chemical reactions and pathways resulting in the formation of any conjugated, w RAB3GAP1 RAB3GAP2	14.29 2/14 14.29 2/14	2.08 2/96	0,034158726 0,034158726
GO:0044089	positive regulation of cellular component biogenesis	Any process that activates or increases the frequency, rate or extent of cellular comp ALOX15 RAB3GAP1 RAB3GAP2	21.43 3/14	0.79 3/382	0,034158726
GO:0006497	protein lipidation	The covalent attachment of lipid groups to an amino acid in a protein. RAB3GAP1 RAB3GAP2 The formation of a double membrane-bounded structure, the autophagosome, that (RAB3GAP1 RAB3GAP2	14.29 2/14	2.20 2/91	0,034158726
GO:0000045	autophagosome assembly		14.29 2/14	2.15 2/93	0,034158726
GO:2001303	lipoxin A4 biosynthetic process	The chemical reactions and pathways resulting in the formation of lipoxin A4. Lipoxir ALOX15	7.14 1/14	33.33 1/3	0,034158726
GO:2001302	lipoxin A4 metabolic process	The chemical reactions and pathways involving lipoxin A4. Lipoxin A4 is a C20 hydrox ALOX15	7.14 1/14	33.33 1/3	0,034158726
	autophagosome organization	A process that is carried out at the cellular level which results in the assembly, arrang RAB3GAP1 RAB3GAP2	14.29 2/14	2.04 2/98	0,034158726
	lipoxin biosynthetic process	The chemical reactions and pathways resulting in the formation of a lipoxin. A lipoxir ALOX15	7.14 1/14	25.00 1/4	0,039277551
GO:0033043	regulation of organelle organization	Any process that modulates the frequency, rate or extent of a process involved in the ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57 4/14	0.44 4/903	0,039277551
GO:2001300	lipoxin metabolic process	The chemical reactions and pathways involving a lipoxin. A lipoxin is a non-classic eic ALOX15	7.14 1/14	25.00 1/4	0,039277551
GO:0010256	endomembrane system organization	A process that is carried out at the cellular level which results in the assembly, arrang RAB3GAP1 RAB3GAP2 SURF4	21.43 3/14	0.73 3/409	0,039277551
GO:0010508	positive regulation of autophagy	Any process that activates, maintains or increases the rate of autophaev, Autophaev, IRAB3GAP1 RAB3GAP2	14.29 2/14		0.039277551
GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formation of a fatty acid, any ol ALOX15 FASN	14.29 2/14	1.61 2/124 20.00 1/5	0,044398083
GO:0032218	riboflavin transport	The directed movement of riboflavin into, out of or within a cell, or between cells, by ABCG2	7.14 1/14		0.045994882
GO:0042157 GO:0006897	lipoprotein metabolic process endocytosis	The chemical reactions and pathways involving any conjugated, water-soluble protein RAB3GAP1 RAB3GAP2	14.29 2/14	1.49 2/134 0.64 3/466	0,047892584 0,047892584
GO:0015747	urate transport	A vesicle-mediated transport process in which cells take up external materials or mer ALOX15 MYO6 SURF4 The directed movement of urate into, out of or within a cell, or between cells, by me ABC62 The changing accidence and extravars conviluent in the formation of charcen of there are ESN.	21.43 3/14 7.14 1/14 7.14 1/14	16.67 1/6	0,051234879
GO:0008611	glycerol ether biosynthetic process	The chemical reactions and pathways resulting in the formation of glycerol ethers, ar FASN	7.14 1/14	12.50 1/8	0,05409999
	ether lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of ether lipids, lipids FASN	7.14 1/14	12.50 1/8	0,05409999
GO:0007033	vacuole organization	A process that is carried out at the cellular level which results in the assembly, arrang RAB3GAP1 RAB3GAP2	14.29 2/14	1.25 2/160	0,05409999
GO:0051122	hepoxilin biosynthetic process	The chemical reactions and pathways resulting in the formation of hepoxilins, a class ALOX15	7.14 1/14	14.29 1/7	0,05409999
GO:0051121	neutrophil differentiation	The process in which a myeloid precursor cell acquires the specialized features of a n FASN	7.14 1/14	12.50 1/8	0,05409999
	hepoxilin metabolic process	The chemical reactions and pathways involving hepoxilins, a class of bioactive icosan(ALOX15	7.14 1/14	14.29 1/7	0,05409999
GO:0097384	cellular lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of lipids, as carried o FASN	7.14 1/14	12.50 1/8	0,05409999
GO:1905153	regulation of membrane invagination	Any process that modulates the frequency, rate or extent of membrane invagination. ALOX15	7.14 1/14	12.50 1/8	0,05409999
GO:0072330	monocarboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of monocarboxylic ar ALOX15 FASN	14.29 2/14	1.31 2/153	0,05409999
GO:0060099	regulation of phagocytosis, engulfment	Any process that modulates the frequency, rate or extent of the internalization of bar ALOX15	7.14 1/14	12.50 1/8	0,05409999
	linoleic acid metabolic process regulation of organelle assembly	The chemical reactions and pathways involving linoleic acid, an unsaturated omega-6 ALOX15 Any process that modulates the frequency, rate or extent of organelle assembly. RAB3GAP1 RAB3GAP2	7.14 1/14 14.29 2/14	12.50 1/8 1.20 2/166	0,05409999 0,055179087
GO:0090557	establishment of endothelial intestinal barrier	The establishment of a barrier between endothelial cell layers of the intestine to exe FASN The chemical reactions and pathways resulting in the formation of ether. FASN	7.14 1/14	11.11 1/9	0,057583388
GO:1901503	ether biosynthetic process		7.14 1/14	11.11 1/9	0,057583388
GO:0015937	coenzyme A biosynthetic process	The chemical reactions and pathways resulting in the formation of coenzyme A, 3'-pl-COASY	7.14 1/14	10.00 1/10	0,060708626
	lipoxygenase pathway	The chemical reactions and pathways by which an unsaturated fatty acid (such as ara ALOX15	7.14 1/14	10.00 1/10	0,060708626
GO:0006646 GO:0021854	phosphatidylethanolamine biosynthetic process hypothalamus development	The chemical reactions and pathways or which an unsubative net you got got got an ACOXIS The chemical reactions and pathways resulting in the formation of phosphatidyletha ALOXIS The progression of the hypothalamus region of the forebrain, from its initial formatic RAB3GAP1	7.14 1/14 7.14 1/14 7.14 1/14	10.00 1/10 10.00 1/10 8.33 1/12	0,060708626 0.068180864
GO:0046415	urate metabolic process	The chemical reactions and pathways involving urate, the anion of uric acid, 2,6,8-tric ABCG2	7.14 1/14	8.33 1/12	0,068180864
GO:0097254	ether lipid metabolic process	The chemical reactions and pathways involving ether lipids, lipids that contain (norm FASN	7.14 1/14	8.33 1/12	0,068180864
	renal tubular secretion	The elimination of substances from peritubular capillaries (or surrounding hemolym; ABCG2	7.14 1/14	8.33 1/12	0,068180864
GO:0016236		The major inducible pathway for the general turnover of cytoplasmic constituents in RAB3GAP1 RAB3GAP2	14.29 2/14	0.98 2/205	0,06999336
GO:0035358		Any process that modulates the frequency, rate or extent of the peroxisome prolifer; ALOX15	7.14 1/14	7.69 1/13	0,071566786
GO:0090150	establishment of protein localization to membrane	The directed movement of a protein to a specific location in a membrane. RAB3GAP1 RAB3GAP2 The directed movement of a protein to a specific location. MYO6 RAB3GAP1 RAB3GAP2 SURF4	14.29 2/14	0.94 2/212	0,072397037
GO:0045184	establishment of protein localization		28.57 4/14	0.31 4/1286	0,072487065
GO:0010232	vascular transport	The directed movement of substances, into, out of or within a cell, either in a vascula ABCG2	7.14 1/14	7.14 1/14	0,072487065
GO:0042759	long-chain fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formation of long-chain fatty at ALOX15	7.14 1/14	6.67 1/15	0,072487065
GO:0042953	lipoprotein transport	The directed movement of any conjugated, water-soluble protein in which the nonpr SURF4	7.14 1/14	6.67 1/15	0,072487065
GO:0006662	glycerol ether metabolic process	The chemical reactions and pathways involving glycerol ethers, any anhydride former FASN	7.14 1/14	6.67 1/15	0,072487065
	transport across blood-brain barrier	The directed movement of substances (e.g. macromolecules, small molecules, ions) t ABCG2	7.14 1/14	7.14 1/14	0,072487065
	coenzyme A metabolic process	The chemical reactions and pathways involving coenzyme A, 3'-phosphoadenosine-(5 COASY	7.14 1/14	7.14 1/14	0,072487065
	lipoprotein localization regulation of autophagy	Any process in which a lipoprotein is transported to, or maintained in, a specific local SURF4 Any process that modulates the frequency, rate or extent of autophagy. Autophagy i: RAB3GAP1 RAB3GAP2	7.14 1/14 14.29 2/14	6.67 1/15 0.87 2/229	0,072487065
GO:0046394	carboxylic acid biosynthetic process oreanic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of carboxylic acids, a ALOXIS FASN The chemical reactions and pathways resulting in the formation of carboxylic acids, any ALOXIS FASN	14.29 2/14	0.84 2/239	0,079096213
GO:0018279	protein N-linked glycosylation via asparagine peroxisome proliferator activated receptor signaling pathway	The glycosylation of protein via the N4 atom of peptidyl-asparagine forming N4-glyco RPN1	7.14 1/14	5.26 1/19 5.26 1/19	0,085894731
GO:0018196	peptidyl-asparagine modification	The series of molecular signals initiated by binding of a ligand to any of the peroxisor ALOX15 The modification of peptidyl-asparagine. RPN1	7.14 1/14	5.00 1/20	0,086030352 0.086030352
	ether metabolic process engulfment of apoptotic cell	The chemical reactions and pathways involving organic ethers, any anhydride of the <code># FASN</code> The removal of the apoptotic cell by phagocytosis, by a neighboring cell or by a phage ALOX15	7.14 1/14 7.14 1/14	5.00 1/20 5.00 1/20	0,086030352
GO:0071353	lipid droplet organization	A process that is carried out at the cellular level which results in the assembly, arrang RAB3GAP1	7.14 1/14	5.00 1/20	0,086030352
	cellular response to interleukin-4	Any process that results in a change in state or activity of a cell (in terms of movemer FASN	7.14 1/14	4.76 1/21	0,087152618
GO:0044087	regulation of cellular component biogenesis	Any process that modulates the frequency, rate or extent of cellular component biog ALOX15 RAB3GAP1 RAB3GAP2	21.43 3/14	0.39 3/762	0,087152618
GO:1901570	fatty acid derivative biosynthetic process	The chemical reactions and pathways resulting in the formation of fatty acid derivativ ALOX15	7.14 1/14	4.76 1/21	0,087152618
	glandular epithelial cell development	The process whose specific outcome is the progression of a glandular epithelial cell o FASN	7.14 1/14	4.55 1/22	0,088085295
	response to interleukin-4	Any process that results in a change in state or activity of a cell or an organism (in ter FASN	7.14 1/14	4.55 1/22	0,088085295
GO:0006082	organic acid metabolic process	The chemical reactions and pathways involving organic acids, any acidic compound cr ABCG2 ALOX15 FASN	21.43 3/14	0.39 3/774	0,088085295
GO:0044281	small molecule metabolic process	The chemical reactions and pathways involving small molecules, any low molecular w ABCG2 ALOX15 COASY FASN	28.57 4/14	0.27 4/1460	0,088085295
GO:0043087	regulation of GTPase activity transeoithelial transport	Any process that modulates the rate of GTP hydrolysis by a GTPase. RAB3GAP1 RAB3GAP2 The directed movement of a substance from one side of an epithelium to the other. ABCG2	14.29 2/14 7.14 1/14	0.70 2/287	0,092016845
GO:0007588		The elimination by an organism of the waste products that arise as a result of metability and CG2 The elimination by an organism of the waste products that arise as a result of metability ABCG2 The process in which the anatomical structures of the face are generated and organi RAB3GAP1	7.14 1/14 7.14 1/14 7.14 1/14	4.17 1/24 4.00 1/25	0,092016845 0.093802689
GO:0046337	phosphatidylethanolamine metabolic process	The process in which the anatomical structures of the face are generated and organic KNBSGAP1 The chemical reactions and pathways involving phosphatidylethanolamine, any of a c ALOX15 The process in which a relatively unspecialized myeloid precursor cell acquires the sp FASN	7.14 1/14	4.00 1/25	0,093802689 0,093802689 0,100186942
	monocyte differentiation granulocyte differentiation	The process in which a myeloid precursor cell acquires the specialized features of a g FASN	7.14 1/14 7.14 1/14	3.70 1/27 3.57 1/28	0,101744377
GO:0006631	tricarboxylic acid cycle fatty acid metabolic process	A nearly universal metabolic pathway in which the acetyl group of acetyl coenzyme A SDHA The chemical reactions and pathways involving fatty acids, alighatic monocarboxylic : ALOX15 FASN	7.14 1/14 14.29 2/14	3.57 1/28 0.63 2/316	0,101744377 0,10242527
GO:1901566	organonitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formation of organonitrogen cc COASY RAB3GAP1 RAB3GAP2 RPN1	28.57 4/14	0.25 4/1575	0,10242527
GO:0042908	xenobiotic transport	The directed movement of a xenobiotic into, out of or within a cell, or between cells, ABCG2	7.14 1/14	3.33 1/30	0,104669299
	head morphogenesis	The process in which the anatomical structures of the head are generated and organi RAB3GAP1	7.14 1/14	3.33 1/30	0,104669299
	positive regulation of cellular catabolic process	Any process that activates or increases the frequency, rate or extent of the chemical RAB3GAP1 RAB3GAP2	14.29 2/14	0.58 2/342	0,114870543
GO:0072594	establishment of protein localization to organelle	The directed movement of a protein to a specific location on or in an organelle. Enco RAB3GAP1 RAB3GAP2	14.29 2/14	0.56 2/357	0,120920032
GO:0019369	arachidonic acid metabolic process	The chemical reactions and pathways involving arachidonic acid, a straight chain fatt ₁ ALOX15	7.14 1/14	2.78 1/36	0,120920032
GO:0002066	columnar/cuboidal epithelial cell development	The process whose specific outcome is the progression of a columnar/cuboidal epithir FASN	7.14 1/14	2.78 1/36	0,120920032
GO:0033866	nucleoside bisphosphate biosynthetic process	The chemical reactions and pathways resulting in the formation of a nucleoside bispl COASY	7.14 1/14	2.56 1/39	0,123561824
	ribonucleoside bisphosphate biosynthetic process	The chemical reactions and pathways resulting in the formation of a ribonucleoside t COASY	7.14 1/14	2.56 1/39	0,123561824
	body morphogenesis	The process in which the anatomical structures of the soma are generated and organ RAB3GAP1	7.14 1/14	2.63 1/38	0,123561824
GO:0034033	purine nucleoside bisphosphate biosynthetic process	The chemical reactions and pathways resulting in the formation of a purine nucleosic COASY	7.14 1/14	2.56 1/39	0,123561824
	establishment of endothelial barrier fatty acid derivative metabolic process	The establishment of a barrier between endothelial cell layers, such as those in the b FASN The chemical reactions and pathways involving fatty acid derivative. ALOX15 Automatic the padulate the foreuroper critical parts and the padulate the padulate the foreuroper critical parts and the padulate the padulate the foreuroper critical parts and the padulate	7.14 1/14 7.14 1/14	2.56 1/39 2.63 1/38	0,123561824 0,123561824 0,124371884
GO:0006914		Any process that modulates the frequency, rate or extent of a process involved in the ALOX15 RAB3GAP1 RAB3GAP2 SURF4 The cellular catabolic process in which cells digest parts of their own cytoplasm; allow RAB3GAP1 RAB3GAP2 The cellular catabolic process in which cells digest parts of their own cytoplasm; allow RAB3GAP1 RAB3GAP2 RAB3GAP2	28.57 4/14 14.29 2/14	0.23 4/1732 0.52 2/382	0,124271984 0,125939179
GO:0061919	process utilizing autophagic mechanism	A cellular process involving delivery of a portion of the cytoplasm to lysosomes or to RAB3GAP1 RAB3GAP2	14.29 2/14	0.52 2/382	0,125939179
GO:0043277	apoptotic cell clearance	The recognition and removal of an apoptotic cell by a neighboring cell or by a phagor ALOX15	7.14 1/14	2.33 1/43	0,125939179
GO:0043407	negative regulation of MAP kinase activity	Any process that stops, prevents, or reduces the frequency, rate or extent of MAP kir STK38	7.14 1/14	2.38 1/42	0,125939179
GO:0060324	face development	The biological process whose specific outcome is the progression of a face from an in RAB3GAP1	7.14 1/14	2.33 1/43	0,125939179
GO:0030838	positive regulation of actin filament polymerization	Any process that activates or increases the frequency, rate or extent of actin polymer ALOX15	7.14 1/14	2.38 1/42	0,125939179
GO:0051180	vitamin transport	The directed movement of vitamins into, out of or within a cell, or between cells, by ABCG2	7.14 1/14	2.33 1/43	0,125939179
GO:0002820	negative regulation of adaptive immune response	Any process that stops, prevents, or reduces the frequency, rate, or extent of an ada ALOX15	7.14 1/14	2.33 1/43	0,125939179
	glandular epithelial cell differentiation	The process in which a relatively unspecialized cell acquires specialized features of a FASN	7.14 1/14	2.27 1/44	0,126731734
	unsaturated fatty acid biosynthetic process positive regulation of catabolic process	The process in which a relatively dispectance centre of the optimized relatives of a prostary of the optimized relatives of a prostary of the optimized relatives of a prostary of a unsaturated far ALOXIS Any process that activates or increases the frequency, rate or extent of the chemical RAB3GAP1 RAB3GAP2	7.14 1/14 7.14 1/14 14.29 2/14	2.27 1/44 0.50 2/400	0,126731734 0,127616256
GO:0009898 GO:0021536 GO:0090407	diencephalon development organophosphate biosynthetic process	Any process that activates of increases the requerity, rate of extend of the chemical increases and activates of increases and activates of the process whose specific outcome is the progression of the diencephalon over tim RAB3GAP1 The chemical reactions and pathways resulting in the biosynthesis of deoxyribose ph ALOX15 COASY	14.29 2/14 7.14 1/14 14.29 2/14	2.13 1/47 0.46 2/439	0,133077868 0,145527383
GO:0044283	small molecule biosynthetic process	The chemical reactions and pathways resulting in the formation of small molecules, a ALOX15 FASN	14.29 2/14	0.46 2/437	0,145527383
GO:0030330		The progression of an endothelial cell over time, from its formation to the mature str FASN A cascade of processes induced by the cell cycle regulator phosphoprotein p53, or an MYO6	7.14 1/14 7.14 1/14	1.89 1/53 1.89 1/53	0,145527383 0,145527383
GO:0008104	protein localization	Any process in which a protein is transported to, or maintained in, a specific location. MYO6 RAB3GAP1 RAB3GAP2 SURF4		0.20 4/1967	0,161053768
GO:0044249	cellular biosynthetic process	The chemical reactions and pathways resulting in the formation of substances, carrie ALOX15 COASY FASN MYO6 RAB3GAP1		0.14 7/5094	0,161053768
	monocarboxylic acid metabolic process	The chemical reactions and pathways involving monocarboxylic acids, any organic aci ALOX15 FASN	14.29 2/14	0.43 2/470	0,161053768
	protein localization to membrane	A process in which a protein is transported to, or maintained in, a specific location in RAB3GAP1 RAB3GAP2	14.29 2/14	0.42 2/473	0,161700279

GO:0006911 phagocytosis, engulfment phagocytosis, engulfment phagocytosis, engulfment regulation of cellular macromolecule biosynthetic process organic substance biosynthetic process establishment of localization limbic system development regulation of protein modification process renal system process long-chain fatty acid metabolic process liosynthetic process regulation of phagocytosis regulation of phagocytosis GO:0006487 GO:2000112 GO:1901576 GO:0009058 GO:0050764 GO:0051049 regulation of transport plasma membrane invagination GO:0099024 positive regulation of protein polymerization GO:0032273 GO:0071277 cellular response to calcium ion columnar/cuboidal epithelial cell differentiation
 GO:1901137
 carbohydrate derivative biosynthetic process

 GO:0008610
 lipid biosynthetic process

 GO:001408
 regulation of MAPK cascade

 GO:001626
 localization within membrane
 localization within membrane endothelial cell differentiation vesicle-mediated transport ribonucleoside bisphosphate metabolic process GO:0045446 GO:0045440 GO:0033875 GO:0019395 fatty acid oxidation GO:0006690 icosanoid metabolic process) icosanoid metabolic process i regulation of lipid transport j purine nucleoside bisphosphate metabolic process i nucleoside bisphosphate metabolic process in control of the sentence of the sentence of the sentence negative regulation of profile sentency/threadine kinase activity protein modification process positive regulation of cell-substrate adhesion endothelium development cellular protein modification process lipid oxidation MARY errorstence GO:0032368 GO:0034032 GO:0033865 GO:0033865 GO:0071901 GO:0036211 GO:0010811 GO:0003158 GO:0006464 GO:0034440 MAPK cascade GO:0000165 unsaturated fatty acid metabolic process bone mineralization regulation of cellular catabolic process 60:0033559 GO:0030282 GO:0031329 GO:0051592 response to calcium ion cellular detoxification cellular detoxification
 cellular response to toxshance
 metabolic process
 regulation of lipid localization
 regulation of lipid localization
 cellular macromolecule biosynthetic process
 macromolecule modification
 cellular response to cytokine stimulus
 lefinic compound metabolic process
 (odgi organization
 signal transduction by p33 class mediator
 macromolecule localization GO:1990748 GO:0097237 GO:0008152 GO:1905952 GO:0034645 GO:0043412 GO:0071345 GO:0120254 GO:0072331 macromolecule localization mammary gland development negative regulation of immune response 60:0033036 GO:0030879 GO:0050777 GO:0033554 cellular response to stress cellular response to DNA damage stimulus GO:0006974 GU:00097 cellular response to DNA damage stimulus
GO:009873 devinčation
GO:005088 lipid homeostasis
GO:004238 primary metabolic process
GO:0031214 biomineral tissue development
GO:000765 sensory perception of sound
GO:0101564 organointrogen compound metabolic process
GO:0110144 biomineralization egative regulation GO:0034097 response to cytokine vascular process in circulatory system G0:000318 vascular process in circulatory system G0:003010 vaguitation of endocytosis G0:003102 vaguitation of endocytosis G0:002300 electron transport chain G0:002300 electron transport chain G0:0014237 carboxylic acid metabolic process G0:0042437 carboxylic acid metabolic process G0:003954 sensory perception of mechanical stimulus G0:003954 regulation of catabolic process G0:003954 regulation of catabolic process G0:004437 coacid metabolic process G0:004436 regulation of MAP kinase activity G0:01920360 sosibili regulation of MAP kinase activity G0:01920360 spotier egulation of Syaramlectuar fiber or G0:1920365 positive regulation of Syaramlectuar fiber or GO:0003018 Co-0004305 regulation of APC hase activity
 G0:109205 positive regulation of supramolecular fiber organization
 G0:0071241 co-lellar response to inorganic substance
 G0:0071241 co-lellar response to inorganic substance
 G0:0071270 signal transduction in response to DNA damage
 G0:0070370 signal transduction of Cellular biosynthetic process
 G0:0070370 signal transduction of ERL1 and ERL2 cascade
 G0:00703142 positive regulation of aKI and ERL2 cascade
 G0:00703931 positive regulation of a biosynthetic process
 G0:00703931 positive regulation of biosynthetic process
 G0:00703931 positive regulation of protein-containing complex assembly
 G0:007031401 positive regulation of protein modification process
 G0:007030401 positive regulation of protein modification process
 G0:0070401401 positive regulation of protein modification process
 G0:0070401401 positive regulation of protein modification process
 G0:0070401401 positive regulation protein positive regulation
 G0:0070401401 positive regulation positive regulation
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 G0:0070401401
 G0:0070401401
 G0:007040140
 G0:007040140
 G0:007040140
 G0:007040140
 G0:0070401 GO:0009636 response to toxic substance negative regulation of protein kinase activity GO:0006469 GO:0051495 positive regulation of cytoskeleton organization GO:0070925 GO:0070925 organelle assembly GO:0046474 glycerophospholipid biosynthetic process G0:004674 giverophospholipid biosynthetic process G0:000262 infonucleotide biosynthetic process G0:000253 infonucleotide biosynthetic process G0:000253 organophosphate metabolic process G0:0002634 purine nucleotide biosynthetic process G0:0005136 purine nucleotide biosynthetic process G0:005136 purine nucleotide biosynthetic process G0:0005136 purine nucleotide biosynthetic process G0:0005136 purine nucleotide biosynthetic process G0:0005230 purine-uncleotide biosynthetic process G0:0005222 purine-unclaining compound biosynthetic process G0:0003523 purine-unclaining compound biosynthetic process
 G0:007252
 purine-containing compound biosynthetic proces

 G0:0033673
 negative regulation of kinase activity

 G0:003154
 actin polymerization or depolymerization

 G0:004257
 cellular lipid metabolic process

 G0:001574
 protein metabolic process

 G0:0015758
 protein metabolic process

 G0:0015758
 protein metabolic process

 G0:001582
 hopsholipid biosynthetic process

 G0:0008564
 phospholipid biosynthetic process

 G0:0008564
 phospholipid biosynthetic process

 G0:0008564
 phaeoxtoxis
 GO:0006909 phagocytosis GO:0045017 glycerolipid biosynthetic process cellular catabolic process GO:0044248 GO:0010038 response to metal ion negative regulation of transferase activity GO:0051348 GO:0043413 lecule glycosylation G0:0043413 macromolecule głycosylation G0:006486 protein głycosylation G0:006487 positiw regulation of GTPase activity G0:0045333 cellular respiration G0:000730 regulation of catalytic activity G0:0007327 regulation of FKI and EKIZ cascade G0:0002228 regulation of cellular protein metabolic process G0:0009170 rudeotide biosynthetic process G0:0009727 regulation of inflammatory response G0:0009727 regulation of inflammatory response GO:0070085 glycosylation nucleoside phosphate biosynthetic process GO:1901293 GO:1901293 nucleoside prosprate plosynthetic process GO:0070371 ERK1 and ERK2 cascade GO:0034976 response to endoplasmic reticulum stress GO:0071704 organic substance metabolic process GO:0051179 localization

1.61 1/62 0,162969827 1.61 1/62 1.59 1/63 0.42 2/480 0.14 7/5165 0.15 6/4033 1.49 1/67 0.25 3/1192 1.45 1/69 1.47 1/68 0,163110603 0,163110603 0,165118173 0.13 7/5231 0.167845322 1.49 1/67 0.167845322 0.25 3/1201 0,167845322 1.43 1/70 0.16844096 1.41 1/71 0,168484318 1.41 1/71 1.39 1/72 0,168484318 0.38 2/521 0.38 2/525 0.38 2/524 1.32 1/76 0.37 2/541 0,170716373 0,170799473 0,170799473 0,17417539 0,17789631 1.23 1/81 0.24 3/1276 18177204 0 18177204 1.16 1/86 0 18440803 1.19 1/84 0.184408033 1.16 1/86 0,184408033 1.19 1/84 0,184408033 0,184408033 1.16 1/86 1.16 1/86 1.16 1/86 1.19 1/84 0.15 5/3236 1.11 1/90 1.12 1/89 0.15 5/3236 1.10 1/91 0,184408033 0,184408033 0,184408033 0,188120909 0,188120909 0,188120909 0,188120909 0,188120909 0.34 2/591 0.18970690 1.08 1/93 1.05 1/95 0 19077730 0,193616032 0.33 2/613 0.198814088 0.96 1/104 0,20890399 0.95 1/105 0,209633292 0.91 1/110 0,2105094 0.09 12/1291 0,2105094 0.09 12/1291 0.91 1/110 0.21 3/1449 0.15 5/3413 0.30 2/660 0.89 1/112 0.88 1/113 0.90 1/11 0,21050944 0,21050944 0,21050944 0,21050944 0,21050944 0,21050944 0,21050944 0.21050944 0.17 4/2363 0.21050944 0.89 1/112 0,21050944 0.88 1/113 0,21050944 0.21 3/1463 0,211100224 0.30 2/668 0,211396823 0.85 1/118 0,215988336 0.85 1/118 0.83 1/120 0.10 11/1142! 0.80 1/125 0.80 1/125 0.12 7/5915 0.79 1/127 0.79 1/127 0,21835313 0,22137561 0,22355731 0,22355731 0,22375599
0,22375599 0,22375599 0.28 2/713 0.22468135 0.78 1/129 0.22468135 0.77 1/130 0,225128826 0.76 1/131 0,225654031 0.76 1/132 0,2261729 0,22668565 0,226949411 0,226949411 0.75 1/133 0.75 1/133 0.27 2/736 0.09 11/1158: 0.74 1/136 0.27 2/729 0.27 2/732 0.19 3/1587 0 2284050 0.27 2/745 0.72 1/139 0.22840596 0 22840596 0.70 1/142 0,229327675 0.70 1/143 0,229327675 0.19 3/1596 0,229327675 0.70 1/143 0,229327675 0.70 1/143 0.68 1/147 0.68 1/147 0.68 1/146 0.19 3/1617 0.68 1/147 0.68 1/148 0.67 1/149 0.26 2/774 0,230065715 0,230065715 0,230065715 0,230065715 0,230065715 0,230504212 0,23050421 0 230576642 0.66 1/151 0.230755608 0.66 1/151 0,230755608 0.63 1/158 0,232606043 0.63 1/158 0,232606043 0.25 2/786 0.64 1/156 0,232606043 0,23260604 0.63 1/158 0.65 1/155 0.64 1/157 0.25 2/793 0.62 1/161 0,232606043 0,232606043 0 235779 0.61 1/163 0.24 2/819 0.23753634 23861535 0.61 1/165 0.23861535 0.59 1/169 0.24269719 0.58 1/172 0,244704036 0.58 1/172 0,244704036 0.57 1/174 0,24636070 0,246360704 0,246669739 0,248595335 0,248595335 0,251179609 0,254247743 0,254651631 0,256199111 0.57 1/175 0.57 1/175 0.23 2/852 0.56 1/178 0.12 6/5108 0.23 2/870 0.54 1/185 0.53 1/187 0.53 1/18/ 0.25644882 0.53 1/190 0 25797165 0.17 3/1814 0,2602415 0.52 1/194 0.260971001 0.51 1/196 0,26244789 0.49 1/203 0,269080263 0.49 1/203 0,269080263 0.48 1/207 0,26978464 0.48 1/207 0.49 1/206 0.16 3/1868 0.49 1/205 0.47 1/211 0.16 3/1884 0.46 1/217 0.46 1/218 0,269784649 0,269784649 0,269784649 0,272535417 0,272535417 0.27880601 0.45 1/220 0.27905482 0.45 1/220 0,279054825 0.45 1/224 0,281633931 0.45 1/224 0,281633931 0.09 11/12360 0.285763876 0.11 6/5413 0,285763876

GO:0110053	regulation of actin filament organization	Any proce The proce
GO:0071702	protein polymerization organic substance transport negative regulation of protein phosphorylation	The direct Any proce
GO:0051246	regulation of protein metabolic process	Any proce
GO:0030900 GO:0051716	forebrain development cellular response to stimulus	The proce Any proce
GO:0042060	wound healing regulation of localization	The series Any proce
GO:0006650	glycerophospholipid metabolic process camera-type eye development	The chem The proce
GO:0032270	positive regulation of cellular protein metabolic process glycoprotein biosynthetic process	Any proce
GO:0009101 GO:0031589	glycoprotein biosynthetic process cell-substrate adhesion	The chem The attach
	negative regulation of phosphorylation intracellular signal transduction	Any proce The proce
GO:0009056 GO:0015980	catabolic process energy derivation by oxidation of organic compounds	The chem The chem
GO:0032535	regulation of cellular component size	A process
GO:0071900 GO:0030099	regulation of protein serine/threonine kinase activity myeloid cell differentiation lipid metabolic process	Any proce The proce
GO:0006629 GO:0018193	lipid metabolic process peptidyl-amino acid modification	The chem The altera
GO:0018105	peptidyl-serine phosphorylation positive regulation of cellular process	The phosp Any proce
GO:0044267	cellular protein metabolic process	The chem
GO:0001503 GO:0002683	ossification negative regulation of immune system process	The forma Any proce
GO:0051247 GO:0032956	positive regulation of protein metabolic process regulation of actin cytoskeleton organization	Any proce Any proce
GO:0006996	organelle organization	A process The chem
GO:0015711	purine ribonucleotide metabolic process organic anion transport gland development	The direct The proce
GO:0010035	response to inorganic substance	Any proce
GO:0001654	peptidyl-serine modification eye development	The modif The proce
GO:0150063 GO:0045936	visual system development negative regulation of phosphate metabolic process	The proce Any proce
GO:0002250	adaptive immune response	An immur Any proce
GO:0019693	regulation of supramolecular fiber organization ribose phosphate metabolic process purine nucleotide metabolic process	The chem
GO:0009611	response to wounding	The chem Any proce
	negative regulation of phosphorus metabolic process regulation of actin filament-based process	Any proce Any proce
GO:0048880	sensory system development glycoprotein metabolic process	The proce The chem
GO:0015031	protein transport	The direct
GO:0043254	ribonucleotide metabolic process regulation of protein-containing complex assembly	The chem Any proce
GO:0006869	lipid transport negative regulation of response to stimulus	The direct Any proce
GO:0006644	phospholipid metabolic process circulatory system process	The chem A organ sy
GO:0045785	positive regulation of cell adhesion	Any proce
	glycerolipid metabolic process purine-containing compound metabolic process	The chem The chem
	mononuclear cell differentiation regulation of intracellular signal transduction	The proce Any proce
	cellular response to chemical stimulus lipid localization	Any proce Any proce
GO:0043410	positive regulation of MAPK cascade	Any proce The chem
GO:0031347	phosphate-containing compound metabolic process regulation of defense response	Any proce
GO:0090066 GO:0006793	regulation of anatomical structure size phosphorus metabolic process	Any proce The chem
GO:0065009 GO:0060627	regulation of molecular function regulation of vesicle-mediated transport	Any proce Any proce
GO:0006091	generation of precursor metabolites and energy	The chem
GO:0031400 GO:0007015	negative regulation of protein modification process actin filament organization positive regulation of nitrogen compound metabolic process	Any proce A process
GO:1901615	organic hydroxy compound metabolic process	Any proce The chem
GO:0051046	regulation of secretion	Any proce The chem
GO:0048518 GO:0006753	positive regulation of biological process nucleoside phosphate metabolic process	Any proce The chem
GO:1902532	negative regulation of intracellular signal transduction	Any proce
GO:0051493	positive regulation of hydrolase activity regulation of cytoskeleton organization	Any proce Any proce
GO:0009888 GO:0002521	tissue development leukocyte differentiation	The proce The proce
GO:0070727	cellular macromolecule localization cellular protein localization	Any proce Any proce
GO:0048513	animal organ development	Developm
GO:0031325	anion transport positive regulation of cellular metabolic process	The direct Any proce
GO:0007420 GO:0006810	brain development transport	The proce The direct
GO:0007423	sensory organ development	The proce The imme
GO:0030855	epithelial cell differentiation	The proce
GO:0055086 GO:0045859	regulation of protein kinase activity	The cellul Any proce
GO:0050896 GO:0060322	response to stimulus head development	Any proce The biolog
GO:0044260	cellular macromolecule metabolic process positive regulation of macromolecule metabolic process	The chem Any proce
GO:0006950	response to stress	Any proce
GO:0043086	phosphorylation negative regulation of catalytic activity	The proce Any proce
GU:0006508	proteolysis regulation of cell adhesion	The hydro Any proce
GO:0043549	regulation of kinase activity ubiquitin-dependent protein catabolic process	Any proce The chem
GO:0019941	modification-dependent protein catabolic process	The chem
GO:0030036 GO:0043632	actin cytoskeleton organization modification-dependent macromolecule catabolic process	A process The chem
GO:0061024	regulation of immune response membrane organization	Any proce A process
GO:0009893	positive regulation of metabolic process macromolecule biosynthetic process	Any proce The chem
GO:0097435	supramolecular fiber organization	A process
GO:0046903	regulation of response to external stimulus secretion	Any proce The contro
GO:0007417 GO:0071310	central nervous system development cellular response to organic substance	The proce Any proce
GO:0030097	hemopoiesis actin filament-based process	The proce Any cellul
GO:0051338	regulation of transferase activity	Any proce
GO:0016567	proteolysis involved in cellular protein catabolic process protein ubiquitination	The hydro The proce
GO:0048534 GO:0044257	hematopoietic or lymphoid organ development cellular protein catabolic process	The proce The chem
GO:0010556	regulation of macromolecule biosynthetic process positive regulation of intracellular signal transduction	Any proce Any proce
GO:0032446	protein modification by small protein conjugation	A protein
GO:0051171	immune system development regulation of nitrogen compound metabolic process	The proce Any proce
GO:0002376 GO:0031326	immune system process regulation of cellular biosynthetic process	Any proce Any proce
GO:0032269	negative regulation of cellular protein metabolic process regulation of biosynthetic process	Any proce Any proce
GO:0044092	negative regulation of molecular function	Any proce

1	Any process that modulates the frequency, rate or extent of actin filament organizati ALC he process of creating protein polymers, compounds composed of a large number c ALC	.OX15	7.14 1/14 7.14 1/14	0.43 1/231 0.43 1/234	0,2 0,28
1	he directed movement of organic substances into, out of or within a cell, or betwee ABC ny process that stops, prevents or reduces the rate of addition of phosphate groups STK	3CG2 MYO6 SURF4	21.43 3/14 7.14 1/14	0.15 3/1968 0.41 1/242	0,28
,	iny process that modulates the frequency, rate or extent of the chemical reactions a RAE	B3GAP1 RAB3GAP2 STK38	21.43 3/14	0.15 3/2025	0,303
,	he process whose specific outcome is the progression of the forebrain over time, frα RAB my process that results in a change in state or activity of a cell (in terms of movemer ABG	CG2 ALOX15 FASN GNG12 MYO6 STK		0.38 1/260 0.10 7/6878	0,310 0,310
,	he series of events that restore integrity to a damaged tissue, following an injury. ALC my process that modulates the frequency, rate or extent of any process in which a c ALC	.0X15 .0X15 MYO6 SURF4	7.14 1/14 21.43 3/14	0.38 1/260 0.15 3/2055	0,310 0,310
1	he chemical reactions and pathways involving glycerophospholipids, any derivative ALC	.0X15	7.14 1/14 7.14 1/14	0.38 1/262 0.38 1/264	0,311
,	he process whose specific outcome is the progression of the camera-type eye over t RAE iny process that activates or increases the frequency, rate or extent of the chemical RAE	AB3GAP1 RAB3GAP2	14.29 2/14	0.19 2/1072	0,311
	he chemical reactions and pathways resulting in the formation of glycoproteins, a pi RPN he attachment of a cell to the underlying substrate via adhesion molecules. ALC		7.14 1/14 7.14 1/14	0.38 1/263 0.37 1/268	0,311 0,313
,	my process that stops, prevents or decreases the rate of addition of phosphate grou STK	K38	7.14 1/14	0.37 1/271	0,314
	he process in which a signal is passed on to downstream components within the cel ALC he chemical reactions and pathways resulting in the breakdown of substances, inclu RAE		21.43 3/14 21.43 3/14	0.14 3/2097 0.14 3/2106	0,314 0,316
	he chemical reactions and pathways by which a cell derives energy from organic cor SDH process that modulates the size of a cellular component. ALC		7.14 1/14 7.14 1/14	0.36 1/280	0,321
,	my process that modulates the rate, frequency, or extent of protein serine/threonin STK	K38	7.14 1/14	0.35 1/282	0,321
	he process in which a relatively unspecialized myeloid precursor cell acquires the sp FAS he chemical reactions and pathways involving lipids, compounds soluble in an orgar ALC		7.14 1/14 14.29 2/14	0.34 1/290 0.18 2/1124	0,321 0,321
1	he alteration of an amino acid residue in a peptide. RPM	N1 STK38	14.29 2/14 7.14 1/14	0.18 2/1125 0.35 1/284	0,321 0,321
,	iny process that activates or increases the frequency, rate or extent of a cellular proi ALC	OX15 MYO6 RAB3GAP1 RAB3GAP2 SI	35.71 5/14	0.11 5/4480	0,321
	he chemical reactions and pathways involving a specific protein, rather than of prot RAE he formation of bone or of a bony substance, or the conversion of fibrous tissue or ALC		35.71 5/14 7.14 1/14	0.11 5/4461 0.35 1/289	0,321
	iny process that stops, prevents, or reduces the frequency, rate, or extent of an imm ALC iny process that activates or increases the frequency, rate or extent of the chemical RAE		7.14 1/14	0.34 1/294	0,324
,	iny process that modulates the frequency, rate or extent of the formation, arrangen ALC	OX15	7.14 1/14	0.34 1/296	0,325
	v process that is carried out at the cellular level which results in the assembly, arrang ALC he chemical reactions and pathways involving a purine ribonucleotide, a compound CO/		28.57 4/14 7.14 1/14	0.12 4/3330 0.33 1/301	0,327
1	he directed movement of organic anions into, out of or within a cell, or between cel ABO	3CG2	7.14 1/14 7.14 1/14	0.33 1/306	0,328
	he process whose specific outcome is the progression of a gland over time, from its FAS my process that results in a change in state or activity of a cell or an organism (in ter ALC		7.14 1/14 7.14 1/14	0.33 1/306	0,328
	he modification of peptidyl-serine. STK he process whose specific outcome is the progression of the eye over time, from its RAE		7.14 1/14 7.14 1/14	0.33 1/306 0.32 1/309	0,328
1	he process whose specific outcome is the progression of the visual system over time RAB	AB3GAP1	7.14 1/14	0.32 1/312	0,331
	Any process that stops, prevents, or reduces the frequency, rate or extent of the cheir STK an immune response mediated by cells expressing specific receptors for antigen prov ALC		7.14 1/14 7.14 1/14	0.31 1/321 0.31 1/325	0,332 0,332
,	Any process that modulates the frequency, rate or extent of supramolecular fiber ore ALC the chemical reactions and pathways involving ribose phosphate, any phosphorylate CO/	.0X15	7.14 1/14 7.14 1/14	0.32 1/315 0.31 1/327	0,332
1	he chemical reactions and pathways involving a purine nucleotide, a compound con CO/	DASY	7.14 1/14	0.31 1/323	0,332
	Any process that results in a change in state or activity of a cell or an organism (in ter ALC Any process that decreases the frequency, rate or extent of the chemical reactions ar STK		7.14 1/14 7.14 1/14	0.31 1/326 0.31 1/321	0,332 0,332
,	iny process that modulates the frequency, rate or extent of any cellular process that ALC	.0X15	7.14 1/14	0.31 1/324	0,332
1	he process whose specific outcome is the progression of a sensory system over time RAE he chemical reactions and pathways involving glycoproteins, a protein that contains RPN	N1	7.14 1/14 7.14 1/14	0.32 1/317 0.31 1/325	0,332 0,332
	he directed movement of proteins into, out of or within a cell, or between cells, by I MY he chemical reactions and pathways involving a ribonucleotide, a compound consist CO/		14.29 2/14 7.14 1/14	0.17 2/1193 0.31 1/318	0,332
,	iny process that modulates the frequency, rate or extent of protein complex assemb ALC	.0X15	7.14 1/14	0.30 1/330	0,334
	he directed movement of lipids into, out of or within a cell, or between cells, by me: SUF my process that stops, prevents, or reduces the frequency, rate or extent of a respoi ALC		7.14 1/14 14.29 2/14	0.30 1/332 0.16 2/1236	0,335 0,338
	he chemical reactions and pathways involving phospholipids, any lipid containing pł ALC organ system process carried out by any of the organs or tissues of the circulatory : AB(7.14 1/14 7.14 1/14	0.30 1/338 0.29 1/342	0,338 0,341
,	iny process that activates or increases the frequency, rate or extent of cell adhesion. ALC	.0X15	7.14 1/14	0.29 1/345	0,342
	he chemical reactions and pathways involving glycerolipids, any lipid with a glycerol ALC he chemical reactions and pathways involving a purine-containing compound, i.e. a CO/		7.14 1/14 7.14 1/14	0.29 1/347 0.29 1/346	0,342 0,342
1	he process in which a relatively unspecialized cell acquires the specialized features (FAS	SN	7.14 1/14 14.29 2/14	0.29 1/349 0.16 2/1270	0,343 0,346
,	wy process that modulates the frequency, rate or extent of intracellular signal transi ALC wy process that results in a change in state or activity of a cell (in terms of movemer ABC)	3CG2 ALOX15 FASN	21.43 3/14	0.13 3/2376	0,351
	wy process in which a lipid is transported to, or maintained in, a specific location. SUF sup process that activates or increases the frequency, rate or extent of signal transd. ALC		7.14 1/14 7.14 1/14	0.27 1/373 0.27 1/373	0,358 0,358
1	he chemical reactions and pathways involving the phosphate group, the anion or sa ALC	OX15 COASY STK38	21.43 3/14 7.14 1/14	0.12 3/2404 0.27 1/376	0,358
			7.14 1/14	0.26 1/379	0,355
	he chemical reactions and pathways involving the nonmetallic element phosphorus ALC iny process that modulates the frequency, rate or extent of a molecular function, an RAE		21.43 3/14 21.43 3/14	0.12 3/2425 0.12 3/2439	0,360 0,362
,	my process that modulates the rate, frequency, or extent of vesicle-mediated transp ALC	.0X15	7.14 1/14	0.26 1/385	0,362
	he chemical reactions and pathways resulting in the formation of precursor metabo SDF my process that stops, prevents, or reduces the frequency, rate or extent of the cov; STK		7.14 1/14 7.14 1/14	0.26 1/386 0.26 1/388	0,362 0,36
,	A process that is carried out at the cellular level which results in the assembly, arrang ALC Any process that activates or increases the frequency, rate or extent of the chemical IMY	.0X15	7.14 1/14 21.43 3/14	0.25 1/396 0.12 3/2473	0,367 0,367
1	he chemical reactions and pathways involving organic hydroxy compound. ALC	.0X15	7.14 1/14	0.25 1/398	0,368
	Any process that modulates the frequency, rate or extent of the controlled release of MY ine chemical reactions and pathways involving a nucleotide, a nucleoside that is este CO/		7.14 1/14 7.14 1/14	0.25 1/400 0.25 1/402	0,368 0,369
,	my process that activates or increases the frequency, rate or extent of a biological pi ALC	OX15 MYO6 RAB3GAP1 RAB3GAP2 SI	35.71 5/14 7.14 1/14	0.10 5/4958 0.24 1/412	0,371
,	iny process that stops, prevents or reduces the frequency, rate or extent of intracelli STK	K38	7.14 1/14	0.24 1/415	0,376
	iny process that activates or increases the frequency, rate or extent of hydrolase act RAE iny process that modulates the frequency, rate or extent of the formation, arrangem ALC		7.14 1/14 7.14 1/14	0.24 1/420 0.23 1/437	0,379 0,387
1	he process whose specific outcome is the progression of a tissue over time, from its ALC	OX15 FASN	14.29 2/14	0.14 2/1431	0,387
	he process in which a relatively unspecialized hemopoietic precursor cell acquires tl FAS ony process in which a macromolecule is transported to, and/or maintained in, a spe RAE		7.14 1/14 14.29 2/14	0.23 1/437 0.14 2/1438	0,387 0,387
	iny process in which a protein is transported to, and/or maintained in, a specific loca RAE		14.29 2/14 21.43 3/14	0.14 2/1432	0,387
1	Development of a tissue or tissues that work together to perform a specific function (ALC he directed movement of anions, atoms or small molecules with a net negative char ABC	3CG2	7.14 1/14	0.11 3/2612 0.22 1/449	0,393 0,394
	Any process that activates or increases the frequency, rate or extent of the chemical MY ine process whose specific outcome is the progression of the brain over time, from it RAE		21.43 3/14 7.14 1/14	0.11 3/2631 0.22 1/463	0,397
1	he directed movement of substances (such as macromolecules, small molecules, ior ABC	3CG2 ALOX15 MYO6 SURF4	28.57 4/14	0.10 4/3886	0,401
	he process whose specific outcome is the progression of sensory organs over time, I RAE he immediate defensive reaction (by vertebrate tissue) to infection or injury caused ALC		7.14 1/14 7.14 1/14	0.21 1/472 0.21 1/472	0,404 0,404
	he process in which a relatively unspecialized cell acquires specialized features of ar FAS he cellular chemical reactions and pathways involving a nucleobase-containing smal CO/		7.14 1/14 7.14 1/14	0.21 1/470	0,404
,	iny process that modulates the frequency, rate or extent of protein kinase activity. STK	K38	7.14 1/14	0.20 1/496	0,419
	wy process that results in a change in state or activity of a cell or an organism (in ter ABC he biological process whose specific outcome is the progression of a head from an i RAE		50.00 7/14 7.14 1/14	0.09 7/7978 0.20 1/503	0,422 0,422
1	he chemical reactions and pathways involving macromolecules, any molecule of hig RAE	AB3GAP1 RAB3GAP2 RPN1 STK38 UBA		0.09 5/5305	0,422
,	Iny process that increases the frequency, rate or extent of the chemical reactions an MY iny process that results in a change in state or activity of a cell or an organism (in ter ALC	OX15 MYO6 UBA1	21.43 3/14 21.43 3/14	0.11 3/2809	0,433
	he process of introducing a phosphate group into a molecule, usually with the form CO/ Any process that stops or reduces the activity of an enzyme.		14.29 2/14 7.14 1/14	0.12 2/1608 0.18 1/555	0,433 0,452
1	he hydrolysis of proteins into smaller polypeptides and/or amino acids by cleavage (UB/	BA1 UQCRC2	14.29 2/14	0.12 2/1674	0,455
	Iny process that modulates the frequency, rate or extent of attachment of a cell to a ALC iny process that modulates the frequency, rate or extent of kinase activity, the cataly STK		7.14 1/14 7.14 1/14	0.17 1/573 0.17 1/588	0,461
1	he chemical reactions and pathways resulting in the breakdown of a protein or pept UB/	3A1	7.14 1/14 7.14 1/14	0.17 1/589 0.17 1/603	0,469
	he chemical reactions and pathways resulting in the breakdown of a protein or pepI UB/ process that is carried out at the cellular level which results in the assembly, arrang ALC		7.14 1/14	0.16 1/611	0,477
1	he chemical reactions and pathways resulting in the breakdown of a macromolecule UB/ my process that modulates the frequency, rate or extent of the immune response, tl ALC	3A1	7.14 1/14 7.14 1/14	0.16 1/611 0.16 1/616	0,480 0,482
,	process which results in the assembly, arrangement of constituent parts, or disasse ALC	.0X15	7.14 1/14	0.16 1/620	0,483
	why process that activates or increases the frequency, rate or extent of the chemical MY the chemical reactions and pathways resulting in the formation of a macromolecule, MY		21.43 3/14 28.57 4/14	0.10 3/3040 0.09 4/4337	0,483 0,483
,	process that is carried out at the cellular level which results in the assembly, arrang ALC	.0X15	7.14 1/14	0.16 1/636	0,48
1		YO6	7.14 1/14 7.14 1/14	0.16 1/642 0.16 1/645	0,491 0,492
1	he process whose specific outcome is the progression of the central nervous system RAE	AB3GAP1	7.14 1/14 14.29 2/14	0.15 1/649 0.11 2/1848	0,493 0,498
1	In process that results in a change in state or activity of a cell (in terms of movemer ALC the process whose specific outcome is the progression of the myeloid and lymphoid FAS	SN	7.14 1/14	0.15 1/670	0,503
	Any cellular process that depends upon or alters the actin cytoskeleton, that part of t ALC strain process that modulates the frequency, rate or extent of transferase activity, the i STK		7.14 1/14 7.14 1/14	0.15 1/675 0.15 1/676	0,504 0,504
1	he hydrolysis of a peptide bond or bonds within a protein as part of the chemical re UB/	3A1	7.14 1/14	0.14 1/696	0,515
	he process in which one or more ubiquitin groups are added to a protein. UB/ he process whose specific outcome is the progression of any organ involved in hem: FAS		7.14 1/14 7.14 1/14	0.14 1/702 0.14 1/705	0,517 0,517
1	he chemical reactions and pathways resulting in the breakdown of a protein by indi UB/	3A1	7.14 1/14	0.14 1/732	0,531
,	iny process that modulates the rate, frequency or extent of the chemical reactions a MY iny process that activates or increases the frequency, rate or extent of intracellular s ALC	.0X15	21.43 3/14 7.14 1/14	0.09 3/3278 0.13 1/741	0,531 0,534
,	v protein modification process in which one or more groups of a small protein, such UB/ ine process whose specific outcome is the progression of an organismal system who: FAS	3A1	7.14 1/14 7.14 1/14	0.13 1/758 0.13 1/758	0,540 0,540
,	my process that modulates the frequency, rate or extent of the chemical reactions a MY	YO6 RAB3GAP1 RAB3GAP2 STK38	28.57 4/14	0.08 4/4722	0,549
	Any process involved in the development or functioning of the immune system, an or ALC any process that modulates the frequency, rate or extent of the chemical reactions a MY		14.29 2/14 21.43 3/14	0.10 2/2045 0.09 3/3385	0,549 0,551
	ny process that stops, prevents, or reduces the frequency, rate or extent of the chei STK ny process that modulates the frequency, rate or extent of the chemical reactions a MY	K38	7.14 1/14	0.13 1/792	0,553
			21.43 3/14 7.14 1/14	0.09 3/3433 0.12 1/816	0,560

	negative regulation of protein metabolic process	Any process that stops, prevents, or reduc
GO:0043085	regulation of primary metabolic process positive regulation of catalytic activity	Any process that modulates the frequency Any process that activates or increases the
GO:0030163	protein catabolic process regulation of protein phosphorylation	The chemical reactions and pathways resu Any process that modulates the frequency
GO:0001932 GO:0060429	epithelium development	The process whose specific outcome is the
	protein modification by small protein conjugation or removal response to organic substance	A protein modification process in which or Any process that results in a change in stat
GO:0048878	chemical homeostasis	Any biological process involved in the main
	system development multicellular organismal process	The process whose specific outcome is the Any biological process, occurring at the lev
GO:0080134	regulation of response to stress	Any process that modulates the frequency
GO:0031323 GO:0022607	regulation of cellular metabolic process cellular component assembly	Any process that modulates the frequency The aggregation, arrangement and bondin
GO:0009966	regulation of signal transduction	Any process that modulates the frequency
	system process negative regulation of signal transduction	A multicellular organismal process carried Any process that stops, prevents, or reduc
GO:0042325	regulation of phosphorylation	Any process that modulates the frequency
GO:0051641	cellular macromolecule catabolic process cellular localization	The chemical reactions and pathways resu A cellular localization process whereby a se
	negative regulation of cell communication	Any process that decreases the frequency,
GO:0045944	negative regulation of signaling positive regulation of transcription by RNA polymerase II	Any process that stops, prevents, or reduce Any process that activates or increases the
	multicellular organism development nitrogen compound metabolic process	The biological process whose specific outco The chemical reactions and pathways invo
GO:0044085	cellular component biogenesis	A process that results in the biosynthesis of
GO:0002682 GO:0007155	regulation of immune system process cell adhesion	Any process that modulates the frequency The attachment of a cell, either to another
GO:0022610	biological adhesion	The attachment of a cell or organism to a s
	regulation of phosphate metabolic process regulation of phosphorus metabolic process	Any process that modulates the frequency Any process that modulates the frequency
GO:0010646	regulation of cell communication	Any process that modulates the frequency
GO:1901565	regulation of signaling organonitrogen compound catabolic process	Any process that modulates the frequency The chemical reactions and pathways resu
GO:0042221	response to chemical	Any process that results in a change in stat
	macromolecule catabolic process positive regulation of molecular function	The chemical reactions and pathways resu Any process that activates or increases the
GO:0009967 GO:0060255	positive regulation of signal transduction	Any process that activates or increases the
GO:0006952	regulation of macromolecule metabolic process defense response	Any process that modulates the frequency Reactions, triggered in response to the pre-
	signal transduction cytoskeleton organization	The cellular process in which a signal is con A process that is carried out at the cellular
GO:0006955	immune response	Any immune system process that function
GO:0010647 GO:0023056	positive regulation of cell communication positive regulation of signaling	Any process that increases the frequency, Any process that activates, maintains or in
GO:0048856	anatomical structure development	The biological process whose specific outc
	positive regulation of nucleic acid-templated transcription homeostatic process	Any process that activates or increases the Any biological process involved in the main
GO:1902680	positive regulation of RNA biosynthetic process	Any process that activates or increases the Any process that activates or increases the
GO:0045893 GO:0006811	positive regulation of transcription, DNA-templated ion transport	The directed movement of charged atoms
	protein phosphorylation regulation of biological quality	The process of introducing a phosphate gr Any process that modulates a qualitative of
GO:0019222	regulation of metabolic process	Any process that modulates the frequency
	transmembrane transport regulation of response to stimulus	The process in which a solute is transporte Any process that modulates the frequency
GO:0023052	signaling	The entirety of a process in which informa
	cell communication sensory perception	Any process that mediates interactions be The series of events required for an organi
GO:0051254	positive regulation of RNA metabolic process	Any process that activates or increases the
	regulation of cellular process positive regulation of macromolecule biosynthetic process	Any process that modulates the frequency Any process that increases the rate, freque
GO:0032502	developmental process	A biological process whose specific outcon
GO:0045935	positive regulation of nucleobase-containing compound metabolic cell development	
GO:0045935 GO:0048468 GO:0016043	cell development cellular component organization	Any cellular process that activates or incre The process whose specific outcome is the A process that results in the assembly, arra
GO:0045935 GO:0048468 GO:0016043 GO:0048584 GO:0034654	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process	Any cellular process that activates or incre The process whose specific outcome is the A process that results in the assembly, arra Any process that activates, maintains or in The chemical reactions and pathways resu
GO:0045935 GO:0048468 GO:0016043 GO:0048584 GO:0034654 GO:0007399	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development	Any cellular process that activates or incre The process whose specific outcome is the A process that results in the assembly, arra Any process that activates, maintains or in The chemical reactions and pathways resu The process whose specific outcome is the
G0:0045935 G0:0048468 G0:0016043 G0:0048584 G0:0034654 G0:0007399 G0:0019438 G0:1901575	cell development cellular component organization positive regulation of response to stimulus nucleobase containing compound biosynthetic process nervous system development aromatic compound biosynthetic process organic substance catabolic process	Any cellular process that activates or incre- The process whose specific outcome is the A process that results in the assembly, arra Any process that activates, maintains or in the chemical reactions and pathways resu The process whose specific outcome is the The chemical reactions and pathways resu The chemical reactions and pathways resu
G0:0045935 G0:0048468 G0:0016043 G0:0048584 G0:0034654 G0:0007399 G0:0019438 G0:1901575 G0:0018130	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process organic substance catabolic process	Any cellular process that activates or incre The process whose specific outcome is the A process that results in the assembly, arra Any process that activates, maintains or in The chemical reactions and pathways resu The process whose specific outcome is the The chemical reactions and pathways resu
G0:0045935 G0:0048468 G0:0016043 G0:0048584 G0:0034654 G0:0007949 G0:0019438 G0:1901575 G0:0018130 G0:0071840 G0:0007186	cel development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process organic substance catabolic process heterocycle biosynthetic process cellular component organization or biogenesis G protein-coupled receptor signaling pathway	Any cellular process that activates or incre- top process whose specific outcome is the A process that results in the assembly arr. The d-minical reactions and pathways resu- The process whose specific outcome is the the c-thical reactions and pathways resu- the c-thical reactions and pathways resu- te c-thical reactions and pathways resu- tations and pathways results and the biosynthesis of a series of molecular signals that proceeds
G0:0045935 G0:0048468 G0:0016043 G0:00148548 G0:0007399 G0:0019438 G0:1901575 G0:0018130 G0:0071840 G0:007186 G0:007186 G0:007186	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process organic substance catabolic process heterocycle biosynthetic process heterocycle biosynthetic process cellular compound roganization or biogenesis	Any cellular process that activates or incre The process that results in the assembly, arra Any process that activates, maintains or in The chemical reactions and pathways resu The process whose specific ouctome is the the chemical reactions and pathways resu The chemical reactions and pathways resu The chemical reactions and pathways resu The chemical reactions and pathways resu
G0:0045935 G0:0048468 G0:0016043 G0:0048584 G0:0034654 G0:007399 G0:0019438 G0:1901575 G0:0018130 G0:0071840 G0:00071840 G0:00071840 G0:00071840 G0:0007185 G0:001362 G0:0050877	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process aromatic compound biosynthetic process aromatic compound biosynthetic process heterocycle biosynthetic process cellular component organization or biogenesis G protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process organic cyclic compound biosynthetic process nervous system process	Any cellular process that activates or incre The process whose specific outcome is the A process that results in the assembly, arri Any process that activates, maintains or in the chemical reactions and pathways resu The process whose specific outcome is the the chemical reactions and pathways resu The chemical reactions and pathways resu the chemical reactions and pathways resu A process that results in the biosynthesis A series of molecular signals that proceed The chemical reactions and pathways resu A organ system process carried out by any the dynamical metations and the pathways the A organ system process carried out by any
G0:0045935 G0:0048468 G0:0016043 G0:0048584 G0:007399 G0:0019438 G0:1901575 G0:0018130 G0:0071840 G0:0071840 G0:0071840 G0:0071862 G0:0050877 G0:0050877 G0:0050877	cell development cellular component organization positive regulation of response to stimulus nucleobase- containing compound biosynthetic process nervous system development aromatic compound biosynthetic process netroucycle biosynthetic process heterocycle biosynthetic process G protein-coupled receptor signaling pathway macromolecule metabolic process organic ryckic compound biosynthetic process nervous system process cellular process	Any cellular process that activates or incre The process that results in the assembly, arr Any process that activates, maintains or in the chemical reactions and pathways resu The process whose specific outcome is the the chemical reactions and pathways resu The chemical reactions and pathways resu The chemical reactions and pathways resu the chemical reactions and pathways resu A process that results in the biosynthesis a series of molecular signals that proceed The chemical reactions and pathways resu A organ system process carried out by any Any process that is carried out at the cellul Any process that is carried out at the cellul any process that is carried out at the cellul
GC:0045935 GO:0048468 GO:0016043 GO:0014054 GO:007399 GO:0019438 GO:1901575 GO:0018130 GO:0071840 GO:0071840 GO:0071840 GO:0071840 GO:001362 GO:01362 GO:0050877 GO:0050789	cell development cellular component organization positive regulation of response to stimulus nucleobase containing compound biosynthetic process nervous system development aromatic compound biosynthetic process organic substance catabolic process heterocycle biosynthetic process cellular component organization or biogenesis G protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process nervous system process cellular process negative regulation of hiological process negative regulation of hiological process	Any cellular process that activates or incre the process whose specific outcome is the A process that results in the assembly, arr. Any process that activates, maintains or in The chemical reactions and pathways resus the chemical reactions and pathways resus the chemical reactions and pathways resus the chemical reactions and pathways resus A process that results in the biosynthesis of A series of molecular signals that proceeds the chemical reactions and pathways resus A process that results in the biosynthesis of the chemical reactions and pathways resus A process that is carried out a the result of a pathways process activate out the cellul Any process that is carried out at the cellul Any process that tops, prevents, or reduc
GC:0045935 GC:0045935 GC:004648 GC:004648 GC:0048584 GC:0019438 GC:0019438 GC:0019438 GC:001840 GC:001840 GC:001840 GC:0048170 GC:0049170 GC:0050877 GC:0050877 GC:0050876 GC:0051172 GC:0050878	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process organic substance catabolic process heterocycle biosynthetic process cellular component organization or biogenesis G protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process negative regulation of nitrogen compound metabolic process response to external stimulus negative regulation of cellular metabolic process	Any cellular process that activates or incre the process whose specific outcome is the A process that securits in the assembly, arr. Any process that activates, maintains or in The chemical reactions and pathways resus the chemical reactions and pathways resus the chemical reactions and pathways resus the chemical reactions and pathways resus A process that clause in the biosynthesis of A series of molecular signals that proceeds the chemical reactions and pathways resus A process that results in the biosynthesis of A series of molecular signals that proceeds the chemical reactions and pathways resus A organ system process carried out by any any process that is carried out at the cellul Any process that is carried out at the cellul Any process that results in a change in stat Any process that tesults in a change in stat
GC:0045935 GO:0046935 GO:0016043 GO:0048584 GO:0034654 GO:0034654 GO:0019438 GO:019438 GO:019438 GO:019438 GO:001840 GO:001840 GO:00071840 GO:00071840 GO:00071840 GO:0005057 GO:0050577 GO:0050577 GO:0050573 GO:0050573	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process heterocyche biosynthetic process cellular component organization or biogenesis & protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process nervous system process cellular process cellular process regulation of hirtogen compound metabolic process regulation of biological process negative regulation of nitrogen compound metabolic process negative regulation of nitrogen compound metabolic process anatomical structure morphogenesis	Any cellular process that activates or incre The process whose specific outcome is the A process that scivates, maintains or in the chemical reactions and pathways resu The process whose specific outcome is the the chemical reactions and pathways resu The chemical reactions and pathways resu The chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways resu A organ system process carried out by any Any process that stops, prevents, or reduc Any process that stops, prevents, or reduc Any process that stops, prevents, or reduc the process in which anatomical structure
C::0045935 C0:0046935 C0:0016043 C0:0048584 C0:0034654 C0:0034654 C0:0034654 C0:0019438 C0:0194137 C0:0191137 C0:0018130 C0:0007184 C0:00043170 C0:0005137 C0:000513 C0:000513 C0:000513 C0:0005137 C0:0005137 C0:0005137	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process cellular component organization or biogenesis G protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process nervous system process cellular process cellular process regulation of hiotogical process regulation of biological process regulation of biological antomical structure morphogeneesis regulation of transcription by RNA polymerase II transcription by RNA polymerase II	Any cellular process that activates or incre the process whose specific outcome is the A process that scivates, smintains or in The chinical reactions and pathways resus The process whose specific outcome is the the chinical reactions and pathways resus the chinical reactions and pathways resus the chinical reactions and pathways resus A process that results in the biosynthesis of a series of molecular signals that proceed The chinical reactions and pathways resus A process that results in the biosynthesis of the chinical reactions and pathways resus A process that results in the the output A process that science and the cellul Ary process that results in a change in stal Any process that modulates the frequency Any process that for Any from a DNA template
GC:0045935 GC:0045935 GC:0048484 GC:0048584 GC:007399 GC:01901575 GC:0011575 GC:00118130 GC:007184 GC:007184 GC:007186 GC:0011372 GC:0051172 GC:0050877 GC:0051172 GC:0050957 GC:0051172 GC:0050957 GC:0051123 GC:0050567 GC:005057 GC:0050567 GC:005057 GC:005567 GC:00557 GC:00	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process nervous system development aromatic compound biosynthetic process nervous system development cellular componer catabolic process heterocycle biosynthetic process cellular compound biosynthetic process organic ryclic compound biosynthetic process nervous system metabolic process cellular process regulation of hiotogical process regulation of hiotogical process regulation of hiotogical process anatomical structure morphogenesis anatomical structure morphogenesis engluton efficiencytion by RNA polymerase II transcription by RNA polymerase II cellular nitrogen compound biosynthetic process	Any cellular process that activates or incre the process whose specific outcome is the A process that results in the assembly, are Any process that activates, maintains or in The chemical reactions and pathways resu The chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways resu the chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways invo A spran system process carried out by any Any process that is carried out at the cellu Any process that is carried out at the cellu Any process that results in a change in stat Any process that results in change in stat Any process that results in change in stat Any process that results in change in stat the pathways resus that could ats the frequency Any process that results in a change in stat the process in which anatomical structures the process in and balax templates the frequency the synthesis of RNA from a DNA template the chemical reactions and pathways resu
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C::0045935 C::0045935 C::0045935 C::0045844 C::0014544 C::0014515 C::0017140	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process aromatic compound biosynthetic process organic substance catabolic process callular component organization or biogenesis G protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process callular compound to process callular compound to process callular process callular of biological process regulation of hirtogen compound metabolic process regulation of sitter morphogenesis antomical structure morphogenesis regulation of sitter process regulation of NAA metabolic process regulation of NAA metabolic process regulation of NAA metabolic process regulation of Sitter	Any cellular process that activates or incre the process whose specific outcome is the A process that results in the assembly arr. The process whose specific outcome is the the chemical reactions and pathways resu The chemical reactions and pathways resu A process that results in the biosynthesis of A series of molecular signals that proceeds the chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways resu A process that correctly and pathways resu A organ system process carried out by any any process that is carried out at the cellul Any process that is carried out at the cellul Any process that tops, prevents, or reduo the process in which anatomical structure Any process that results in a change in ata any process that results in a change in ata any process that modulates the frequency the synthesis of RNA from a DNA template The agregation, arrangement and bondin the agregation, arrangement and bondin the genoress in which macromolecules agg Any process that modulates the frequency Any process that modulates the frequency free chemical reactions and pathways intow the chemical reactions and pathways intow the chemical reactions and pathways intow the chemical reactions and pathways intow
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C::0045935 C::0045935 C::0045935 C::0045844 C::0014643 C::0014514 C::0014515 C::0017140	cell development cellular component organization positive regulation of response to stimulus nucleobase-containing compound biosynthetic process aromatic compound biosynthetic process organic substance catabolic process callular component organization or biogenesis G protein-coupled receptor signaling pathway macromolecule metabolic process organic cyclic compound biosynthetic process callular compound to process callular compound to process callular process callular of biological process regulation of hirtogen compound metabolic process regulation of sitter morphogenesis antomical structure morphogenesis regulation of sitter process regulation of NAA metabolic process regulation of NAA metabolic process regulation of NAA metabolic process regulation of Sitter	Any cellular process that activates or incre the process whose specific outcome is the A process that results in the assembly arr. The process whose specific outcome is the the chemical reactions and pathways resu The chemical reactions and pathways resu A process that results in the biosynthesis of A series of molecular signals that proceeds the chemical reactions and pathways resu A process that results in the biosynthesis of the chemical reactions and pathways resu A process that correctly and pathways resu A organ system process carried out by any any process that is carried out at the cellul Any process that is carried out at the cellul Any process that tops, prevents, or reduo the process in which anatomical structure Any process that results in a change in ata any process that results in a change in ata any process that modulates the frequency the synthesis of RNA from a DNA template The agregation, arrangement and bondin the agregation, arrangement and bondin the genoress in which macromolecules agg Any process that modulates the frequency Any process that modulates the frequency free chemical reactions and pathways intow the chemical reactions and pathways intow the chemical reactions and pathways intow the chemical reactions and pathways intow

process that stops, prevents, or reduces the frequency, rate or extent of chemica	STK38	7.14 1/14	0.12 1/839	0,572619405
r process that modulates the frequency, rate or extent of the chemical reactions a r process that activates or increases the activity of an enzyme.				0,572619405 0,574253899
chemical reactions and pathways resulting in the breakdown of a protein by the	UBA1	7.14 1/14	0.12 1/855	0,577878039
r process that modulates the frequency, rate or extent of addition of phosphate gr process whose specific outcome is the progression of an epithelium over time, fr				0,582444353 0,584527663
rotein modification process in which one or more groups of a small protein, such r process that results in a change in state or activity of a cell or an organism (in ter				0,584527663 0.587962578
biological process involved in the maintenance of an internal steady state of a ch	SURF4	7.14 1/14		0,591401095
process whose specific outcome is the progression of an organismal system over r biological process, occurring at the level of a multicellular organism, pertinent to				0,591401095 0,592544291
process that modulates the frequency, rate or extent of a response to stress. Res	ALOX15	7.14 1/14	0.11 1/909	0,592834395
r process that modulates the frequency, rate or extent of the chemical reactions a aggregation, arrangement and bonding together of a cellular component.				0,593641032 0,596201656
process that modulates the frequency, rate or extent of signal transduction.	ALOX15 STK38	14.29 2/14	0.09 2/2282	0,596201656
nulticellular organismal process carried out by any of the organs or tissues in an or r process that stops, prevents, or reduces the frequency, rate or extent of signal tr				0,604252289 0,611088163
process that modulates the frequency, rate or extent of addition of phosphate gi	STK38	7.14 1/14	0.10 1/986	0,618008138
 chemical reactions and pathways resulting in the breakdown of a macromolecule ellular localization process whereby a substance or cellular entity, such as a protei 		,		0,618008138 0,628623981
r process that decreases the frequency, rate or extent of cell communication. Cell				0,629712767
r process that stops, prevents, or reduces the frequency, rate or extent of a signali process that activates or increases the frequency, rate or extent of transcription			0.10 1/1023 0.10 1/1036	0,629712767 0,63254333
biological process whose specific outcome is the progression of a multicellular or chemical reactions and pathways involving organic or inorganic compounds that			0.08 3/3871 0.07 8/10926	0,63254333 0,633883678
rocess that results in the biosynthesis of constituent macromolecules, assembly, a	ALOX15 RAB3GAP1 RAB3GAP2	21.43 3/14	0.08 3/3907	0,637866152
process that modulates the frequency, rate, or extent of an immune system proc attachment of a cell, either to another cell or to an underlying substrate such as				0,644860067 0,645757013
attachment of a cell or organism to a substrate, another cell, or other organism.	ALOX15	7.14 1/14	0.09 1/1092	0,645757013
r process that modulates the frequency, rate or extent of the chemical reactions a r process that modulates the frequency, rate or extent of the chemical reactions a				0,645757013 0,645757013
process that modulates the frequency, rate or extent of cell communication. Cell	ALOX15 STK38	14.29 2/14	0.08 2/2562	0,650470638
r process that modulates the frequency, rate or extent of a signaling process. chemical reactions and pathways resulting in the breakdown of organonitrogen (0,651899954 0,655063989
process that results in a change in state or activity of a cell or an organism (in ter	ABCG2 ALOX15 FASN	21.43 3/14	0.07 3/4056	0,657076932
 chemical reactions and pathways resulting in the breakdown of a macromolecule r process that activates or increases the rate or extent of a molecular function, an 			0.09 1/1142 0.09 1/1149	0,657076932 0,65824996
process that activates or increases the frequency, rate or extent of signal transdu	ALOX15	7.14 1/14	0.09 1/1161	0,661288298
r process that modulates the frequency, rate or extent of the chemical reactions a locitons, triggered in response to the presence of a foreign body or the occurrence				0,662404929 0,662404929
cellular process in which a signal is conveyed to trigger a change in the activity or				0,677753617
rocess that is carried out at the cellular level which results in the assembly, arrang rimmune system process that functions in the calibrated response of an organism	ALOX15	7.14 1/14	0.08 1/1288	0,685760136 0,69752737
r process that increases the frequency, rate or extent of cell communication. Cell (r process that activates, maintains or increases the frequency, rate or extent of a s			0.08 1/1286	0,69752737 0,69766325
biological process whose specific outcome is the progression of an anatomical st	ALOX15 FASN RAB3GAP1	21.43 3/14	0.07 3/4373	0,707007445
r process that activates or increases the frequency, rate or extent of nucleic acid-to r biological process involved in the maintenance of an internal steady state.				0,708717817 0.708717817
process that activates or increases the frequency, rate or extent of RNA biosynth	MYO6	7.14 1/14	0.07 1/1360	0,708717817
r process that activates or increases the frequency, rate or extent of cellular DNA- e directed movement of charged atoms or small charged molecules into, out of or				0,708717817 0,708717817
process of introducing a phosphate group on to a protein.	STK38	7.14 1/14	0.07 1/1340	0,708717817
r process that modulates a qualitative or quantitative trait of a biological quality. <i>k</i> r process that modulates the frequency, rate or extent of the chemical reactions a			0.07 2/2959 0.07 4/5976	0,715381414 0,71649464
process in which a solute is transported across a lipid bilayer, from one side of a	ABCG2	7.14 1/14	0.07 1/1405	0,71649464
r process that modulates the frequency, rate or extent of a response to a stimulus entirety of a process in which information is transmitted within a biological syste			0.07 2/2982 0.07 4/6020	0,71649464 0,721192617
r process that mediates interactions between a cell and its surroundings. Encompa				0,726342259 0,726342259
series of events required for an organism to receive a sensory stimulus, convert i process that activates or increases the frequency, rate or extent of the chemical	MYO6	7.14 1/14	0.07 1/1459	0,726342259
r process that modulates the frequency, rate or extent of a cellular process, any of r process that increases the rate, frequency or extent of the chemical reactions an				0,727114876 0,742766646
iological process whose specific outcome is the progression of an integrated living	ALOX15 FASN RAB3GAP1	21.43 3/14	0.06 3/4755	0,750906813
r cellular process that activates or increases the frequency, rate or extent of the ch process whose specific outcome is the progression of the cell over time, from its				0,756512816 0,756512816
rocess that results in the assembly, arrangement of constituent parts, or disassem	ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57 4/14	0.06 4/6354	0,759641517
r process that activates, maintains or increases the rate of a response to a stimulu: e chemical reactions and pathways resulting in the formation of nucleobases, nucleoba				0,759641517 0,773683427
process whose specific outcome is the progression of nervous tissue over time, fi	RAB3GAP1			0,778296517
 chemical reactions and pathways resulting in the formation of aromatic compounts chemical reactions and pathways resulting in the breakdown of an organic substration 				0,781020446 0,781020446
chemical reactions and pathways resulting in the formation of heterocyclic comp rocess that results in the biosynthesis of constituent macromolecules, assembly, a	COASY MYO6			0,781020446 0,781266358
eries of molecular signals that proceeds with an activated receptor promoting the				0,781200558
chemical reactions and pathways involving macromolecules, any molecule of hig chemical reactions and pathways resulting in the formation of organic cyclic com				0,783789594 0,791862207
rgan system process carried out by any of the organs or tissues of neurological sys	MYO6	7.14 1/14	0.05 1/1827	0,791862207
r process that is carried out at the cellular level, but not necessarily restricted to a r process that stops, prevents, or reduces the frequency, rate or extent of the cher				0,798722877 0,807079065
process that modulates the frequency, rate or extent of a biological process. Biol	ALOX15 GNG12 MYO6 RAB3GAP1 RAB3	50.00 7/14	0.06 7/11175	0,807079065
r process that results in a change in state or activity of a cell or an organism (in ter r process that stops, prevents, or reduces the frequency, rate or extent of the cher				0,821021545 0,825128758
process in which anatomical structures are generated and organized. Morphogen	RAB3GAP1	7.14 1/14	0.05 1/2107	0,836386121 0,841566107
r process that modulates the frequency, rate or extent of transcription mediated t synthesis of RNA from a DNA template by RNA polymerase II (RNAP II), originatir				0,854141339
chemical reactions and pathways resulting in the formation of organic and inorga process that modulates a measurable attribute of any biological process, quality			0.05 2/4213 0.06 7/11905	0,87037813
aggregation, arrangement and bonding together of a set of macromolecules to fu				0,889763164
r process that decreases the frequency, rate or extent of the chemical reactions ar r process that stops, prevents, or reduces the frequency, rate or extent of a biolog				0,893374164 0.899092454
process in which macromolecules aggregate, disaggregate, or are modified, resul	ALOX15	7.14 1/14	0.04 1/2678	0,903374055
r process that stops, prevents, or reduces the frequency, rate or extent of the cher r process that modulates the frequency, rate or extent of cellular DNA-templated				0,904796064 0,917593805
process that modulates the frequency, rate or extent of nucleic acid-templated t	MY06	7.14 1/14	0.03 1/2881	0,917593805
r process that modulates the frequency, rate or extent of RNA biosynthetic proces e chemical reactions and pathways resulting in the formation of RNA, ribonucleic a				0,917593805 0,925341895
	MY06	7.14 1/14		0,925341895
e cellular synthesis of RNA on a template of nucleic acid (DNA or RNA). process in which relatively unspecialized cells, e.g. embryonic or regenerative ce			0.03 1/3019 0.03 1/3098	0,925341895 0,92917094
process that modulates the frequency, rate or extent of the chemical reactions a	MYO6	7.14 1/14		0,930203762
iological process whose specific outcome is the progression of a cell over time fro r cellular process that modulates the frequency, rate or extent of the chemical rea	MY06	7.14 1/14	0.03 1/3162 0.03 1/3342	0,93053958 0,941626338
r process that stops, prevents, or reduces the frequency, rate or extent of a cellula r process that modulates the frequency, rate or extent of gene expression. Gene ϵ	STK38	7.14 1/14	0.03 1/3856	0,968037034 0,983946915
chemical reactions and pathways involving heterocyclic compounds, those with a	COASY MYO6	14.29 2/14	0.03 2/6828	0,988191314
r cellular metabolic process involving nucleobases, nucleosides, nucleotides and n chemical reactions and pathways involving aromatic compounds, any organic cor				0,988191314 0,988191314
chemical reactions and pathways involving organic cyclic compound.	COASY MYO6	14.29 2/14	0.03 2/7066	0,989591243
chemical reactions and pathways involving various organic and inorganic nitroge cellular chemical reactions and pathways involving RNA, ribonucleic acid, one of				0,995338681 0,997632807
cellular metabolic process involving nucleic acids.	MY06	7.14 1/14	0.02 1/6311	0,998751976
iological process represents a specific objective that the organism is genetically pr process in which a gene's sequence is converted into a mature gene product (pro-			0.07 14/2011(0.01 1/7489	1

sPLS_LPLactiv	ity_Enrichment_GO_BP_of_17prot_contributing_to_HL_g	roup			
GO_BP	Name	Function Gene Name	Term freque	er Term frequ	P-value (fdr)
GO:0090206	negative regulation of cholesterol metabolic process	Any process that decreases the rate, frequency, or extent (ERLIN2	7.14 1/14	25.00 1/4	0,079087858
GO:0006102	isocitrate metabolic process	The chemical reactions and pathways involving isocitrate, 1 IDH1	7.14 1/14	33.33 1/3	0,079087858
GO:0006097	glyoxylate cycle	A modification of the TCA cycle occurring in some plants a IDH1	7.14 1/14	50.00 1/2	0,079087858
GO:0006081 GO:1903778	cellular aldehyde metabolic process protein localization to vacuolar membrane	The chemical reactions and pathways involving aldehydes, ALPL IDH1 A process in which a protein is transported to, or maintain SH3GLB1	14.29 2/14 7.14 1/14	3.85 2/52 100.00 1/1	0,079087858 0,079087858
GO:1903527	positive regulation of membrane tubulation	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	25.00 1/4	0,079087858
GO:0045541	negative regulation of cholesterol biosynthetic process	Any process that stops, prevents, or reduces the frequency ERLIN2	7.14 1/14	25.00 1/4	0,079087858
GO:0106119	negative regulation of sterol biosynthetic process	Any process that stops, prevents or reduces the frequency ERLIN2	7.14 1/14	25.00 1/4	0,079087858
GO:1901615	organic hydroxy compound metabolic process	The chemical reactions and pathways involving organic hy ALPL ERLIN2 IDH1	21.43 3/14	0.75 3/398	0,079087858
GO:1902652	secondary alcohol metabolic process	The chemical reactions and pathways involving secondary ERLIN2 IDH1	14.29 2/14	1.98 2/101	0,079087858
GO:0003360	brainstem development	The progression of the brainstem from its formation to the CNTFR	7.14 1/14	25.00 1/4	0,079087858
GO:0042822	pyridoxal phosphate metabolic process	The chemical reactions and pathways involving pyridoxal p ALPL	7.14 1/14	25.00 1/4	0,079087858
GO:0015881	creatine transmembrane transport	The directed movement of creatine across a membrane. SLC6A8	7.14 1/14	50.00 1/2	0,079087858
GO:0042816	vitamin B6 metabolic process	The chemical reactions and pathways involving any of the ALPL	7.14 1/14	25.00 1/4	0,079087858
GO:0046890	regulation of lipid biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2 IDH1	14.29 2/14	1.61 2/124	0,08647439
GO:0060696	regulation of phospholipid catabolic process	Any process that modulates the rate, frequency, or extent IDH1	7.14 1/14	20.00 1/5	0,08647439
GO:0046487	glyoxylate metabolic process	The chemical reactions and pathways involving glyoxylate, IDH1	7.14 1/14	14.29 1/7	0,092179749
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway	A series of molecular signals initiated by the binding of a ci CNTFR	7.14 1/14	14.29 1/7	0,092179749
GO:1903525 GO:0090148	regulation of membrane tubulation membrane fission	Any process that modulates the frequency, rate or extent (SH3GLB1 A process that is carried out at the cellular level which rest SH3GLB1	7.14 1/14 7.14 1/14	14.29 1/7 14.29 1/7	0,092179749 0,092179749
GO:0090148 GO:0048102	autophagic cell death	A form of programmed cell death that is accompanied by t SH3GLB1	7.14 1/14	14.29 1/7 16.67 1/6	0,092179749
GO:0048102 GO:0106118	regulation of sterol biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2	7.14 1/14	10.00 1/10	0,103534823
GO:0001967	suckling behavior	Specific behavior of a newborn or infant mammal that rest CNTFR	7.14 1/14	11.11 1/9	0,103534823
GO:1902931	negative regulation of alcohol biosynthetic process	Any process that stops, prevents or reduces the frequency ERLIN2	7.14 1/14	9.09 1/11	0,103534823
GO:0006103	2-oxoglutarate metabolic process	The chemical reactions and pathways involving oxoglutara IDH1	7.14 1/14	10.00 1/10	0,103534823
GO:0072350	tricarboxylic acid metabolic process	The chemical reactions and pathways involving dicarboxyli IDH1	7.14 1/14	9.09 1/11	0,103534823
GO:0071071	regulation of phospholipid biosynthetic process	Any process that modulates the frequency, rate or extent (IDH1	7.14 1/14	8.33 1/12	0,103534823
GO:0006814	sodium ion transport	The directed movement of sodium ions (Na+) into, out of c SLC5A9 SLC6A8	14.29 2/14	1.00 2/200	0,103534823
GO:0051764	actin crosslink formation	The process in which two or more actin filaments are conn MARCKS	7.14 1/14	9.09 1/11	0,103534823
GO:0045540	regulation of cholesterol biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2	7.14 1/14		0,103534823
GO:0045717	negative regulation of fatty acid biosynthetic process	Any process that stops, prevents, or reduces the frequency ERLIN2	7.14 1/14	8.33 1/12	0,103534823
GO:0051290	protein heterotetramerization	The formation of a protein heterotetramer, a macromoleci KRT10	7.14 1/14	10.00 1/10	0,103534823
GO:0071501	cellular response to sterol depletion	Any process that results in a change in state or activity of a ERLIN2	7.14 1/14	7.69 1/13	0,105530823
GO:0032933	SREBP signaling pathway	A series of molecular signals from the endoplasmic reticult ERLIN2	7.14 1/14	7.69 1/13	0,105530823
GO:1903729	regulation of plasma membrane organization	Any process that modulates the frequency, rate or extent (SH3GLB1	7.14 1/14	7.14 1/14	0,107300105
GO:0006991 GO:2000786	response to sterol depletion	Any process that results in a change in state or activity of a ERLIN2	7.14 1/14 7.14 1/14	7.14 1/14 6.67 1/15	0,107300105
GO:2000786 GO:0033280	positive regulation of autophagosome assembly response to vitamin D	Any process that activates or increases the frequency, rate SH3GLB1 Any process that results in a change in state or activity of a ALPL	7.14 1/14	6.25 1/15	0,111821131 0,116099533
GO:0033280	response to nutrient levels	Any process that results in a change in state of activity of a ALPL SH3GLB1	14.29 2/14		0,119730648
GO:0019216	regulation of lipid metabolic process	Any process that modulates the frequency, rate or extent (ERLIN2 IDH1	14.29 2/14	0.81 2/246	0,119730648
GO:0090181	regulation of cholesterol metabolic process	Any process that modulates the rate, frequency, or extent ERLIN2	7.14 1/14	5.00 1/20	0,119730648
GO:0045939	negative regulation of steroid metabolic process	Any process that stops, prevents, or reduces the frequency ERLIN2	7.14 1/14	5.00 1/20	0,119730648
GO:0097320	plasma membrane tubulation	A membrane tubulation process occurring in a plasma mer SH3GLB1	7.14 1/14	5.26 1/19	0,119730648
GO:0010894	negative regulation of steroid biosynthetic process	Any process that decreases the frequency, rate or extent o ERLIN2	7.14 1/14	5.00 1/20	0,119730648
GO:0044090	positive regulation of vacuole organization	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	5.56 1/18	0,119730648
GO:0051291	protein heterooligomerization	The process of creating protein oligomers, compounds cor KRT10	7.14 1/14	5.56 1/18	0,119730648
GO:0006066	alcohol metabolic process	The chemical reactions and pathways involving alcohols, a ERLIN2 IDH1	14.29 2/14	0.75 2/266	0,120950404
GO:0009991	response to extracellular stimulus	Any process that results in a change in state or activity of a ALPL SH3GLB1	14.29 2/14	0.73 2/273	0,12108921
GO:0045922	negative regulation of fatty acid metabolic process	Any process that stops, prevents, or reduces the frequency ERLIN2	7.14 1/14	4.55 1/22	0,12108921
GO:0032801	receptor catabolic process	The chemical reactions and pathways resulting in the breal SH3GLB1	7.14 1/14	4.55 1/22	0,12108921
GO:0033273	response to vitamin	Any process that results in a change in state or activity of a ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:0001958	endochondral ossification	Replacement ossification wherein bone tissue replaces car ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:0072337	modified amino acid transport	The directed movement of modified amino acids into, out SLC6A8	7.14 1/14	4.35 1/23	0,121119324
GO:0006767 GO:0036075	water-soluble vitamin metabolic process replacement ossification	The chemical reactions and pathways involving any of a div ALPL Ossification that requires the replacement of a preexisting ALPL	7.14 1/14 7.14 1/14	3.85 1/26 3.85 1/26	0,121119324
GO:0030073 GO:0046677	response to antibiotic	Any process that results in a change in state or activity of a ALPL	7.14 1/14	4.35 1/23	0,121119324 0,121119324
GO:0018149	peptide cross-linking	The formation of a covalent cross-link between or within p KRT10	7.14 1/14	4.00 1/25	0,121119324
GO:0072524	pyridine-containing compound metabolic process	The chemical reactions and pathways involving a pyridine- ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:1903725	regulation of phospholipid metabolic process	Any process that modulates the frequency, rate or extent (IDH1	7.14 1/14	4.00 1/25	0,121119324
GO:1902930	regulation of alcohol biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2	, 7.14 1/14	3.70 1/27	0,121614649
GO:0006739	NADP metabolic process	The chemical reactions and pathways involving nicotinami IDH1	7.14 1/14	3.70 1/27	0,121614649
GO:0006099	tricarboxylic acid cycle	A nearly universal metabolic pathway in which the acetyl g IDH1	7.14 1/14	3.57 1/28	0,124044689
GO:0007584	response to nutrient	Any process that results in a change in state or activity of a ALPL	7.14 1/14	2.94 1/34	0,147948184
GO:0042304	regulation of fatty acid biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2	7.14 1/14	2.78 1/36	0,149434108
GO:0006695	cholesterol biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	2.78 1/36	0,149434108
GO:1902653	secondary alcohol biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	2.78 1/36	0,149434108
GO:0009395	phospholipid catabolic process	The chemical reactions and pathways resulting in the breal IDH1	7.14 1/14	2.44 1/41	0,151545566
GO:2000785	regulation of autophagosome assembly	Any process that modulates the frequency, rate or extent (SH3GLB1	7.14 1/14	2.50 1/40	0,151545566
GO:0042149	cellular response to glucose starvation	Any process that results in a change in state or activity of a SH3GLB1	7.14 1/14	2.50 1/40	0,151545566
GO:0061919	process utilizing autophagic mechanism	A cellular process involving delivery of a portion of the cyti ANXA7 SH3GLB1	14.29 2/14 7 14 1/14	0.52 2/382	0,151545566
GO:0051055 GO:0006914	negative regulation of lipid biosynthetic process autophagy	Any process that stops, prevents, or reduces the frequency ERLIN2 The cellular catabolic process in which cells digest parts of ANXA7 SH3GLB1	7.14 1/14 14.29 2/14	2.50 1/40 0.52 2/382	0,151545566 0,151545566
GO:0016126	sterol biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	2.56 1/39	0,151545566
GO:0010120 GO:0006984	ER-nucleus signaling pathway	Any series of molecular signals that conveys information fr ERLIN2	7.14 1/14	2.63 1/38	0,151545566
GO:0000384 GO:0034198	cellular response to amino acid starvation	Any process that results in a change in state or activity of a SH3GLB1	7.14 1/14	2.38 1/42	0,153122546
GO:1990928	response to amino acid starvation	Any process that results in a change in state or activity of a SH3GLB1	7.14 1/14	2.33 1/43	0,154655727
GO:0044088	regulation of vacuole organization	Any process that redulates the frequency, rate or extent (SH3GLB1	7.14 1/14	2.27 1/44	0,156146816
GO:0044248	cellular catabolic process	The chemical reactions and pathways resulting in the breachXA7 ERLIN2 IDH			0,161534441
GO:0050994	regulation of lipid catabolic process	Any process that modulates the frequency, rate, or extent IDH1	7.14 1/14	2.04 1/49	0,169215648
GO:0050810	regulation of steroid biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2	7.14 1/14	2.00 1/50	0,170455749
GO:0060350	endochondral bone morphogenesis	The process in which bones are generated and organized a ALPL	7.14 1/14	1.96 1/51	0,171663082
GO:0006766	vitamin metabolic process	The chemical reactions and pathways involving vitamins. V ALPL	7.14 1/14	1.89 1/53	0,176105947
GO:0006749	glutathione metabolic process	The chemical reactions and pathways involving glutathion IDH1	7.14 1/14	1.85 1/54	0,177209833
GO:0016239	positive regulation of macroautophagy	Any process, such as recognition of nutrient depletion, tha SH3GLB1	7.14 1/14	1.79 1/56	0,181468483
GO:0072665	protein localization to vacuole	A process in which a protein is transported to, or maintain SH3GLB1	7.14 1/14	1.67 1/60	0,184241808
GO:0031638	zymogen activation	The proteolytic processing of an inactive enzyme to an acti CD5L	7.14 1/14	1.69 1/59	0,184241808
GO:0030855	epithelial cell differentiation	The process in which a relatively unspecialized cell acquire ANXA7 KRT10	14.29 2/14	0.43 2/470	0,184241808

GO:0032787 monocarboxylic acid metabolic process GO:0043648 dicarboxylic acid metabolic process GO:0120162 positive regulation of cold-induced thermogenesis GO:0007631 feeding behavior negative regulation of small molecule metabolic process GO:0062014 GO:0051262 protein tetramerization positive regulation of organelle assembly GO:1902117 GO:0019217 regulation of fatty acid metabolic process GO:0019218 regulation of steroid metabolic process GO:0045833 negative regulation of lipid metabolic process GO:0008610 lipid biosynthetic process GO:0009056 catabolic process GO:0032465 regulation of cytokinesis glucose transmembrane transport GO·1904659 GO:0060349 bone morphogenesis GO:1990823 response to leukemia inhibitory factor GO:0008645 hexose transmembrane transport GO:0030433 ubiquitin-dependent ERAD pathway GO:0015718 monocarboxylic acid transport GO:1990830 cellular response to leukemia inhibitory factor GO:0015749 monosaccharide transmembrane transport GO:0034219 carbohydrate transmembrane transport GO:0010033 response to organic substance GO:0016241 regulation of macroautophagy GO-0008203 cholesterol metabolic process GO:0030216 keratinocyte differentiation GO:0030282 bone mineralization GO:0010565 regulation of cellular ketone metabolic process GO:0031329 regulation of cellular catabolic process GO:0106106 cold-induced thermogenesis GO:000045 autophagosome assembly GO:1990266 neutrophil migration GO:1905037 autophagosome organization GO:0120161 regulation of cold-induced thermogenesis GO:1990845 adaptive thermogenesis GO:0016125 sterol metabolic process GO:0036503 ERAD pathway GO:0043524 negative regulation of neuron apoptotic process GO:0009888 tissue development GO:0046165 alcohol biosynthetic process GO:0010508 positive regulation of autophagy GO:0071345 cellular response to cytokine stimulus GO:0003006 developmental process involved in reproduction GO:0044281 small molecule metabolic process temperature homeostasis GO:0001659 GO:0008643 carbohydrate transport GO:0006694 steroid biosynthetic process GO:0097530 granulocyte migration GO:0060538 skeletal muscle organ development GO:0007009 plasma membrane organization GO:0043112 receptor metabolic process GO:0031214 biomineral tissue development GO:0051017 actin filament bundle assembly GO:0061572 actin filament bundle organization GO:0006633 fatty acid biosynthetic process GO:0034097 response to cytokine organophosphate catabolic process GO·0046434 GO·0110148 hiomineralization GO:1901215 negative regulation of neuron death GO:0030001 metal ion transport GO:0043523 regulation of neuron apoptotic process GO:0000910 cytokinesis GO:0009267 cellular response to starvation GO:0009894 regulation of catabolic process GO:0019752 carboxylic acid metabolic process regulation of cell division GO:0051302 GO:0043436 oxoacid metabolic process GO:0006575 cellular modified amino acid metabolic process GO:0031334 GO:0006836 neurotransmitter transport GO:0006082 organic acid metabolic process GO:0072330 monocarboxylic acid biosynthetic process GO:0035725 sodium ion transmembrane transport GO:0042594 response to starvation GO:0009913 epidermal cell differentiation GO:0019637 organophosphate metabolic process GO:0031669 cellular response to nutrient levels vacuole organization GO:0007033 GO:0097529 myeloid leukocyte migration GO:1902115 regulation of organelle assembly GO:0051402 neuron apoptotic process GO:0009060 aerobic respiration GO:0042180 cellular ketone metabolic process GO:0060348 bone development GO:1901617 organic hydroxy compound biosynthetic process GO:1901575 organic substance catabolic process GO:0044255 cellular lipid metabolic process GO:1901214 regulation of neuron death GO:0031668 cellular response to extracellular stimulus

The chemical reactions and pathways involving monocarbc ERLIN2 IDH1 14.29 2/14 0.43 2/470 0,184241808 The chemical reactions and pathways involving dicarboxyli IDH1 7.14 1/14 1.67 1/60 0,184241808 Any process that activates or increases the frequency, rate ALPL 7.14 1/14 1.61 1/62 0.187155616 Behavior associated with the intake of food. CNTER 7.14 1/14 1.59 1/63 0.18802391 Any process that stops, prevents or reduces the frequency ERLIN2 0.196879758 7.14 1/14 1.45 1/69 0.196879758 The formation of a protein tetramer, a macromolecular str KRT10 7.14 1/14 1.45 1/69 Any process that activates or increases the frequency, rate SH3GLB1 0,196879758 7.14 1/14 1.49 1/67 Any process that modulates the frequency, rate or extent (ERLIN2 7.14 1/14 1.45 1/69 0,196879758 Any process that modulates the frequency, rate or extent (ERLIN2 7.14 1/14 1.41 1/71 0,198281792 Any process that stops, prevents, or reduces the frequency ERLIN2 7.14 1/14 1.41 1/71 0,198281792 14.29 2/14 0,202907868 The chemical reactions and pathways resulting in the form ERLIN2 IDH1 0.38 2/525 0,202907868 The chemical reactions and pathways resulting in the breal ANXA7 ERLIN2 IDH1 28.57 4/14 0.19 4/2106 Any process that modulates the frequency, rate or extent (SH3GLB1 7.14 1/14 1.33 1/75 0,202907868 The process in which glucose is transported across a memł SLC5A9 7 14 1/14 1.27 1/79 0 211341563 The process in which bones are generated and organized. ALPL 7.14 1/14 1.20 1/83 0.21422839 0.21422839 Any process that results in a change in state or activity of a BSPRY 7.14 1/14 1.18 1/85 The process in which hexose is transported across a memb SLC5A9 7.14 1/14 0.21422839 1.23 1/81 0,21422839 The series of steps necessary to target endoplasmic reticul ERLIN2 7.14 1/14 1.20 1/83 The directed movement of monocarboxylic acids into, out SLC6A8 7.14 1/14 1.18 1/85 0,21422839 Any process that results in a change in state or activity of a BSPRY 7.14 1/14 1.19 1/84 0,21422839 The process in which a monosaccharide is transported acrc SLC5A9 7.14 1/14 1.15 1/87 0,217099264 The process in which a carbohydrate is transported across SLC5A9 7.14 1/14 0.217912025 1.12 1/89 Any process that results in a change in state or activity of ALPL BSPRY CNTFR 28.57 4/14 0.18 4/2222 0.217912025 Any process that modulates the frequency, rate or extent (SH3GLB1 7.14 1/14 1.09 1/92 0.21798349 The chemical reactions and pathways involving cholesterol ERLIN2 7.14 1/14 1.04 1/96 0.21798349 The process in which a relatively unspecialized cell acquire KRT10 7 14 1/14 1 05 1/95 0 21798349 0,21798349 The deposition of hydroxyapatite, a form of calcium phosp ALPL 7.14 1/14 1.05 1/95 0,21798349 Any process that modulates the chemical reactions and pa ERLIN2 7.14 1/14 1.02 1/98 0,21798349 Any process that modulates the frequency, rate or extent (IDH1 SH3GLB1 14.29 2/14 0.33 2/613 The process by which heat is generated by increasing meta ALPL 7.14 1/14 1.08 1/93 0,21798349 The formation of a double membrane-bounded structure, SH3GLB1 7.14 1/14 1.08 1/93 0,21798349 7.14 1/14 The movement of a neutrophil within or between different GP2 1.04 1/96 0,21798349 A process that is carried out at the cellular level which resu SH3GLB1 7.14 1/14 0.21798349 1.02 1/98 Any process that modulates the frequency, rate or extent (ALPL 7.14 1/14 1.08 1/93 0.21798349 The regulated production of heat in response to short tern ALPL 7.14 1/14 0.98 1/102 0,22271412 The chemical reactions and pathways involving sterols, ste ERLIN2 7.14 1/14 0.97 1/103 0.22271412 The protein catabolic pathway which targets endoplasmic | ERLIN2 7.14 1/14 0.97 1/103 0.22271412 0.223005828 Any process that stops, prevents, or reduces the frequency CNTFR 7.14 1/14 0.96 1/104 The process whose specific outcome is the progression of ALPL ANXA7 KRT10 21.43 3/14 0,229156697 0.21 3/143: 0.229677896 The chemical reactions and pathways resulting in the form ERLIN2 7.14 1/14 0.92 1/109 Any process that activates, maintains or increases the rate SH3GLB1 7.14 1/14 0.88 1/114 0.231020925 Any process that results in a change in state or activity of a BSPRY CNTFR 14.29 2/14 0.30 2/660 0.231020925 A developmental process in which a progressive change in ALPL CNTFR 14.29 2/14 0.30 2/666 0,231020925 0,231020925 The chemical reactions and pathways involving small mole ALPL ERLIN2 IDH1 21.43 3/14 0.21 3/1460 0.88 1/114 A homeostatic process in which an organism modulates its ALPL 7.14 1/14 0,231020925 The directed movement of carbohydrate into, out of or wil SLC5A9 7.14 1/14 0.86 1/116 0.231139951 The chemical reactions and pathways resulting in the form ERLIN2 7.14 1/14 0.86 1/116 0.231139951 The movement of a granulocyte within or between differe GP2 7.14 1/14 0.85 1/118 0.233233916 The progression of a skeletal muscle organ over time from CNTFR 7.14 1/14 0.78 1/129 0.23507163 7.14 1/14 0.80 1/125 0.23507163 A process that is carried out at the cellular level which rest SH3GLB1 7.14 1/14 0.23507163 The chemical reactions and pathways involving a receptor SH3GLB1 0.77 1/130 7.14 1/14 0.80 1/125 0.23507163 Formation of hard tissues that consist mainly of inorganic (ALPL The assembly of actin filament bundles; actin filaments are MARCKS 7.14 1/14 0.79 1/126 0,23507163 7.14 1/14 A process that results in the assembly, arrangement of con MARCKS 0.78 1/128 0,23507163 The chemical reactions and pathways resulting in the form ERLIN2 7.14 1/14 0.81 1/124 0,23507163 Any process that results in a change in state or activity of a BSPRY CNTFR 14.29 2/14 0.28 2/713 0,23507163 The chemical reactions and pathways resulting in the breal IDH1 7.14 1/14 0 79 1/126 0 23507163 The process where mineral crystals are formed and deposi ALPL 7 14 1/14 0 79 1/127 0 23507163 Any process that stops, prevents or reduces the frequency CNTFR 7.14 1/14 0.77 1/130 0.23507163 The directed movement of metal ions, any metal ion with (SLC5A9 SLC6A8 14.29 2/14 0.23507163 0.28 2/708 Any process that modulates the occurrence or rate of cell (CNTFR 7.14 1/14 0.76 1/132 0,236923618 0.75 1/134 The division of the cytoplasm and the plasma membrane o SH3GLB1 7.14 1/14 0.238746302 Any process that results in a change in state or activity of a SH3GLB1 7.14 1/14 0.73 1/137 0,23904417 Any process that modulates the frequency, rate, or extent IDH1 SH3GLB1 14.29 2/14 0.27 2/732 0,23904417 The chemical reactions and pathways involving carboxylic : ERLIN2 IDH1 14.29 2/14 0.27 2/736 0,23904417 Any process that modulates the frequency, rate or extent (SH3GLB1 7.14 1/14 0.72 1/138 0.239138704 The chemical reactions and pathways involving any oxoaci ERLIN2 IDH1 14.29 2/14 0.27 2/745 0.240236722 The chemical reactions and pathways involving compound IDH1 7.14 1/14 0.65 1/153 0.24920429 positive regulation of protein-containing complex assembl Any process that activates or increases the frequency, rate SH3GLB1 7.14 1/14 0.68 1/148 0 24920429 0.67 1/149 0.24920429 The directed movement of a neurotransmitter into, out of SLC6A8 7.14 1/14 0,24920429 The chemical reactions and pathways involving organic aci ERLIN2 IDH1 14.29 2/14 0.26 2/774 7.14 1/14 0.65 1/153 0,24920429 The chemical reactions and pathways resulting in the form ERLIN2 A process in which a sodium ion is transported from one si SLC6A8 0,24920429 7.14 1/14 0.67 1/149 Any process that results in a change in state or activity of a SH3GLB1 7.14 1/14 0.66 1/151 0.24920429 The process in which a relatively unspecialized cell acquire KRT10 7.14 1/14 0.65 1/153 0,24920429 The chemical reactions and pathways involving organopho ALPL IDH1 14.29 2/14 0.25 2/793 0,252377521 Any process that results in a change in state or activity of a SH3GLB1 7.14 1/14 0.256809463 0.62 1/161 0,256809463 A process that is carried out at the cellular level which resu SH3GLB1 7.14 1/14 0.62 1/160 The movement of a myeloid leukocyte within or between (GP2 7.14 1/14 0.60 1/166 0,259641729 Any process that modulates the frequency, rate or extent (SH3GLB1 7.14 1/14 0.60 1/166 0.259641729 0.259641729 Any apoptotic process in a neuron, the basic cellular unit o CNTER 7.14 1/14 0.61 1/164 0.262434639 The enzymatic release of energy from inorganic and organi IDH1 7.14 1/14 0.59 1/169 0.59 1/170 0,262434639 The chemical reactions and pathways involving any of a cla ERLIN2 7.14 1/14 The process whose specific outcome is the progression of | ALPL 7.14 1/14 0.57 1/175 0.265045347 The chemical reactions and pathways resulting in the form ERLIN2 7.14 1/14 0.57 1/175 0.265045347 The chemical reactions and pathways resulting in the breal ERLIN2 IDH1 SH3GL 21.43 3/14 0.17 3/1742 0.265045347 The chemical reactions and pathways involving lipids, as ca ERLIN2 IDH1 14.29 2/14 0.23 2/852 0,266687742 Any process that modulates the frequency, rate or extent (CNTFR 7.14 1/14 0.56 1/179 0,267663455 Any process that results in a change in state or activity of a SH3GLB1 7.14 1/14 0.55 1/181 0,268944706 GO:0008654 phospholipid biosynthetic process GO:0060429 epithelium development GO:0044242 cellular lipid catabolic process GO:0016485 protein processing GO:0048705 skeletal system morphogenesis GO:0071310 cellular response to organic substance GO:0007548 sex differentiation GO:0045333 cellular respiration macroautophagy GO:0016236 GO:0051259 protein complex oligomerization GO:0043588 skin development GO:0070997 neuron death GO:0071496 cellular response to external stimulus GO·0007517 muscle organ development GO:0051179 localization GO:0008202 steroid metabolic process GO:0010506 regulation of autophagy GO:0046942 carboxylic acid transport GO:0044262 cellular carbohydrate metabolic process GO:0034976 response to endoplasmic reticulum stress GO:0071702 organic substance transport GO:0006812 cation transport epidermis development GO:0008544 GO:0098656 anion transmembrane transport GO:0062012 regulation of small molecule metabolic process GO·0046394 carboxylic acid biosynthetic process GO:0016053 organic acid biosynthetic process GO:000003 reproduction GO:0022414 reproductive process GO:0051604 protein maturation GO:0048856 anatomical structure development GO:0006790 sulfur compound metabolic process GO:0006979 response to oxidative stress GO:0015980 energy derivation by oxidation of organic compounds GO:0016042 lipid catabolic process GO:0006629 lipid metabolic process GO:0001503 ossification GO:0050900 leukocyte migration GO:0009057 macromolecule catabolic process GO:0015711 organic anion transport GO:0006631 fatty acid metabolic process GO:1901564 organonitrogen compound metabolic process GO:0043254 regulation of protein-containing complex assembly GO:0006644 phospholipid metabolic process GO:0031331 positive regulation of cellular catabolic process GO:0032502 developmental process GO:0016192 vesicle-mediated transport GO:0070887 cellular response to chemical stimulus GO:0006915 apoptotic process GO:0048871 multicellular organismal homeostasis GO:0051301 cell division GO:0048731 system development GO:0071407 cellular response to organic cyclic compound positive regulation of cellular component biogenesis GO:0044089 GO:0043161 GO:0012501 programmed cell death GO:0006091 generation of precursor metabolites and energy GO:0006811 ion transport GO:0009896 positive regulation of catabolic process GO:0016311 dephosphorylation GO:0007015 actin filament organization GO:0010638 positive regulation of organelle organization GO:0001501 skeletal system development GO:0019221 cytokine-mediated signaling pathway GO:0010256 endomembrane system organization transmembrane transport GO:0055085 GO:0007610 behavior GO:0008219 cell death GO·0044283 small molecule biosynthetic process GO:0070727 cellular macromolecule localization GO:0034613 cellular protein localization GO:0090407 organophosphate biosynthetic process GO:0033554 cellular response to stress GO:0006820 anion transport GO:0061061 muscle structure development GO:0048513 animal organ development GO:0006810 transport GO:0006897 endocytosis GO:0033993 response to lipid GO:0010498 proteasomal protein catabolic process GO:0007275 multicellular organism development GO:0072657 protein localization to membrane GO:0005975 carbohydrate metabolic process GO:0014070 response to organic cyclic compound GO:0051234 establishment of localization GO:0071705 nitrogen compound transport GO:0010564 regulation of cell cycle process response to chemical GO:0042221 GO:0006950 response to stress

The chemical reactions and pathways resulting in the form IDH1 7.14 1/14 0.54 1/185 0,272499475 The process whose specific outcome is the progression of ANXA7 KRT10 14.29 2/14 0.23 2/875 0,272499475 The chemical reactions and pathways resulting in the breal IDH1 7.14 1/14 0.53 1/188 0.274051847 Any protein maturation process achieved by the cleavage (CD5L 7.14 1/14 0.52 1/192 0.277973286 The process in which the anatomical structures of the skel ALPL 7.14 1/14 0.50 1/199 0.285877842 Any process that results in a change in state or activity of a ALPL BSPRY CNTFR 21.43 3/14 0.16 3/1848 0.287438919 0,288890774 The establishment of the sex of an organism by physical di CNTFR 7.14 1/14 0.49 1/205 The enzymatic release of energy from inorganic and organ IDH1 7.14 1/14 0.49 1/206 0.288890774 The major inducible pathway for the general turnover of c SH3GLB1 7.14 1/14 0.49 1/205 0,288890774 The process of creating protein oligomers, compounds cor KRT10 7.14 1/14 0.48 1/209 0,291243947 7.14 1/14 0.47 1/212 0,293286893 The process whose specific outcome is the progression of I KRT10 0,293286893 The process of cell death in a neuron. 7.14 1/14 0.47 1/213 CNTFR Any process that results in a change in state or activity of a SH3GLB1 7.14 1/14 0.45 1/222 0,301249335 The process whose specific outcome is the progression of I CNTFR 7 14 1/14 0.45 1/224 0 301249335 Any process in which a cell, a substance, or a cellular entity CD5L GP2 NAPA SH: 42.86 6/14 0.11 6/5413 0.301249335 The chemical reactions and pathways involving steroids, cc ERLIN2 7.14 1/14 0.44 1/229 0.301249335 Any process that modulates the frequency, rate or extent (SH3GLB1 0.44 1/229 0.301249335 7.14 1/14 0,301249335 The directed movement of carboxylic acids into, out of or \ SLC6A8 7.14 1/14 0.44 1/228 0,301249335 The chemical reactions and pathways involving carbohydra IDH1 7.14 1/14 0.44 1/229 Any process that results in a change in state or activity of a ERLIN2 7.14 1/14 0.45 1/224 0,301249335 The directed movement of organic substances into, out of NAPA SLC5A9 SLC6A 21.43 3/14 0.15 3/1968 0,301725763 The directed movement of cations, atoms or small molecu SLC5A9 SLC6A8 14.29 2/14 0.301725763 0.20 2/999 The process whose specific outcome is the progression of #KRT10 7.14 1/14 0.42 1/236 0.301725763 The process in which an anion is transported across a merr SLC6A8 7.14 1/14 0.43 1/232 0.301725763 Any process that modulates the rate, frequency or extent (ERLIN2 7.14 1/14 0.42 1/236 0.301725763 The chemical reactions and pathways resulting in the form ERLIN2 7.14 1/14 0 42 1/239 0 303759134 0,305746757 The chemical reactions and pathways resulting in the form ERLIN2 7.14 1/14 0.41 1/242 The production of new individuals that contain some porti ALPL CNTFR 0,305746757 14.29 2/14 0.20 2/1024 0,305746757 A biological process that directly contributes to the proces ALPL CNTFR 14.29 2/14 0.20 2/102: Any process leading to the attainment of the full functiona CD5L 7.14 1/14 0.39 1/254 0,315052273 The biological process whose specific outcome is the progr ALPL ANXA7 CNTFR 35.71 5/14 0.11 5/4373 0,32699463 The chemical reactions and pathways involving the nonme IDH1 7.14 1/14 0.37 1/272 0,332234638 0,333974491 7.14 1/14 Any process that results in a change in state or activity of a IDH1 0.36 1/275 The chemical reactions and pathways by which a cell deriv IDH1 7.14 1/14 0.337892402 0.36 1/280 The chemical reactions and pathways resulting in the breal IDH1 7.14 1/14 0.35 1/284 0,34066382 The chemical reactions and pathways involving lipids, com ERLIN2 IDH1 14.29 2/14 0.18 2/1124 0,341261655 The formation of bone or of a bony substance, or the conv ALPL 7.14 1/14 0.35 1/289 0.341261655 The movement of a leukocyte within or between different GP2 7.14 1/14 0.35 1/289 0.341261655 The chemical reactions and pathways resulting in the breal ERLIN2 SH3GLB1 14.29 2/14 0.18 2/1142 0,346305827 . 7.14 1/14 0,356072443 The directed movement of organic anions into, out of or w SLC6A8 0.33 1/306 The chemical reactions and pathways involving fatty acids, ERLIN2 7.14 1/14 0.32 1/316 0.364860904 The chemical reactions and pathways involving organonitri ALPL BSPRY CD5L EF 42.86 6/14 0.10 6/591 0.373962119 Any process that modulates the frequency, rate or extent (SH3GLB1 7.14 1/14 0.30 1/330 0,37588299 The chemical reactions and pathways involving phospholip IDH1 7.14 1/14 0.30 1/338 0,38228067 Any process that activates or increases the frequency, rate SH3GLB1 7.14 1/14 0.29 1/342 0,384569779 A biological process whose specific outcome is the progres ALPL ANXA7 CNTFR 35.71 5/14 0.11 5/475 0.394007027 A cellular transport process in which transported substanc CD5L NAPA 14.29 2/14 0.16 2/127(0.395703715 Any process that results in a change in state or activity of a ALPL BSPRY CNTFR 21.43 3/14 0.13 3/2376 0.398667135 A programmed cell death process which begins when a cel CNTFR SH3GLB1 14.29 2/14 0.15 2/1299 0.402320032 0.27 1/369 Any process involved in the maintenance of an internal ste ALPL 7.14 1/14 0.402320032 The process resulting in division and partitioning of compo SH3GLB1 0,40438132 7.14 1/14 0.27 1/373 The process whose specific outcome is the progression of ALPL CNTFR KRT10 128.57 4/14 0,408178997 0.11 4/3612 Any process that results in a change in state or activity of a ALPL 7.14 1/14 0.26 1/383 0,408522312 Any process that activates or increases the frequency, rate SH3GLB1 7.14 1/14 0.26 1/382 0,408522312 proteasome-mediated ubiquitin-dependent protein catab: The chemical reactions and pathways resulting in the breal ERLIN2 7.14 1/14 0,408898892 0.26 1/391 A process which begins when a cell receives an internal or CNTFR SH3GLB1 14.29 2/14 0.15 2/1343 0,408898892 The chemical reactions and pathways resulting in the form IDH1 7.14 1/14 0 26 1/386 0 408898892 The directed movement of charged atoms or small charge(SLC5A9 SLC6A8 14 29 2/14 0 15 2/134 0 408898892 Any process that activates or increases the frequency, rate SH3GLB1 7.14 1/14 0.25 1/400 0.410121831 0.410121831 The process of removing one or more phosphoric (ester or ALPL 7.14 1/14 0.25 1/399 A process that is carried out at the cellular level which rest MARCKS 7.14 1/14 0.25 1/396 0,410121831 7.14 1/14 0.25 1/398 0.410121831 Any process that increases the frequency, rate or extent of SH3GLB1 The process whose specific outcome is the progression of I ALPL 7.14 1/14 0.25 1/405 0,412863711 A series of molecular signals initiated by the binding of a c CNTFR 7.14 1/14 0.25 1/408 0,412963669 A process that is carried out at the cellular level which rest SH3GLB1 7.14 1/14 0.24 1/409 0,412963669 The process in which a solute is transported across a lipid I SLC5A9 SLC6A8 14.29 2/14 0.14 2/1405 0.420001124 The internally coordinated responses (actions or inactions) CNTFR 7.14 1/14 0.24 1/421 0.420001124 Any biological process that results in permanent cessation CNTFR SH3GLB1 14.29 2/14 0.14 2/1432 0.42672106 The chemical reactions and pathways resulting in the form ERLIN2 7 14 1/14 0 23 1/437 0 42672106 Any process in which a macromolecule is transported to, a NAPA SH3GLB1 0.42672106 14.29 2/14 0.14 2/1438 Any process in which a protein is transported to, and/or m NAPA SH3GLB1 14.29 2/14 0,42672106 0.14 2/1432 0,42672106 The chemical reactions and pathways resulting in the biosy IDH1 7.14 1/14 0.23 1/439 Any process that results in a change in state or activity of a ERLIN2 SH3GLB1 0,428211624 14.29 2/14 0.14 2/1463 The directed movement of anions, atoms or small molecul SLC6A8 7.14 1/14 0.22 1/449 0.428211624 The progression of a muscle structure over time, from its f CNTFR 7.14 1/14 0.22 1/445 0,428211624 Development of a tissue or tissues that work together to p ALPL CNTFR KRT10 21.43 3/14 0.11 3/2612 0,428211624 The directed movement of substances (such as macromole CD5L NAPA SLC5A9 28.57 4/14 0.433436809 0.10 4/3886 A vesicle-mediated transport process in which cells take ut CD5L 7.14 1/14 0.21 1/466 0.433436809 Any process that results in a change in state or activity of a ALPL 7.14 1/14 0.22 1/464 0.433436809 The chemical reactions and pathways resulting in the breal ERLIN2 7.14 1/14 0.22 1/464 0.433436809 The biological process whose specific outcome is the progr ALPL CNTFR KRT10 | 28.57 4/14 0.10 4/387 0.433436809 0.437287783 A process in which a protein is transported to, or maintain SH3GLB1 7.14 1/14 0.21 1/473 The chemical reactions and pathways involving carbohydra IDH1 7.14 1/14 0.21 1/484 0.444205924 Any process that results in a change in state or activity of a ALPL 7.14 1/14 0.451008587 0.20 1/495 Any process that localizes a substance or cellular compone CD5L NAPA SLC5A9 28.57 4/14 0.10 4/403 0.462048459 The directed movement of nitrogen-containing compound NAPA SLC6A8 14.29 2/14 0.13 2/158 0.462048459 Any process that modulates a cellular process that is involv SH3GLB1 7.14 1/14 0.19 1/520 0,463737395 Any process that results in a change in state or activity of a ALPL BSPRY CNTFR I 28.57 4/14 0.10 4/4056 0,463737395 Any process that results in a change in state or activity of a ERLIN2 IDH1 SH3GL 21.43 3/14 0.11 3/280! 0,465301685

GO:0051668	localization within membrane	Any process in which a substance or cellular entity, such as SH3GLB1	7.14 1/14	0.18 1/541	0,474974404
GO:0006508	proteolysis		, 14.29 2/14		0,487900758
GO:0006511	ubiquitin-dependent protein catabolic process		7.14 1/14		0,505700048
GO:0019941	modification-dependent protein catabolic process		7.14 1/14		0,513574642
GO:0043632 GO:0030036	actin cytoskeleton organization		7.14 1/14 7.14 1/14		0,515276864 0,515276864
GO:0050050	membrane organization		7.14 1/14	,	0,519503943
GO:0097435	supramolecular fiber organization		, 7.14 1/14	•	0,528353733
GO:0007417	central nervous system development		7.14 1/14		0,532479195
GO:0008284	positive regulation of cell population proliferation		7.14 1/14		0,532479195
GO:0043066 GO:0010243	negative regulation of apoptotic process response to organonitrogen compound		7.14 1/14 7.14 1/14		0,532479195 0,535111914
GO:0010243	negative regulation of programmed cell death		7.14 1/14		0,536415959
GO:0098662	inorganic cation transmembrane transport		, 7.14 1/14		0,540234846
GO:0030029	actin filament-based process		7.14 1/14		0,540234846
GO:0051603			7.14 1/14		0,551506482
GO:0016567 GO:0060548	protein ubiquitination negative regulation of cell death		7.14 1/14 7.14 1/14	0.14 1/702	0,553273348 0,56174767
GO:0098660	inorganic ion transmembrane transport		7.14 1/14		0,562127217
GO:0044257	cellular protein catabolic process	The chemical reactions and pathways resulting in the breal ERLIN2	7.14 1/14	0.14 1/732	0,562127217
GO:0008104	protein localization		14.29 2/14		0,562127217
GO:0033365	protein localization to organelle regulation of metabolic process		7.14 1/14		0,562127217
GO:0019222 GO:1901698	regulation of metabolic process response to nitrogen compound	Any process that modulates the frequency, rate or extent (ALPL ANXA7 ERLIN2 Any process that results in a change in state or activity of a ERLIN2	35.71 5/14 7.14 1/14		0,562127217 0,562360499
GO:0006886	intracellular protein transport		7.14 1/14		0,562360499
GO:0009605	response to external stimulus	Any process that results in a change in state or activity of a ALPL SH3GLB1	14.29 2/14	0.10 2/2004	0,565704898
GO:0044087	regulation of cellular component biogenesis		7.14 1/14		0,566188013
GO:0032446 GO:0051130	protein modification by small protein conjugation positive regulation of cellular component organization		7.14 1/14		0,566188013
GO:0051130 GO:0070925	organelle assembly		7.14 1/14 7.14 1/14		0,566188013 0,577235731
GO:0051726	regulation of cell cycle		7.14 1/14		0,577512781
GO:0098655	cation transmembrane transport	The process in which a cation is transported across a mem SLC6A8	7.14 1/14		0,577781997
GO:0009887	animal organ morphogenesis		7.14 1/14		0,588414518
GO:0030163 GO:0070647	protein catabolic process		7.14 1/14 7.14 1/14		0,606726245 0,616170698
GO:0006518	peptide metabolic process		7.14 1/14		0,624366921
GO:0033043	regulation of organelle organization		, 7.14 1/14	0.11 1/903	0,62533545
GO:0022607	cellular component assembly	The aggregation, arrangement and bonding together of a c KRT10 MARCKS SH3			0,634395658
GO:0019538	protein metabolic process	The chemical reactions and pathways involving a protein. I BSPRY CD5L ERLIN2			0,645112565
GO:0022402 GO:0044265	cell cycle process cellular macromolecule catabolic process	•	7.14 1/14 7.14 1/14		0,649542338 0,652646283
GO:0050896	response to stimulus	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR I			0,652646283
GO:0033036	macromolecule localization		14.29 2/14		0,652646283
GO:0006796	phosphate-containing compound metabolic process		14.29 2/14		0,657397925
GO:0034220	ion transmembrane transport		7.14 1/14		0,657397925 0,659059358
GO:0051240 GO:0006793	positive regulation of multicellular organismal process phosphorus metabolic process		7.14 1/14 14.29 2/14		0,659059358
GO:0051641	cellular localization		14.29 2/14		0,659059358
GO:1901700	response to oxygen-containing compound	Any process that results in a change in state or activity of a ALPL	7.14 1/14		0,659642725
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromole BSPRY ERLIN2 KRT1			0,661370354
GO:0042981 GO:0010629	regulation of apoptotic process negative regulation of gene expression		7.14 1/14 7.14 1/14		0,661370354 0,661370354
GO:0010025	cellular component biogenesis	A process that results in the biosynthesis of constituent mi KRT10 MARCKS SH3			0,663732525
GO:0043067	regulation of programmed cell death	Any process that modulates the frequency, rate or extent (CNTFR	7.14 1/14	0.09 1/106	0,665348444
GO:0065003	protein-containing complex assembly		14.29 2/14		0,670212347
GO:0019220 GO:0051174	regulation of phosphate metabolic process regulation of phosphorus metabolic process		7.14 1/14 7.14 1/14	0.09 1/109 ⁴ 0.09 1/109 ⁴	0,67133047 0,67133047
GO:0031174 GO:0043603	cellular amide metabolic process		7.14 1/14		0,676669002
GO:0051716	cellular response to stimulus	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR I		,	0,67838709
GO:1901565	organonitrogen compound catabolic process		7.14 1/14		0,679383777
GO:0010941	regulation of cell death		7.14 1/14		0,682490344
GO:0042127 GO:0043933	regulation of cell population proliferation protein-containing complex organization		7.14 1/14 14.29 2/14		0,685924626 0,69600714
GO:00455333 GO:0015031	protein transport		7.14 1/14		0,69600714
GO:0016477	cell migration	The controlled self-propelled movement of a cell from one GP2	7.14 1/14	0.08 1/1202	0,697300013
GO:0009892	negative regulation of metabolic process		14.29 2/14		0,697698405
GO:0007010 GO:0031327	cytoskeleton organization negative regulation of cellular biosynthetic process	•	7.14 1/14 7.14 1/14		0,70896947 0,711891578
GO:0009890	negative regulation of biosynthetic process		7.14 1/14		0,716163988
GO:0045184	establishment of protein localization		7.14 1/14		0,717188907
GO:0007049	cell cycle		7.14 1/14		0,721647353
GO:0042592	homeostatic process		7.14 1/14		0,728911121
GO:0046907 GO:0051674	intracellular transport localization of cell		7.14 1/14 7.14 1/14		0,728911121 0,728911121
GO:0031074 GO:0048870	cell motility		7.14 1/14		0,728911121
GO:0044267	cellular protein metabolic process	The chemical reactions and pathways involving a specific p BSPRY ERLIN2 KRT1			0,735627158
GO:0008283	cell population proliferation		7.14 1/14		0,742970078
GO:0048519	negative regulation of biological process	Any process that stops, prevents, or reduces the frequency ANXA7 CNTFR ERLIN			0,747280672
GO:0009893 GO:0040011	positive regulation of metabolic process locomotion		14.29 2/14 7.14 1/14	0.07 2/304(0,749650637 0,7569576
GO:0040011 GO:0030154	cell differentiation		14.29 2/14		0,75795121
GO:0048869	cellular developmental process		14.29 2/14		0,769346524
GO:0006464	cellular protein modification process		14.29 2/14		0,780132201
GO:0036211	protein modification process		14.29 2/14		0,780132201 0,793981459
GO:0032501 GO:0006996	multicellular organismal process organelle organization	Any biological process, occurring at the level of a multicell ALPL CNTFR KRT10 I A process that is carried out at the cellular level which rest MARCKS SH3GLB1	28.57 4/14 14.29 2/14		0,793981459
GO:0051128	regulation of cellular component organization	•	7.14 1/14	0.06 1/1732	
GO:0006928	movement of cell or subcellular component		7.14 1/14	0.06 1/170	
GO:0009889	regulation of biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2 IDH1	14.29 2/14	0.06 2/343	0,79698703

GO:0048518	positive regulation of biological process	Any process that activates or increases the frequency, rate ALPL CNTFR SH3GLE	21.43 3/14	0.06 3/4958	0,79698703
GO:0007399	nervous system development	The process whose specific outcome is the progression of I MARCKS	7.14 1/14	0.06 1/171(0,79698703
GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units ir BSPRY KRT10	14.29 2/14	0.06 2/341:	0,79698703
GO:0031326	regulation of cellular biosynthetic process	Any process that modulates the frequency, rate or extent (ERLIN2 IDH1	14.29 2/14	0.06 2/3385	0,79698703
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent (ERLIN2 IDH1 SH3GL	21.43 3/14	0.06 3/502	0,79698703
GO:0051649	establishment of localization in cell	Any process, occuring in a cell, that localizes a substance o NAPA	7.14 1/14	0.06 1/178:	0,804324588
GO:0071704	organic substance metabolic process	The chemical reactions and pathways involving an organic ALPL ANXA7 BSPRY	57.14 8/14	0.06 8/1236	0,8067419
GO:0009987	cellular process	Any process that is carried out at the cellular level, but not ALPL ANXA7 BSPRY	92.86 13/14	0.07 13/18:	0,81858918
GO:0051239	regulation of multicellular organismal process	Any process that modulates the frequency, rate or extent (ALPL	7.14 1/14	0.05 1/194:	0,832200855
GO:0002376	immune system process	Any process involved in the development or functioning of GP2	7.14 1/14	0.05 1/2045	0,847565399
GO:0031324	negative regulation of cellular metabolic process	Any process that stops, prevents, or reduces the frequency ERLIN2	7.14 1/14	0.05 1/203!	0,847565399
GO:0048523	negative regulation of cellular process	Any process that stops, prevents, or reduces the frequency CNTFR ERLIN2	14.29 2/14	0.05 2/3856	0,848931299
GO:0009653	anatomical structure morphogenesis	The process in which anatomical structures are generated ALPL	7.14 1/14	0.05 1/210	0,854299974
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism ALPL ANXA7 BSPRY	57.14 8/14	0.06 8/129:	0,864376958
GO:0044237	cellular metabolic process	The chemical reactions and pathways by which individual CALPL ANXA7 BSPRY	50.00 7/14	0.06 7/1158	0,864687819
GO:0007166	cell surface receptor signaling pathway	A series of molecular signals initiated by activation of a rec CNTFR	7.14 1/14	0.04 1/2259	0,872935767
GO:0007154	cell communication	Any process that mediates interactions between a cell and CNTFR ERLIN2 SH30	21.43 3/14	0.05 3/6065	0,903627165
GO:0010605	negative regulation of macromolecule metabolic process	Any process that decreases the frequency, rate or extent o ANXA7	7.14 1/14	0.04 1/256:	0,910119162
GO:0048522	positive regulation of cellular process	Any process that activates or increases the frequency, rate CNTFR SH3GLB1	14.29 2/14	0.04 2/4480	0,910119162
GO:0031325	positive regulation of cellular metabolic process	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	0.04 1/263:	0,914830252
GO:0006807	nitrogen compound metabolic process	The chemical reactions and pathways involving organic or ALPL BSPRY CD5L Ef	42.86 6/14	0.05 6/1092	0,919988415
GO:0016043	cellular component organization	A process that results in the assembly, arrangement of con KRT10 MARCKS SHE	3 21.43 3/14	0.05 3/6354	0,919988415
GO:0043170	macromolecule metabolic process	The chemical reactions and pathways involving macromole ANXA7 BSPRY CD5L	42.86 6/14	0.05 6/109:	0,919988415
GO:0080090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent (ERLIN2 IDH1	14.29 2/14	0.04 2/485	0,930689335
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent ma KRT10 MARCKS SHE	321.43 3/14	0.05 3/6564	0,930689335
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent (ALPL ANXA7 CNTFR	42.86 6/14	0.05 6/111	0,931829975
GO:0065008	regulation of biological quality	Any process that modulates a qualitative or quantitative tr ALPL	7.14 1/14	0.03 1/2959	0,932184262
GO:0044249	cellular biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2 IDH1	14.29 2/14	0.04 2/5094	0,941637763
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2 IDH1	14.29 2/14	0.04 2/516	0,944150782
GO:0009058	biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2 IDH1	14.29 2/14	0.04 2/523:	
GO:0007165	signal transduction	The cellular process in which a signal is conveyed to trigger CNTFR ERLIN2	14.29 2/14	0.04 2/5642	0,96237207
GO:0065007	biological regulation	Any process that modulates a measurable attribute of any ALPL ANXA7 CNTFR	42.86 6/14	0.05 6/1190	0,96237207
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	0.03 1/3552	0,96237207
GO:0023052	signaling	The entirety of a process in which information is transmitter CNTFR ERLIN2	14.29 2/14	0.03 2/6020	0,97662684
GO:0044238	primary metabolic process	The chemical reactions and pathways involving those com BSPRY CD5L ERLIN2	35.71 5/14	0.04 5/1142	0,988590329
GO:0010468	regulation of gene expression	Any process that modulates the frequency, rate or extent (ANXA7	7.14 1/14	0.02 1/4340	0,988590329
GO:1901360	organic cyclic compound metabolic process	The chemical reactions and pathways involving organic cyc ALPL ERLIN2	14.29 2/14	0.03 2/706	0,995002214
GO:0050794	regulation of cellular process	Any process that modulates the frequency, rate or extent (CNTFR ERLIN2 IDH1	28.57 4/14	0.04 4/1039	0,995002214
GO:0010467	gene expression	The process in which a gene's sequence is converted into a ANXA7 CD5L	14.29 2/14		0,996675729
GO:0034641	cellular nitrogen compound metabolic process	The chemical reactions and pathways involving various org ALPL IDH1	14.29 2/14		0,996675729
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent (ANXA7	7.14 1/14	0.02 1/5552	0,996675729
GO:0006725	cellular aromatic compound metabolic process	The chemical reactions and pathways involving aromatic c ALPL	, 7.14 1/14	0.01 1/689:	
GO:0046483	heterocycle metabolic process	The chemical reactions and pathways involving heterocycli ALPL	, 7.14 1/14	0.01 1/6828	0,99970648
GO:0008150	biological_process	A biological process represents a specific objective that the ALPL ANXA7 BSPRY			1

GO_BP		Function Gene Name		Term frequer	
GO:1903725 GO:1905667		Any process that modulates the frequency, rate or extent of ACSL3 PHB2	16.67 2/12 8.33 1/12		0,0635563 0,0650423
GO:0150173		Any process that stops, prevents or reduces the frequency, ra ANKRD13A Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12	100.00 1/1	0,0650423
GO:2001247		Any process that activates or increases the frequency, rate or ACSL3		100.00 1/1	0,0650423
GO:0051049 GO:0016192		Any process that modulates the frequency, rate or extent of IACSL3 ANKRD13A NDRG4 PHB2 SURF4 A cellular transport process in which transported substances ACSL3 ANKRD13A AP2B1 NDRG4 SURF4		0.42 5/1201 0.39 5/1276	0,0650423 0,0650423
GO:0033600	negative regulation of mammary gland epithelial cell proliferation	Any process that stops, prevents or reduces the rate or exten PHB2	8.33 1/12	25.00 1/4	0,0677404
GO:0032879 GO:0097384		Any process that modulates the frequency, rate or extent of ACSL3 ANKRD13A NDRG4 PHB2 SURF4 The chemical reactions and pathways resulting in the formati FASN	41.67 5/12 8.33 1/12	0.24 5/2055 12.50 1/8	0,0677404 0,0677404
GO:1904732		Any process that modulates the frequency, rate or extent of (PHB2		14.29 1/7	0,0677404
GO:1904959 GO:0060341		Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12 25.00 3/12	16.67 1/6	0,0677404 0,0677404
GO:0080341 GO:0042695		Any process that modulates the frequency, rate or extent of ACSL3 ANKRD13A NDRG4 The beginning of development of the breasts in the female. PHB2	8.33 1/12	20.00 1/5	0,0677404
GO:0033036		Any process in which a macromolecule is transported to, or r ACSL3 ANKRD13A AP2B1 PHB2 SQLE SURF4		0.25 6/2363	0,0677404
GO:0010637 GO:0042996		Any process that decreases the frequency, rate or extent of r VAT1 Any process that modulates the frequency, rate or extent of I ACSL3	8.33 1/12 8.33 1/12	14.29 1/7 12.50 1/8	0,0677404 0,0677404
GO:0042998		Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12	20.00 1/5	0,0677404
GO:0098876 GO:0060744		The directed movement of substances to the plasma membri ACSL3 NDRG4 The process in which the branching structure of the mammai PHB2	16.67 2/12 8.33 1/12	1.72 2/116 20.00 1/5	0,0677404 0,0677404
GO:2001245		Any process that modulates the frequency, rate or extent of ACSL3	8.33 1/12	50.00 1/2	0,0677404
GO:0034379 GO:0060627		The non-covalent aggregation and arrangement of proteins a ACSL3 Any process that modulates the rate, frequency, or extent of ACSL3 ANKRD13A NDRG4	8.33 1/12 25.00 3/12	16.67 1/6	0,0677404 0,0677404
GO:1990051		Any process that initiates the activity of the inactive enzyme PHB2	8.33 1/12	25.00 1/4	0,0677404
GO:0008611		The chemical reactions and pathways resulting in the formati FASN	8.33 1/12	12.50 1/8	0,0677404
GO:0006629 GO:0060762	lipid metabolic process regulation of branching involved in mammary gland duct morphogen	The chemical reactions and pathways involving lipids, compo ACSL3 FASN PHB2 SQLE Any process that modulates the rate, frequency, or extent of PHB2	33.33 4/12 8.33 1/12	0.36 4/1124 25.00 1/4	0,0677404 0,0677404
GO:0006898		An endocytosis process in which cell surface receptors ensuri ANKRD13A AP2B1	16.67 2/12		0,0677404
GO:0046504 GO:0006897		The chemical reactions and pathways resulting in the formati FASN A vesicle-mediated transport process in which cells take up e ANKRD13A AP2B1 SURF4	8.33 1/12 25.00 3/12		0,0677404 0,0677404
GO:0008104	protein localization	Any process in which a protein is transported to, or maintain ACSL3 ANKRD13A AP2B1 PHB2 SURF4	41.67 5/12	0.25 5/1967	0,0677404
GO:0002091		Any process that stops, prevents, or reduces the frequency, r ANKRD13A	8.33 1/12		0,0677404 0,0677404
GO:0070374 GO:0006810	transport	Any process that activates or increases the frequency, rate or NDRG4 PHB2 The directed movement of substances (such as macromolecu ACSL3 ANKRD13A AP2B1 ATP13A3 NDRG4 PI	16.67 2/12 H 58.33 7/12		0,0677404
GO:0015031	protein transport	The directed movement of proteins into, out of or within a ct ACSL3 AP2B1 PHB2 SURF4	33.33 4/12	0.34 4/1193	0,0677404
GO:0030223 GO:0071073		The process in which a myeloid precursor cell acquires the sp FASN Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12 8.33 1/12	12.50 1/8 14.29 1/7	0,0677404 0,0677404
GO:0150172		Any process that modulates the frequency, rate or extent of ACSL3	8.33 1/12	16.67 1/6	0,0677404
GO:0008610 GO:0045136		The chemical reactions and pathways resulting in the formati ACSL3 FASN SQLE The process whose specific outcome is the progression of the PHB2	25.00 3/12 8.33 1/12	0.57 3/525 12.50 1/8	0,0677404 0,0677404
GO:1900208		Any process that modulates the frequency, rate or extent of (PHB2	8.33 1/12	33.33 1/3	0,0677404
GO:0051179 GO:0051234		Any process in which a cell, a substance, or a cellular entity, s ACSL3 ANKRD13A AP2B1 ATP13A3 NDRG4 PF Any process that localizes a substance or cellular component ACSL3 ANKRD13A AP2B1 ATP13A3 NDRG4 PF			0,0677404 0,0677404
GO:0031234 GO:0031536		Any process that activates or increases the rate of progressio PHB2	8.33 1/12	20.00 1/5	0,0677404
GO:0030879		The process whose specific outcome is the progression of the FASN PHB2	16.67 2/12		0,0677404
GO:0046543 GO:0010876		The process whose specific outcome is the progression of the PHB2 Any process in which a lipid is transported to, or maintained ACSL3 SQLE SURF4	8.33 1/12 25.00 3/12		0,0677404 0,0677404
GO:0045184	establishment of protein localization	The directed movement of a protein to a specific location. ACSL3 AP2B1 PHB2 SURF4	33.33 4/12	0.31 4/1286	0,0697581
GO:1905666 GO:0090557		Any process that modulates the frequency, rate or extent of ANKRD13A The establishment of a barrier between endothelial cell layer FASN		11.11 1/9 11.11 1/9	0,0697581 0,0697581
GO:1901503		The chemical reactions and pathways resulting in the formati FASN	8.33 1/12	11.11 1/9	0,0697581
GO:0140042		A process that results in the assembly, arrangement of consti SQLE	8.33 1/12	11.11 1/9	0,0697581
GO:0033147 GO:1903727	negative regulation of intracellular estrogen receptor signaling pathw positive regulation of phospholipid metabolic process	Any process that scops, prevents, or reduces the frequency, rate or ACSL3	8.33 1/12 8.33 1/12	10.00 1/10 10.00 1/10	0,0707808 0,0707808
GO:0010635	regulation of mitochondrial fusion	Any process that modulates the frequency, rate or extent of IVAT1	8.33 1/12	10.00 1/10	0,0707808
GO:0010642 GO:0007096	negative regulation of platelet-derived growth factor receptor signali regulation of exit from mitosis	Any process that stops, prevents, or reduces the frequency, r NDRG4 Any process involved in the progression from anaphase/telor PHB2	8.33 1/12 8.33 1/12	10.00 1/10 9.09 1/11	0,0707808 0,0751064
GO:0140374	antiviral innate immune response	A defense response against viruses mediated through an inna PHB2	8.33 1/12	9.09 1/11	0,0751064
GO:0014912 GO:0007202		Any process that stops, prevents, or reduces the frequency, r NDRG4 The initiation of the activity of the inactive enzyme phospolic PHB2	8.33 1/12 8.33 1/12	8.33 1/12 8.33 1/12	0,0753061 0,0753061
GO:0070372		Any process that modulates the frequency, rate or extent of : NDRG4 PHB2	16.67 2/12		0,0753061
GO:0071071		Any process that modulates the frequency, rate or extent of LACSL3	8.33 1/12	8.33 1/12	0,0753061
GO:0046485 GO:0070371		The chemical reactions and pathways involving ether lipids, li FASN An intracellular protein kinase cascade containing at least ER NDRG4 PHB2	8.33 1/12 16.67 2/12		0,0753061 0,0786281
GO:0023035		A series of molecular signals initiated by the binding of the ct PHB2		7.69 1/13	0,0790106
GO:0070727 GO:0034613		Any process in which a macromolecule is transported to, and ACSL3 ANKRD13A AP2B1 PHB2 Any process in which a protein is transported to, and/or mair ACSL3 ANKRD13A AP2B1 PHB2	33.33 4/12 33.33 4/12	0.28 4/1438 0.28 4/1432	0,0791132 0,0791132
GO:0019216	regulation of lipid metabolic process	Any process that modulates the frequency, rate or extent of I ACSL3 PHB2	16.67 2/12	0.81 2/246	0,0791132
GO:0034377 GO:0006662		The non-covalent aggregation and arrangement of proteins a ACSL3 The chemical reactions and pathways involving glycerol ether FASN	8.33 1/12 8.33 1/12	6.25 1/16 6.67 1/15	0,0791132 0,0791132
GO:0006656		The chemical reactions and pathways moving gycerol energy and the formati ACSL3	8.33 1/12	6.25 1/16	0,0791132
GO:0033599		Any process that modulates the frequency, rate or extent of I PHB2	8.33 1/12	6.25 1/16	0,0791132
GO:0060973 GO:0035336		The orderly movement of a cell from one site to another thal NDRG4 The chemical reactions and pathways involving long-chain fal ACSL3	8.33 1/12 8.33 1/12	6.67 1/15 6.25 1/16	0,0791132 0,0791132
GO:0140014	mitotic nuclear division	A mitotic cell cycle process comprising the steps by which the CUL9 PHB2	16.67 2/12	0.81 2/248	0,0791132
GO:0010155 GO:0042953		Any process that modulates the frequency, rate or extent of PHB2 The directed movement of any conjugated, water-soluble prc SURF4	8.33 1/12 8.33 1/12	6.25 1/16 6.67 1/15	0,0791132 0,0791132
GO:0044872	lipoprotein localization	Any process in which a lipoprotein is transported to, or main! SURF4	8.33 1/12	6.67 1/15	0,0791132
GO:0048261		Any process that stops, prevents, or reduces the frequency, r ANKRD13A A cellular localization process whereby a substance or cellula ACSL3 ANKRD13A AP2B1 NDRG4 PHB2	8.33 1/12 41.67 5/12	6.67 1/15 0.21 5/2418	0,0791132
GO:0051641 GO:2001135		A cellular localization process whereby a substance or cellula ACSL3 ANKRD13A AP2B1 NDRG4 PHB2 Any process that modulates the frequency, rate or extent of + NDRG4	41.67 5/12 8.33 1/12	0.21 5/2418 5.88 1/17	0,0791132 0,0815475
GO:0032048	cardiolipin metabolic process	The chemical reactions and pathways involving cardiolipin, 1, PHB2	8.33 1/12	5.88 1/17	0,0815475
GO:0006650 GO:0060749		The chemical reactions and pathways involving glycerophosp ACSL3 PHB2 The progression of the mammary gland alveolus over time, fr PHB2	16.67 2/12 8.33 1/12	0.76 2/262 5.26 1/19	0,0816634 0,0826025
GO:0065005	protein-lipid complex assembly	The aggregation, arrangement and bonding together of prote ACSL3	8.33 1/12	5.00 1/20	0,0826025
GO:0034389 GO:0018904		A process that is carried out at the cellular level which result: SQLE The chemical reactions and pathways involving organic ether FASN	8.33 1/12 8.33 1/12	5.00 1/20 5.00 1/20	0,0826025 0,0826025
GO:0018904 GO:0140354		The directed movement of a lipid from outside of a cell into (ACSL3	8.33 1/12 8.33 1/12	5.26 1/19	0,0826025
GO:0036010	protein localization to endosome	A process in which a protein is transported to, or maintained ANKRD13A	8.33 1/12	5.26 1/19	0,0826025
GO:0010863 GO:0010458		Any process that increases the rate of phospholipase C activil PHB2 The cell cycle transition where a cell leaves M phase and entr PHB2	8.33 1/12 8.33 1/12	5.00 1/20 5.00 1/20	0,0826025 0,0826025
GO:0039529	RIG-I signaling pathway	Any series of molecular signals generated as a consequence c PHB2	8.33 1/12	5.00 1/20	0,0826025
GO:0044539 GO:0061377		The directed movement of a long-chain fatty acid from outsi ACSL3 The progression of the mammary gland lobule over time, fro: PHB2	8.33 1/12 8.33 1/12	5.56 1/18 5.26 1/19	0,0826025 0,0826025
GO:0061377 GO:0071705		The directed movement of nitrogen-containing compounds ii ACSL3 AP2B1 PHB2 SURF4		0.25 4/1587	0,0826025
GO:0010640	regulation of platelet-derived growth factor receptor signaling pathw	Any process that modulates the frequency, rate or extent of INDRG4	8.33 1/12	4.76 1/21	0,0826635
GO:1900274 GO:0060444		Any process that modulates the frequency, rate or extent of PHB2 The process in which the branching structure of the mammai PHB2	8.33 1/12 8.33 1/12	4.76 1/21 4.76 1/21	0,0826635 0,0826635
GO:0044255	cellular lipid metabolic process	The chemical reactions and pathways involving lipids, as carri ACSL3 FASN PHB2	25.00 3/12	0.35 3/852	0,0826635
GO:0071353 GO:0035337		Any process that results in a change in state or activity of a c4 FASN The chemical reactions and pathways involving a fatty-acyl-C ACSL3	8.33 1/12 8.33 1/12	4.76 1/21 4.55 1/22	0,0826635 0,0836905
GO:0035337 GO:0070670		Any process that results in a change in state or activity of a crFASN	8.33 1/12 8.33 1/12	4.55 1/22 4.55 1/22	0,0836905
GO:0002068		The process whose specific outcome is the progression of a g FASN	8.33 1/12	4.55 1/22	0,0836905
GO:0048732 GO:0000423		The process whose specific outcome is the progression of a g FASN PHB2 The selective autophagy process in which a mitochondrion is PHB2	16.67 2/12 8.33 1/12	0.65 2/306 4.17 1/24	0,0874493 0,0886417
GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in respon	Any series of molecular signals generated as a consequence c PHB2	8.33 1/12	4.17 1/24	0,0886417
GO:0006631 GO:0033043		The chemical reactions and pathways involving fatty acids, al ACSL3 FASN Any process that modulates the frequency, rate or extent of : CUL9 SURF4 VAT1	16.67 2/12 25.00 3/12		0,0895066 0,0895066
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GO:0006869	lipid transport	The directed movement of lipids into, out of or within a cell, ACSL3 SURF4	16.67 2/12	0.60 2/332	0,0906447
GO:0033598	mammary gland epithelial cell proliferation	The multiplication or reproduction of mammary gland epithe PHB2	8.33 1/12	3.70 1/27	0,0906447
GO:0014910 GO:0033146	regulation of smooth muscle cell migration	Any process that modulates the frequency, rate or extent of : NDRG4	8.33 1/12 8.33 1/12	3.85 1/26	0,0906447
GO:0033146 GO:0060603	regulation of intracellular estrogen receptor signaling pathway mammary gland duct morphogenesis	Any process that modulates the frequency, rate or extent of PHB2 The process in which anatomical structures of the mammary PHB2	8.33 1/12 8.33 1/12	3.85 1/26 3.70 1/27	0,0906447 0,0906447
GO:0046471	phosphatidylglycerol metabolic process	The chemical reactions and pathways involving phosphatidyl PHB2	8.33 1/12	3.70 1/27	0,0906447
GO:0030224	monocyte differentiation	The process in which a relatively unspecialized myeloid preci FASN	8.33 1/12	3.70 1/27	0,0906447
GO:0008053 GO:0051128	mitochondrial fusion regulation of cellular component organization	Merging of two or more mitochondria within a cell to form a VAT1 Any process that modulates the frequency, rate or extent of : ANKRD13A CUL9 SURF4 VAT1	8.33 1/12 33.33 4/12	3.85 1/26 0.23 4/1732	0,0906447 0,0906447
GO:0048662	negative regulation of smooth muscle cell proliferation	Any process that stops, prevents or reduces the rate or exten NDRG4	8.33 1/12		0,0914053
GO:0006644	phospholipid metabolic process	The chemical reactions and pathways involving phospholipid: ACSL3 PHB2		0.59 2/338	0,0914053
GO:0030851 GO:0045806	granulocyte differentiation negative regulation of endocytosis	The process in which a myeloid precursor cell acquires the sr FASN Any process that stops, prevents, or reduces the frequency, r ANKRD13A	8.33 1/12 8.33 1/12	3.57 1/28 3.45 1/29	0,0914053 0,0928188
GO:0043001	Golgi to plasma membrane protein transport	The directed movement of proteins from the Golgi to the pla ACSL3	8.33 1/12	3.45 1/29	0,0928188
GO:0046486	glycerolipid metabolic process	The chemical reactions and pathways involving glycerolipids, ACSL3 PHB2		0.58 2/347	0,0936966
GO:0033144 GO:0008542	negative regulation of intracellular steroid hormone receptor signalin visual learning	Any process that stops, prevents, or reduces the frequency, r PHB2 Any process in an organism in which a change in behavior of NDRG4	8.33 1/12 8.33 1/12	3.33 1/30 3.23 1/31	0,0944323 0,0944809
GO:0008342 GO:0007346	regulation of mitotic cell cycle	Any process that modulates the rate or extent of progress thi CUL9 PHB2		0.57 2/353	0,0944809
GO:0010518	positive regulation of phospholipase activity	Any process that increases the frequency, rate or extent of pl PHB2	8.33 1/12	3.23 1/31	0,0944809
GO:0071827	plasma lipoprotein particle organization	A protein-lipid complex subunit organization process that res ACSL3	8.33 1/12	3.23 1/31 3.12 1/32	0,0944809
GO:0014909 GO:0000280	smooth muscle cell migration nuclear division	The orderly movement of a smooth muscle cell from one site NDRG4 The division of a cell nucleus into two nuclei, with DNA and o CUL9 PHB2	8.33 1/12 16.67 2/12	3.12 1/32 0.54 2/372	0,0967403 0,0988684
GO:0007632	visual behavior	The behavior of an organism in response to a visual stimulus. NDRG4	8.33 1/12		0,0988684
GO:0043410	positive regulation of MAPK cascade	Any process that activates or increases the frequency, rate or NDRG4 PHB2		0.54 2/373	0,0988684
GO:0010823 GO:0071825	negative regulation of mitochondrion organization protein-lipid complex subunit organization	Any process that decreases the frequency, rate or extent of a VAT1 Any process in which macromolecules aggregate, disaggregal ACSL3	8.33 1/12 8.33 1/12	2.94 1/34 2.94 1/34	0,0988684 0,0988684
GO:0002090	regulation of receptor internalization	Any process that modulates the frequency, rate or extent of (ANKRD13A	8.33 1/12	2.78 1/36	0,1015722
GO:0002066	columnar/cuboidal epithelial cell development	The process whose specific outcome is the progression of a c FASN	8.33 1/12	2.78 1/36	0,1015722
GO:1902808 GO:0010517	positive regulation of cell cycle G1/S phase transition regulation of phospholipase activity	Any signalling pathway that activates or increases the activity PHB2 Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12 8.33 1/12	2.78 1/36 2.78 1/36	0,1015722 0,1015722
GO:0061028	establishment of endothelial barrier	The establishment of a barrier between endothelial cell layer FASN	8.33 1/12	2.56 1/39	0,1046019
GO:0060443	mammary gland morphogenesis	The process in which anatomical structures of the mammary PHB2	8.33 1/12	2.56 1/39	0,1046019
GO:0016126	sterol biosynthetic process	The chemical reactions and pathways resulting in the formati SQLE	8.33 1/12 8.33 1/12	2.56 1/39	0,1046019
GO:0002753 GO:1901568	cytoplasmic pattern recognition receptor signaling pathway fatty acid derivative metabolic process	Any series of molecular signals generated as a consequence (PHB2 The chemical reactions and pathways involving fatty acid der ACSL3	8.33 1/12	2.56 1/39 2.63 1/38	0,1046019 0,1046019
GO:0030520	intracellular estrogen receptor signaling pathway	Any series of molecular signals generated as a consequence (PHB2	8.33 1/12	2.63 1/38	0,1046019
GO:0002639	positive regulation of immunoglobulin production	Any process that activates or increases the frequency, rate, o PHB2	8.33 1/12	2.63 1/38	0,1046019
GO:0060688 GO:0071702	regulation of morphogenesis of a branching structure organic substance transport	Any process that modulates the rate, frequency, or extent of PHB2 The directed movement of organic substances into, out of or ACSL3 AP2B1 PHB2 SURF4	8.33 1/12	2.50 1/40 0.20 4/1968	0,106515 0,1066871
GO:0048285	organelle fission	The creation of two or more organeles by division of one org CUL9 PHB2		0.48 2/414	0,1075817
GO:0072583	clathrin-dependent endocytosis	An endocytosis process that begins when material is taken ut AP2B1	8.33 1/12	2.44 1/41	0,1075817
GO:0060193 GO:0002067	positive regulation of lipase activity	Any process that increases the frequency, rate or extent of lip PHB2	8.33 1/12	2.33 1/43 2.27 1/44	0,1113385 0,1123881
GO:0002087 GO:0006893	glandular epithelial cell differentiation Golgi to plasma membrane transport	The process in which a relatively unspecialized cell acquires s FASN The directed movement of substances from the Golgi to the ACSL3	8.33 1/12 8.33 1/12	2.27 1/44 2.27 1/44	0,1123881
GO:0014812	muscle cell migration	The orderly movement of a muscle cell from one site to anot NDRG4	8.33 1/12	2.22 1/45	0,1141551
GO:0007005	mitochondrion organization	A process that is carried out at the cellular level which result: PHB2 VAT1	16.67 2/12		0,1170456
GO:1903078 GO:0061951	positive regulation of protein localization to plasma membrane establishment of protein localization to plasma membrane	Any process that activates or increases the frequency, rate or ACSL3 The directed movement of a protein to a specific location in : ACSL3	8.33 1/12 8.33 1/12	2.08 1/48 2.13 1/47	0,1170456 0,1170456
GO:0097006	regulation of plasma lipoprotein particle levels	Any process involved in the maintenance of internal levels of ACSL3	8.33 1/12	2.08 1/48	0,1170456
GO:1905330	regulation of morphogenesis of an epithelium	Any process that modulates the frequency, rate or extent of IPHB2	8.33 1/12	2.08 1/48	0,1170456
GO:0042127	regulation of cell population proliferation	Any process that modulates the frequency, rate or extent of INDRG4 PHB2 SQLE		0.26 3/1156	0,1170456
GO:0046470 GO:0048856	phosphatidylcholine metabolic process anatomical structure development	The chemical reactions and pathways involving phosphatidyli ACSL3 The biological process whose specific outcome is the progres ACSL3 CMTM8 FASN NDRG4 PHB2 VAT1	8.33 1/12	2.04 1/49 0.14 6/4373	0,1179583 0,1179583
GO:0048278	vesicle docking	The initial attachment of a transport vesicle membrane to the NDRG4	8.33 1/12	2.00 1/50	0,1188472
GO:0048008	platelet-derived growth factor receptor signaling pathway	The series of molecular signals generated as a consequence c NDRG4	8.33 1/12	2.00 1/50	0,1188472
GO:0008306	associative learning	Learning by associating a stimulus (the cause) with a particul: NDRG4	8.33 1/12	1.96 1/51	0,1197131
GO:0007062 GO:0032787	sister chromatid cohesion monocarboxylic acid metabolic process	The cell cycle process in which the sister chromatids of a repl PHB2 The chemical reactions and pathways involving monocarboxy ACSL3 FASN	8.33 1/12 16.67 2/12	0.43 2/470	0,1197131 0,120659
GO:0008285	negative regulation of cell population proliferation	Any process that stops, prevents or reduces the rate or exten NDRG4 PHB2	16.67 2/12	0.43 2/469	0,120659
GO:0060191	regulation of lipase activity	Any process that modulates the frequency, rate or extent of I PHB2	8.33 1/12		0,120659
GO:0001885 GO:1904377	endothelial cell development positive regulation of protein localization to cell periphery	The progression of an endothelial cell over time, from its forr FASN Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12 8.33 1/12	1.89 1/53 1.85 1/54	0,1213794 0,1229043
GO:0098586	cellular response to virus	Any process that results in a change in state or activity of a cr PHB2	8.33 1/12	1.82 1/55	0,12441
GO:0002637	regulation of immunoglobulin production	Any process that modulates the frequency, rate, or extent of PHB2	8.33 1/12	1.79 1/56	0,125165
GO:0033143 GO:1901224	regulation of intracellular steroid hormone receptor signaling pathwa	Any process that modulates the frequency, rate or extent of 1 PHB2 Any process that activates or increases the frequency, rate or PHB2	8.33 1/12		0,125165
GO:1901224 GO:0046889	positive regulation of NIK/NF-kappaB signaling positive regulation of lipid biosynthetic process	Any process that activates or increases the frequency, rate of PHB2 Any process that activates or increases the frequency, rate of ACSL3	8.33 1/12 8.33 1/12	1.75 1/57	0,1266291 0,1280752
GO:0015909	long-chain fatty acid transport	The directed movement of long-chain fatty acids into, out of ACSL3	8.33 1/12	1.69 1/59	0,1295036
GO:0006996	organelle organization	A process that is carried out at the cellular level which result: CUL9 PHB2 SQLE SURF4 VAT1		0.15 5/3330	0,130146
GO:0061180 GO:0051129	mammary gland epithelium development negative regulation of cellular component organization	The process whose specific outcome is the progression of the PHB2 Any process that stops, prevents, or reduces the frequency, r ANKRD13A VAT1	8.33 1/12 16.67 2/12	1.67 1/60 0.39 2/507	0,130146 0,130146
GO:0061912	selective autophagy	The macroautophagy process in which specific structures are PHB2	8.33 1/12	1.64 1/61	0,1308302
GO:0010564	regulation of cell cycle process	Any process that modulates a cellular process that is involvec CUL9 PHB2		0.38 2/520	0,1340659
GO:0048259 GO:0043408	regulation of receptor-mediated endocytosis	Any process that modulates the frequency, rate or extent of I ANKRD13A Any process that modulates the frequency, rate or extent of I NDRG4 PHB2	8.33 1/12	1.59 1/63 0.38 2/524	0,1340659
GO:0043408 GO:0000422	regulation of MAPK cascade autophagy of mitochondrion	The autophagic process in which mitochondria are delivered PHB2	8.33 1/12	0.38 2/524 1.52 1/66	0,1352115 0,1375199
GO:0061726	mitochondrion disassembly	The disaggregation of a mitochondrion into its constituent cc PHB2	8.33 1/12	1.52 1/66	0,1375199
GO:1901992 GO:0001676	positive regulation of mitotic cell cycle phase transition	Any process that activates or increases the frequency, rate or PHB2 The chemical reactions and pathways involving long-chain fat ACSL3	8.33 1/12 8.33 1/12	1.49 1/67 1.47 1/68	0,1380196
GO:0001676 GO:0051668	long-chain fatty acid metabolic process localization within membrane	The chemical reactions and pathways involving long-chain fal ACSL3 Any process in which a substance or cellular entity, such as a ACSL3 NDRG4		0.37 2/541	0,1380196 0,1380196
GO:0032456	endocytic recycling	The directed movement of membrane-bounded vesicles fron NDRG4	8.33 1/12	1.47 1/68	0,1380196
GO:0140056	organelle localization by membrane tethering	The process by which an organelle membrane interacts with NDRG4	8.33 1/12	1.49 1/67	0,1380196
GO:0019915 GO:0046907	lipid storage intracellular transport	The accumulation and maintenance in cells or tissues of lipid SQLE The directed movement of substances within a cell. AP2B1 NDRG4 PHB2	8.33 1/12 25.00 3/12	1.45 1/69 0.22 3/1335	0,1391169 0,1396249
GO:0051341	regulation of oxidoreductase activity	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	1.43 1/70	0,1396249
GO:0002065	columnar/cuboidal epithelial cell differentiation	The process in which a relatively unspecialized cell acquires s FASN	8.33 1/12	1.39 1/72	0,1398364
GO:0032502 GO:0035383	developmental process thioester metabolic process	A biological process whose specific outcome is the progressic ACSL3 CMTM8 FASN NDRG4 PHB2 VAT1 The chemical reactions and pathways involving a thioester, a ACSL3	50.00 6/12 8.33 1/12	0.13 6/4755 1.39 1/72	0,1398364 0,1398364
GO:0015908	fatty acid transport	The directed movement of fatty acids into, out of or within a ACSL3	8.33 1/12	1.41 1/71	0,1398364
GO:0006637	acyl-CoA metabolic process	The chemical reactions and pathways involving acyl-CoA, any ACSL3	8.33 1/12	1.39 1/72	0,1398364
GO:0048660	regulation of smooth muscle cell proliferation	Any process that modulates the frequency, rate or extent of : NDRG4	8.33 1/12	1.41 1/71	0,1398364
GO:0048659 GO:0022406	smooth muscle cell proliferation membrane docking	The multiplication or reproduction of smooth muscle cells, re NDRG4 The initial attachment of a membrane or protein to a target I NDRG4	8.33 1/12 8.33 1/12	1.37 1/73 1.35 1/74	0,1403721 0,141545
GO:1905477	positive regulation of protein localization to membrane	Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12	1.32 1/76	0,1438528
GO:0006892	post-Golgi vesicle-mediated transport	The directed movement of substances from the Golgi to othe ACSL3	8.33 1/12	1.32 1/76	0,1438528
GO:1903047 GO:0000165	mitotic cell cycle process MAPK cascade	A process that is part of the mitotic cell cycle. CUL9 PHB2 An intracellular protein kinase cascade containing at least a N NDRG4 PHB2	16.67 2/12 16.67 2/12	0.34 2/584 0.34 2/591	0,1476475 0,1479802
GO:1901222	regulation of NIK/NF-kappaB signaling	An intracential protein mass cascade containing at least a monor PhB2		1.23 1/81	0,1479802
GO:0008283	cell population proliferation	The multiplication or reproduction of cells, resulting in the e> NDRG4 PHB2 SQLE	25.00 3/12	0.21 3/1409	0,1479802
GO:0032880 GO:0045446	regulation of protein localization endothelial cell differentiation	Any process that modulates the frequency, rate or extent of : ACSL3 ANKRD13A The process in which a mesodermal, bone marrow or neural FASN		0.34 2/594 1.23 1/81	0,1479802 0,1479802
GO:0045446 GO:0002377	endothelial cell differentiation immunoglobulin production	The appearance of immunoglobulin due to biosynthesis or se PHB2	8.33 1/12 8.33 1/12	1.23 1/81 1.23 1/81	0,1479802 0,1479802
GO:0032368	regulation of lipid transport	Any process that modulates the frequency, rate or extent of I SURF4	8.33 1/12	1.19 1/84	0,149056
GO:0048731	system development	The process whose specific outcome is the progression of an ACSL3 CMTM8 FASN NDRG4 PHB2	41.67 5/12		0,149056
GO:0030518 GO:0034032	intracellular steroid hormone receptor signaling pathway purine nucleoside bisphosphate metabolic process	A series of molecular signals generated as a consequence of PHB2 The chemical reactions and pathways involving a purine nucl ACSL3	8.33 1/12 8.33 1/12	1.19 1/84 1.16 1/86	0,149056 0,149056
GO:0007088	regulation of mitotic nuclear division	Any process that modulates the frequency, rate or extent of I CUL9	8.33 1/12	1.18 1/85	0,149056
GO:1903076	regulation of protein localization to plasma membrane	Any process that modulates the frequency, rate or extent of ACSL3	8.33 1/12	1.16 1/86	0,149056
GO:0033865	nucleoside bisphosphate metabolic process	The chemical reactions and pathways involving a nucleoside ACSL3	8.33 1/12	1.10 1/86	0,149056

GO:1901989	positive regulation of cell cycle phase transition	Any process that activates or increases the frequency, rate or PHB2		1.18 1/85	0,149056
GO:0002702	positive regulation of production of molecular mediator of immune n			1.20 1/83	0,149056
GO:0033875 GO:0031623	ribonucleoside bisphosphate metabolic process receptor internalization	The chemical reactions and pathways involving a ribonucleos ACSL3 A receptor-mediated endocytosis process that results in the r ANKRD13A		1.16 1/86 1.19 1/84	0,149056 0,149056
GO:0031623 GO:0016043	cellular component organization	A receptor-mediated endocyclosis process that results in the rankwolsa. A process that results in the assembly, arrangement of consti ACSL3 ANKRD13A CUL9 PHB2 SQLE SURF4 VA			0,149038
GO:0010043	small molecule metabolic process	The chemical reactions and pathways involving small molecu ACSL3 FASN SQLE		0.21 3/1460	0,1493738
GO:0003158	endothelium development	The process whose specific outcome is the progression of an FASN		1.12 1/89	0,1520562
GO:0040011	locomotion	Self-propelled movement of a cell or organism from one loca CMTM8 NDRG4 PHB2		0.20 3/1476	0,153326
GO:2000027	regulation of animal organ morphogenesis	Any process that modulates the frequency, rate or extent of PHB2		1.10 1/91	0,153326
GO:1903008		The disaggregation of an organelle into its constituent compt PHB2		1.10 1/91	0,153326
GO:0045931	positive regulation of mitotic cell cycle	Any process that activates or increases the rate or extent of r PHB2		1.08 1/93	0,1545588
GO:0042552		The process in which myelin sheaths are formed and maintai CMTM8		1.08 1/93	0,1545588
GO:0007612	learning	Any process in an organism in which a relatively long-lasting NDRG4	8.33 1/12	1.08 1/93	0,1545588
GO:0008366	axon ensheathment	Any process in which the axon of a neuron is insulated, and tl CMTM8	8.33 1/12	1.05 1/95	0,1564306
GO:0007272	ensheathment of neurons	The process in which glial cells envelop neuronal cell bodies (CMTM8	8.33 1/12	1.05 1/95	0,1564306
GO:0032147	activation of protein kinase activity	Any process that initiates the activity of an inactive protein ki PHB2		1.04 1/96	0,1566777
GO:0008203		The chemical reactions and pathways involving cholesterol, c SQLE		1.04 1/96	0,1566777
GO:0043401	steroid hormone mediated signaling pathway	A series of molecular signals mediated by a steroid hormone PHB2		1.01 1/99	0,1593899
GO:0038061	NIK/NF-kappaB signaling	The process in which a signal is passed on to downstream cor PHB2		1.01 1/99	0,1593899
GO:0022612		The process in which the anatomical structures of a gland are PHB2		1.01 1/99	0,1593899
GO:0050680	negative regulation of epithelial cell proliferation	Any process that stops, prevents or reduces the rate or exten PHB2		0.99 1/101	0,1602184
GO:0022603 GO:0016125	regulation of anatomical structure morphogenesis sterol metabolic process	Any process that modulates the frequency, rate or extent of : PHB2 VAT1 The chemical reactions and pathways involving sterols, steroi SQLE	16.67 2/12 8.33 1/12	0.30 2/6/1	0,1602184 0,1602184
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent macr ACSL3 ANKRD13A CUL9 PHB2 SQLE SURF4 VA			0,1602184
GO:0010821	regulation of mitochondrion organization	Any process that modulates the frequency, rate or extent of VAT1		0.98 1/102	0,1602184
GO:0043467	regulation of generation of precursor metabolites and energy	Any process that modulates the frequency, rate or extent of PHB2		1.00 1/100	0,1602184
GO:1902806	regulation of cell cycle G1/S phase transition	Any signalling pathway that modulates the activity of a cell c PHB2		0.97 1/103	0,1602184
GO:1902652	secondary alcohol metabolic process	The chemical reactions and pathways involving secondary alc SQLE		0.99 1/101	0,1602184
GO:1904375	regulation of protein localization to cell periphery	Any process that modulates the frequency, rate or extent of ACSL3	8.33 1/12	0.96 1/104	0,1604151
GO:0045834	positive regulation of lipid metabolic process	Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12	0.96 1/104	0,1604151
GO:0010562	positive regulation of phosphorus metabolic process	Any process that increases the frequency, rate or extent of th ACSL3 PHB2	16.67 2/12		0,1653601
GO:0051783	regulation of nuclear division	Any process that modulates the frequency, rate or extent of I CUL9		0.91 1/110	0,1653601
GO:0033002	muscle cell proliferation	The expansion of a muscle cell population by cell division. NDRG4		0.91 1/110	0,1653601
GO:0045937	positive regulation of phosphate metabolic process	Any process that activates or increases the frequency, rate or ACSL3 PHB2 The biological process where creatific outcome is the progress ACSL3 CMTM8 EASN NDPG4 PHP2	16.67 2/12		0,1653601
GO:0007275	multicellular organism development	The biological process whose specific outcome is the progres ACSL3 CMTM8 FASN NDRG4 PHB2 Any process that modulates the frequency, rate or extent of I SURF4		0.13 5/3871 0.91 1/110	0,1653601
GO:1905952 GO:0007030	regulation of lipid localization			0.91 1/110 0.88 1/113	0,1653601 0,1690606
GO:0007030 GO:0000278	Golgi organization mitotic cell cycle	A process that is carried out at the cellular level which result: SURF4 Progression through the phases of the mitotic cell cycle, the I CUL9 PHB2	8.33 1/12 16.67 2/12		0,1690606
GO:0006694	steroid biosynthetic process	The chemical reactions and pathways resulting in the formati SQLE		0.86 1/116	0,1720475
GO:0002700	regulation of production of molecular mediator of immune response			0.85 1/117	0,1728058
GO:0033365	protein localization to organelle	A process in which a protein is transported to, or maintained ANKRD13A PHB2	16.67 2/12		0,1732908
GO:0055088	lipid homeostasis	Any process involved in the maintenance of an internal stead SURF4		0.83 1/120	0,1743679
GO:0048284	organelle fusion	The creation of a single organelle from two or more organelle VAT1	8.33 1/12	0.83 1/120	0,1743679
GO:0019752	carboxylic acid metabolic process	The chemical reactions and pathways involving carboxylic aci ACSL3 FASN	16.67 2/12	0.27 2/736	0,1743679
GO:1902533	positive regulation of intracellular signal transduction	Any process that activates or increases the frequency, rate or NDRG4 PHB2	16.67 2/12	0.27 2/741	0,1756061
GO:0006886	intracellular protein transport	The directed movement of proteins in a cell, including the mi AP2B1 PHB2	16.67 2/12	0.27 2/743	0,1757661
GO:0043436		The chemical reactions and pathways involving any oxoacid; ACSL3 FASN	16.67 2/12		0,1758757
GO:0043433	negative regulation of DNA-binding transcription factor activity	Any process that stops, prevents, or reduces the frequency, r PHB2		0.81 1/123	0,1758757
GO:0046890	regulation of lipid biosynthetic process	Any process that modulates the frequency, rate or extent of I ACSL3		0.81 1/124	0,1759247
GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formati FASN		0.81 1/124	0,1759247
GO:0065007	biological regulation	Any process that modulates a measurable attribute of any bir ACSL3 ANKRD13A ATP13A3 CMTM8 CUL9 NDI			
GO:0007399 GO:0030100	nervous system development regulation of endocytosis	The process whose specific outcome is the progression of nei ACSL3 CMTM8 NDRG4 Any process that modulates the frequency, rate or extent of (ANKRD13A		0.18 3/1710 0.77 1/130	0,1798833 0,1798833
GO:0002221	pattern recognition receptor signaling pathway	Any process that modulates the nequency, face of extent of rankholds. Any series of molecular signals generated as a consequence (PHB2		0.76 1/130	0,1798833
GO:0048754		The process in which the anatomical structures of branches ii PHB2		0.77 1/130	0,1798833
GO:0006082		The chemical reactions and pathways involving organic acids, ACSL3 FASN	16.67 2/12		0,1798833
GO:0006606	protein import into nucleus	The directed movement of a protein from the cytoplasm to t PHB2		0.78 1/128	0,1798833
GO:0071383	cellular response to steroid hormone stimulus	Any process that results in a change in state or activity of a cr PHB2		0.77 1/130	0,1798833
GO:0043112	receptor metabolic process	The chemical reactions and pathways involving a receptor mi ANKRD13A	8.33 1/12	0.77 1/130	0,1798833
GO:0051170	import into nucleus	The directed movement of substances into the nucleus. PHB2	8.33 1/12	0.76 1/132	0,1800977
GO:1903828	negative regulation of protein localization	Any process that stops, prevents or reduces the frequency, rc ANKRD13A		0.75 1/134	0,1820676
GO:1905475	regulation of protein localization to membrane	Any process that modulates the frequency, rate or extent of ACSL3		0.74 1/135	0,1827169
GO:0051726	regulation of cell cycle	Any process that modulates the rate or extent of progression CUL9 PHB2	16.67 2/12		0,1837433
GO:0019637	organophosphate metabolic process	The chemical reactions and pathways involving organophosp ACSL3 PHB2	16.67 2/12		0,1840459
GO:0098655	cation transmembrane transport	The process in which a cation is transported across a membra ATP13A3 PHB2	16.67 2/12		0,1840459
GO:0009755 GO:0002440	hormone-mediated signaling pathway production of molecular mediator of immune response	A series of molecular signals mediated by the detection of a I PHB2 The synthesis or release of any molecular mediator of the im PHB2		0.70 1/142 0.70 1/143	0,1891055 0,1897128
GO:0002440 GO:0044843		The cell cycle process by which a cell in G1 phase commits to PHB2		0.69 1/143	0,1903151
GO:0051649	establishment of localization in cell	Any process, occuring in a cell, that localizes a substance or c AP2B1 NDRG4 PHB2		0.17 3/1783	0,1916847
GO:0050821	protein stabilization	Any process involved in maintaining the structure and integri PHB2		0.68 1/147	0,1927645
GO:1902600	proton transmembrane transport	The directed movement of a proton across a membrane. PHB2	8.33 1/12	0.67 1/149	0,1946008
GO:0048545	response to steroid hormone	Any process that results in a change in state or activity of a cr PHB2	8.33 1/12	0.66 1/152	0,1976688
GO:0072330	monocarboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formati FASN	8.33 1/12	0.65 1/153	0,198227
GO:0061138	morphogenesis of a branching epithelium	The process in which the anatomical structures of a branchec PHB2		0.64 1/156	0,2005615
GO:0046474		The chemical reactions and pathways resulting in the formati ACSL3		0.64 1/156	0,2005615
GO:0002573		The process in which a relatively unspecialized myeloid preci FASN		0.64 1/157	0,2011014
GO:0050794 GO:0007611	regulation of cellular process	Any process that modulates the frequency, rate or extent of ACSL3 ANKRD13A CMTM8 CUL9 NDRG4 PHB2 The acquisition and processing of information and/or the sto NDRG4		0.09 9/10398 0.62 1/161	0,2028349 0,2039067
GO:0007611 GO:0002064	learning or memory epithelial cell development	The acquisition and processing of information and/or the sto NDRG4 The process whose specific outcome is the progression of an FASN		0.62 1/161 0.62 1/161	0,2039067
GO:0002084 GO:0060429		The process whose specific outcome is the progression of an FASN The process whose specific outcome is the progression of an FASN PHB2	8.55 1/12 16.67 2/12		0,2059087
GO:0002699	positive regulation of immune effector process	Any process that activates or increases the frequency, rate, o PHB2		0.59 1/169	0,2107181
GO:0001763	morphogenesis of a branching structure	The process in which the anatomical structures of branches a PHB2		0.60 1/168	0,2107181
GO:0032412	regulation of ion transmembrane transporter activity	Any process that modulates the activity of an ion transporter PHB2	8.33 1/12	0.59 1/169	0,2107181
GO:0048878	chemical homeostasis	Any biological process involved in the maintenance of an inte ATP13A3 SURF4	16.67 2/12	0.22 2/900	0,2139191
GO:1901617	organic hydroxy compound biosynthetic process	The chemical reactions and pathways resulting in the formati SQLE		0.57 1/175	0,2163975
GO:0000819	sister chromatid segregation	The cell cycle process in which sister chromatids are organize PHB2		0.56 1/178	0,2184768
GO:0022898	regulation of transmembrane transporter activity	Any process that modulates the frequency, rate or extent of 1 PHB2		0.56 1/178	0,2184768
GO:0090068	positive regulation of cell cycle process	Any process that increases the rate, frequency or extent of a PHB2		0.55 1/181	0,2205231
GO:0017038		The targeting and directed movement of proteins into a cell (PHB2		0.55 1/181	0,2205231
GO:0051222 GO:0008654	positive regulation of protein transport phospholipid biosynthetic process	Any process that activates or increases the frequency, rate or ACSL3 The chemical reactions and pathways resulting in the formati ACSL3		0.54 1/184 0.54 1/185	0,2232642 0,2236859
GO:0008034 GO:0051047	positive regulation of secretion	Any process that activates or increases the frequency, rate or ACSL3		0.53 1/185	0,2250859
GO:0032409	regulation of transporter activity	Any process that activates of increases the nequency, rate of ACSLS Any process that modulates the activity of a transporter. PHB2		0.53 1/187	0,2252481
GO:0050890	cognition	The operation of the mind by which an organism becomes av NDRG4		0.53 1/189	0,226066
GO:0045017		The chemical reactions and pathways resulting in the formati ACSL3		0.53 1/190	0,2264701
GO:0009968	negative regulation of signal transduction	Any process that stops, prevents, or reduces the frequency, r NDRG4 PHB2	16.67 2/12		0,2307464
GO:0022402		The cellular process that ensures successive accurate and cor CUL9 PHB2	16.67 2/12		0,2307464
GO:0030336	negative regulation of cell migration	Any process that stops, prevents, or reduces the frequency, r NDRG4		0.51 1/197	0,2321305
GO:1904951	positive regulation of establishment of protein localization	Any process that activates or increases the frequency, rate or ACSL3		0.50 1/199	0,2336164
GO:0098657	import into cell	The directed movement of some substance from outside of a ACSL3		0.50 1/200	0,233984
GO:0016197		The directed movement of substances mediated by an endos NDRG4		0.50 1/201	0,2343488
GO:0016236	macroautophagy	The major inducible pathway for the general turnover of cytc PHB2		0.49 1/205	0,2372573
GO:0030522	intracellular receptor signaling pathway	Any series of molecular signals initiated by a ligand binding tr PHB2		0.49 1/205	0,2372573
GO:0006812	cation transport	The directed movement of cations, atoms or small molecules ATP13A3 PHB2		0.20 2/999	0,2384555
GO:2000146	negative regulation of cell motility	Any process that stops, prevents, or reduces the frequency, r NDRG4 Reactions triggered in response to the presence of a symbion PHR2		0.48 1/207	0,2384555
GO:0140546 GO:0034220	defense response to symbiont ion transmembrane transport	Reactions triggered in response to the presence of a symbior PHB2 A process in which an ion is transported across a membrane. ATP13A3 PHB2		0.48 1/210 0.20 2/1004	0,2389703 0,2389703
GO:0051607	defense response to virus	Reactions triggered in response to the presence of a virus the PHB2		0.20 2/1004	0,2389703
GO:0051271	negative regulation of cellular component movement	Any process that stops, prevents, or reduces the frequency, r NDRG4		0.47 1/211	0,2393048
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GO:0090150					
	establishment of protein localization to membrane	The directed movement of a protein to a specific location in ACSL3	8.33 1/12		0,2396367
GO:0010648	negative regulation of cell communication	Any process that decreases the frequency, rate or extent of c NDRG4 PHB2		0.20 2/1021	0,2420058
GO:0051091 GO:0023057	positive regulation of DNA-binding transcription factor activity negative regulation of signaling	Any process that activates or increases the frequency, rate or PHB2 Any process that stops, prevents, or reduces the frequency, r NDRG4 PHB2	8.33 1/12	0.47 1/215 0.20 2/1023	0,2420058 0,2420576
GO:0032386	regulation of intracellular transport	Any process that modulates the frequency, rate or extent of I NDRG4	8.33 1/12	0.45 1/220	0,245135
GO:1901990	regulation of mitotic cell cycle phase transition	Any process that modulates the frequency, rate or extent of I PHB2	8.33 1/12	0.45 1/221	0,2454391
GO:0009416	response to light stimulus	Any process that results in a change in state or activity of a ct NDRG4	8.33 1/12	0.44 1/229	0,250745
GO:0008202 GO:1904062	steroid metabolic process regulation of cation transmembrane transport	The chemical reactions and pathways involving steroids, com SQLE	8.33 1/12	0.44 1/229 0.44 1/228	0,250745
GO:1904082 GO:0034504	protein localization to nucleus	Any process that modulates the frequency, rate or extent of I PHB2 A process in which a protein transports or maintains the loca PHB2	8.33 1/12 8.33 1/12	0.44 1/228	0,250745 0,250745
GO:0031647	regulation of protein stability	Any process that affects the structure and integrity of a prote PHB2	8.33 1/12	0.43 1/231	0,2512982
GO:0072659	protein localization to plasma membrane	A process in which a protein is transported to, or maintained ACSL3	8.33 1/12	0.43 1/231	0,2512982
GO:0040013	negative regulation of locomotion	Any process that stops, prevents, or reduces the frequency, r NDRG4	8.33 1/12	0.43 1/232	0,2515714
GO:0042113 GO:0046394	B cell activation carboxylic acid biosynthetic process	The change in morphology and behavior of a mature or imm: PHB2 The chemical reactions and pathways resulting in the formati FASN	8.33 1/12 8.33 1/12	0.43 1/235 0.42 1/239	0,2538673 0,2571514
GO:0016053	organic acid biosynthetic process	The chemical reactions and pathways resulting in the formati FASN	8.33 1/12	0.42 1/233	0,2586473
GO:0045787	positive regulation of cell cycle	Any process that activates or increases the rate or extent of r PHB2	8.33 1/12	0.41 1/242	0,2586473
GO:0019220	regulation of phosphate metabolic process	Any process that modulates the frequency, rate or extent of I ACSL3 PHB2	16.67 2/12	0.18 2/1094	0,258661
GO:0051174	regulation of phosphorus metabolic process	Any process that modulates the frequency, rate or extent of I ACSL3 PHB2		0.18 2/1094	0,258661
GO:0048193	Golgi vesicle transport	The directed movement of substances into, out of or within t ACSL3	8.33 1/12	0.40 1/247	0,2613431
GO:0098813	nuclear chromosome segregation	The process in which genetic material, in the form of nuclear PHB2	8.33 1/12 8.33 1/12	0.40 1/248 0.40 1/252	0,2615723
GO:0002697 GO:0015849	regulation of immune effector process organic acid transport	Any process that modulates the frequency, rate, or extent of PHB2 The directed movement of organic acids, any acidic compour ACSL3	8.33 1/12	0.40 1/252	0,2647397 0,2669057
GO:0050678	regulation of epithelial cell proliferation	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.39 1/256	0,2671126
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent of ACSL3 ANKRD13A CMTM8 CUL9 NDRG4 PH	B2 75.00 9/12	0.08 9/11175	0,2675604
GO:0051235	maintenance of location	Any process in which a cell, substance or cellular entity, such SQLE	8.33 1/12	0.38 1/262	0,2713765
GO:0060562	epithelial tube morphogenesis	The process in which the anatomical structures of a tube are PHB2	8.33 1/12	0.38 1/265	0,273483
GO:0006066 GO:0009615	alcohol metabolic process response to virus	The chemical reactions and pathways involving alcohols, any SQLE Any process that results in a change in state or activity of a cr PHB2	8.33 1/12 8.33 1/12	0.38 1/266 0.37 1/269	0,2736637 0,2741964
GO:0006913	nucleocytoplasmic transport	The directed movement of molecules between the nucleus a PHB2	8.33 1/12	0.37 1/269	0,2741964
GO:0051169	nuclear transport	The directed movement of substances into, out of, or within PHB2	8.33 1/12	0.37 1/269	0,2741964
GO:0009967	positive regulation of signal transduction	Any process that activates or increases the frequency, rate or NDRG4 PHB2	16.67 2/12	0.17 2/1161	0,2746106
GO:0051051	negative regulation of transport	Any process that stops, prevents, or reduces the frequency, r ANKRD13A	8.33 1/12	0.37 1/272	0,2747156
GO:0006790	sulfur compound metabolic process	The chemical reactions and pathways involving the nonmetal ACSL3	8.33 1/12	0.37 1/272	0,2747156
GO:1990778 GO:0010639	protein localization to cell periphery negative regulation of organelle organization	A process in which a protein is transported to, or maintained ACSL3 Any process that decreases the frequency, rate or extent of a VAT1	8.33 1/12 8.33 1/12	0.36 1/274 0.36 1/279	0,2758183 0,279697
GO:0016477	cell migration	The controlled self-propelled movement of a cell from one si NDRG4 PHB2		0.30 1/2/3	0,2864115
GO:0030099	myeloid cell differentiation	The process in which a relatively unspecialized myeloid prect FASN	8.33 1/12	0.34 1/290	0,2882686
GO:1901987	regulation of cell cycle phase transition	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.34 1/298	0,2947726
GO:0045860	positive regulation of protein kinase activity	Any process that activates or increases the frequency, rate or PHB2	8.33 1/12	0.33 1/299	0,2948722
GO:0009150	purine ribonucleotide metabolic process	The chemical reactions and pathways involving a purine riboi ACSL3	8.33 1/12	0.33 1/301	0,2954114
GO:0048585 GO:0002764	negative regulation of response to stimulus immune response-regulating signaling pathway	Any process that stops, prevents, or reduces the frequency, r NDRG4 PHB2 The cascade of processes by which a signal interacts with a re PHB2	8.33 1/12	0.16 2/1236 0.33 1/303	0,2954114 0,2960626
GO:0002704 GO:0007059	chromosome segregation	The process in which genetic material, in the form of chrome PHB2	8.33 1/12	0.33 1/303	0,2961552
GO:1903829	positive regulation of protein localization	Any process that activates or increases the frequency, rate or ACSL3	8.33 1/12	0.33 1/305	0,2962468
GO:0050673	epithelial cell proliferation	The multiplication or reproduction of epithelial cells, resultin PHB2	8.33 1/12	0.32 1/308	0,298114
GO:0044772	mitotic cell cycle phase transition	The cell cycle process by which a cell commits to entering the PHB2	8.33 1/12	0.32 1/311	0,2999668
GO:0009314	response to radiation	Any process that results in a change in state or activity of a cr NDRG4	8.33 1/12	0.32 1/314	0,3009983
GO:0051223 GO:1902531	regulation of protein transport regulation of intracellular signal transduction	Any process that modulates the frequency, rate or extent of I ACSL3 Any process that modulates the frequency, rate or extent of I NDRG4 PHB2	8.33 1/12	0.32 1/314 0.16 2/1270	0,3009983 0,3018567
GO:0006874	cellular calcium ion homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.32 1/317	0,3018507
GO:0009259	ribonucleotide metabolic process	The chemical reactions and pathways involving a ribonucleot ACSL3	8.33 1/12	0.31 1/318	0,3020824
GO:0006163	purine nucleotide metabolic process	The chemical reactions and pathways involving a purine nucl ACSL3	8.33 1/12	0.31 1/323	0,3048038
GO:0010647	positive regulation of cell communication	Any process that increases the frequency, rate or extent of ct NDRG4 PHB2		0.16 2/1286	0,3048038
GO:0023056	positive regulation of signaling	Any process that activates, maintains or increases the freque NDRG4 PHB2		0.15 2/1293	0,3049732
GO:0022411 GO:0034765	cellular component disassembly regulation of ion transmembrane transport	A cellular process that results in the breakdown of a cellular (PHB2 Any process that modulates the frequency, rate or extent of (PHB2	8.33 1/12 8.33 1/12	0.31 1/325 0.31 1/326	0,3049732 0,3049732
GO:0034703 GO:0019693	ribose phosphate metabolic process	The chemical reactions and pathways involving ribose phospi ACSL3	8.33 1/12	0.31 1/320	0,3050282
GO:0055074	calcium ion homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.30 1/328	0,3050824
GO:0007049	cell cycle	The progression of biochemical and morphological phases an CUL9 PHB2	16.67 2/12	0.15 2/1305	0,3069113
GO:0051090	regulation of DNA-binding transcription factor activity	Any process that modulates the frequency, rate or extent of I PHB2	8.33 1/12	0.30 1/333	0,3077154
GO:0070201	regulation of establishment of protein localization	Any process that modulates the frequency, rate or extent of I ACSL3	8.33 1/12	0.30 1/336	0,3094363
GO:0048523 GO:0140694	negative regulation of cellular process non-membrane-bounded organelle assembly	Any process that stops, prevents, or reduces the frequency, r ANKRD13A NDRG4 PHB2 VAT1 The aggregation, arrangement and bonding together of a set SQLE	33.33 4/12 8.33 1/12	0.10 4/3856 0.28 1/351	0,309986 0,314588
GO:0042592	homeostatic process	Any biological process involved in the maintenance of an inte ATP13A3 SURF4		0.15 2/1352	0.314588
		Any process involved in the controlled self-propelled movem NDRG4 PHB2			0.244500
GO:0048870	cell motility		16.67 2/12	0.15 2/1350	0,314588
GO:0048870 GO:1903131	cell motility mononuclear cell differentiation	The process in which a relatively unspecialized cell acquires t FASN	16.67 2/12 8.33 1/12	0.15 2/1350 0.29 1/349	0,314588
GO:1903131 GO:0071396	mononuclear cell differentiation cellular response to lipid	Any process that results in a change in state or activity of a cr PHB2	8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347	0,314588 0,314588
GO:1903131 GO:0071396 GO:0051674	mononuclear cell differentiation cellular response to lipid localization of cell	Any process that results in a change in state or activity of a ci PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2	8.33 1/12 8.33 1/12 16.67 2/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350	0,314588 0,314588 0,314588
GO:1903131 GO:0071396 GO:0051674 GO:0006811	mononuclear cell differentiation cellular response to lipid localization of cell ion transport	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2	8.33 1/12 8.33 1/12 16.67 2/12 16.67 2/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347	0,314588 0,314588 0,314588 0,314588
GO:1903131 GO:0071396 GO:0051674	mononuclear cell differentiation cellular response to lipid localization of cell	Any process that results in a change in state or activity of a ci PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2	8.33 1/12 8.33 1/12 16.67 2/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350	0,314588 0,314588 0,314588
GO:1903131 GO:0071396 GO:0051674 GO:0006811 GO:0072521	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small changed n ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3	8.33 1/12 8.33 1/12 16.67 2/12 16.67 2/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/346	0,314588 0,314588 0,314588 0,314588 0,314588
G0:1903131 G0:0071396 G0:0051674 G0:0006811 G0:0072521 G0:0072503 G0:0072594 G0:0072507	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small changed n APT13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead APT13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead APT13A3	8.33 1/12 8.33 1/12 16.67 2/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/346 0.29 1/347 0.28 1/357 0.27 1/364	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,3178959 0,3217928
G0:1903131 G0:0071396 G0:0051674 G0:0006811 G0:0072521 G0:0072594 G0:0072594 G0:0072507 G0:0033674	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process that activates or increases the frequency, rate on PHB2	8.33 1/12 8.33 1/12 16.67 2/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/346 0.29 1/347 0.28 1/357 0.27 1/364 0.27 1/364	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,3178959 0,3217928 0,3217928
G0:1903131 G0:0071396 G0:0051674 G0:0076811 G0:0072521 G0:0072593 G0:0072594 G0:0072507 G0:0033674 G0:0048513	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development	Any process that results in a change in state or activity of a c PHB2 Any process that results in a change in state or activity of a c PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process involved in the maintenance of an internal stead ATP13A3 Any process involved in the maintenance of an internal stead ATP13A3 Development of a tissue or tissues that work together to peri FASN NDRG4 PHB2	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/347 0.29 1/347 0.29 1/347 0.28 1/357 0.27 1/364 0.27 1/364 0.11 3/2612	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,3178959 0,3217928 0,3217928
G0:1903131 G0:0071396 G0:0051674 G0:0006811 G0:0072521 G0:0072594 G0:0072594 G0:0072507 G0:0033674	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process that activates or increases the frequency, rate on PHB2	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/346 0.29 1/347 0.28 1/357 0.27 1/364 0.27 1/364	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,3178959 0,3217928 0,3217928
G0:1903131 G0:0071396 G0:0051674 G0:0006811 G0:0072521 G0:0072503 G0:0072507 G0:003674 G0:0048513 G0:0055085	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmembrane transport	Any process that results in a change in state or activity of a c PHB2 Any process that results in a change in state or activity of a c PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process involved in the maintenance of an internal stead ATP13A3 Development of a tissue or tissues that work together to peri FASN NDRG4 PHB2 The process in which a solute is transported across a lipid bil; ATP13A3 PHB2 A cellular process involving delivery of a portion of the cytop PHB2 Any process that tesults in a change in state or activity of a c PHB2	8.33 1/12 8.33 1/12 16.67 2/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.19 1/347 0.15 2/1350 0.15 2/1347 0.29 1/347 0.29 1/347 0.28 1/357 0.27 1/364 0.27 1/364 0.11 3/2612 0.14 2/1405 0.26 1/382	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,3178959 0,3217928 0,3217928 0,3217928 0,3217928
G0:1903131 G0:0071396 G0:0051674 G0:00051674 G0:0072521 G0:0072507 G0:0072507 G0:003674 G0:0048513 G0:0055085 G0:0061919 G0:0071407 G0:0006914	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmembrane transport process utilizing autophagic mechanism cellular response to organic cyclic compound autophagy	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process that activates or increases the frequency, rate on PHB2 Development of a tissue or tissues that work together to pert FASN NDRG4 PHB2 The process involved is transported across a lipid bil: ATP13A3 PHB2 A cellular process involving delivery of a portion of the cytop PHB2 Any process that results in a change in state or activity of a cr PHB2 The cellular catabolic process in which cells digest parts of th PHB2	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.15 2/1350 0.15 2/1347 0.29 1/346 0.29 1/347 0.28 1/357 0.27 1/364 0.11 3/2612 0.14 2/1405 0.26 1/382	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,317928 0,3217928 0,3217928 0,3217928 0,32297505 0,3328304 0,3328304 0,3328304
G0:1903131 G0:0071396 G0:0051674 G0:0072501 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0035085 G0:0055085 G0:0061919 G0:0071407 G0:00061919 G0:00071407	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmebrane transport process utilizing autophagic mechanism cellular response to organic cyclic compound autophagy generation of precursor metabolites and energy	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small changed n AP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process that activates or increases the frequency, rate on PHB2 Development of a tissue or tissues that work together to perl FASN NDRG4 PHB2 The process in which a solute is transported across a lipid bil ATP13A3 PHB2 A cellular process that tesults in a change in state or activity of a cr PHB2 Any process that results in a change in state or activity of a cr PHB2 The cellular catabolic process in which cells digest parts of th PHB2 The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/347 0.29 1/347 0.27 1/364 0.27 1/364 0.14 2/1405 0.14 2/1405 0.26 1/382 0.26 1/386	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,317928 0,3217928 0,3217928 0,3217928 0,3227905 0,328304 0,3328304 0,3328304 0,3328304
G0:1903131 G0:0071396 G0:0051674 G0:00068111 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0038674 G0:0048513 G0:0048513 G0:0055085 G0:0061919 G0:00071407 G0:0006914 G0:0006914 G0:00060914	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmembrane transport process utilizing autophagic mechanism cellular response to organic cyclic compound autophagy generation of transmembrane transport	Any process that results in a change in state or activity of a c PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process involved in the maintenance of an internal stead ATP13A3 Development of a tissue or tissues that work together to perl FASN NDRG4 PHB2 The process in which a solute is transported across a lipid bil ATP13A3 PHB2 A cellular process in which cells digest parts of the PHB2 The collular catabolic process in which cells digest parts of the PHB2 The chemical reactions and pathways resulting in the formati PHB2 Any process that results in a change in state or activity of a c PHB2 The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 25.00 3/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/347 0.29 1/347 0.29 1/347 0.27 1/364 0.27 1/364 0.27 1/364 0.11 3/2612 0.42 1/362 0.26 1/382 0.26 1/382 0.26 1/386 0.26 1/386	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,3178959 0,3217928 0,3217928 0,3217928 0,32297505 0,3328304 0,3328304 0,3328304 0,3328316
G0:1903131 G0:0071396 G0:0051674 G0:0072501 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0035085 G0:0055085 G0:0061919 G0:0071407 G0:00061919 G0:00071407	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmebrane transport process utilizing autophagic mechanism cellular response to organic cyclic compound autophagy generation of precursor metabolites and energy	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small changed n AP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process that activates or increases the frequency, rate on PHB2 Development of a tissue or tissues that work together to perl FASN NDRG4 PHB2 The process in which a solute is transported across a lipid bil ATP13A3 PHB2 A cellular process that tesults in a change in state or activity of a cr PHB2 Any process that results in a change in state or activity of a cr PHB2 The cellular catabolic process in which cells digest parts of th PHB2 The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 25.00 3/12 16.67 2/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/347 0.29 1/347 0.27 1/364 0.27 1/364 0.14 2/1405 0.14 2/1405 0.26 1/382 0.26 1/386	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,317928 0,3217928 0,3217928 0,3217928 0,3227905 0,328304 0,3328304 0,3328304 0,3328304
G0:1903131 G0:0071396 G0:0051674 G0:0072521 G0:0072521 G0:0072507 G0:003674 G0:0048513 G0:0055085 G0:0061919 G0:0071407 G0:00061914 G0:00060914 G0:0007200 G0:0007200 G0:0000 G0:00000 G0:00000 G0:0000 G0:00000 G0:00000 G0:00000000	mononuclear cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmembrane transport process utilizing autophagic mechanism cellular response to organic cyclic compound autophagy generation of precursor metabolites and energy regulation of transmembrane transport tissue development	Any process that results in a change in state or activity of a cr PHB2 Any process in which a cell is transported to, and/or maintair NDRG4 PHB2 The directed movement of charged atoms or small charged r ATP13A3 PHB2 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PHB2 Any process involved in the maintenance of an internal stead ATP13A3 Any process that activates or increases the frequency, rate on PHB2 Development of a tissue or tissues that work together to pert FASN NDRG4 PHB2 The process involving delivery of a portion of the cytop PHB2 Any process that results in a change in state or activity of a cr PHB2 The cellular catabolic process in which cells digest parts of th PHB2 The chemical reactions and pathways resulting in the formati PHB2 Any process that moulates the frequency, rate or extent of 1PHB2 The chemical reactions and pathways resulting in the formati PHB2 Any process that moulates the frequency, rate or extent of 1PHB2 The process that moulates the frequency, rate or activity of a cr PHB2 The process that moulates the frequency rate or extent of 1PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 The process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 The process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate or activity of a cr PHB2 Any process that moulates the frequency rate	8.33 1/12 8.33 1/12 16.67 2/12 16.67 2/12 8.33 1/12 8.33 1/12	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1350 0.29 1/347 0.29 1/346 0.29 1/347 0.28 1/357 0.27 1/364 0.27 1/364 0.11 3/2612 0.14 2/1405 0.26 1/382 0.26 1/382 0.26 1/386 0.14 2/1431	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,317928 0,3217928 0,3217928 0,3227505 0,32297505 0,3328304 0,3328304 0,3328304 0,3335216 0,334179
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ATP13A3 PHB2 A cellular catabolic process in which cells digest parts of th PHB2 The celludar catabolic process in which cells digest parts of th PHB2 The chemical reactions and pathways resulting in the formati PHB2 Any process that modulates the frequency, rate or extent of 1 PHB2 The cell cycle process by which a cell commits to entering the PHB2 The cell cycle process by which a cell commits to entering the PHB2 The chemical reactions and pathways involving organic hydrc SQLE Any process that modulates the frequency, rate or extent of a SURF4 The chemical reactions and pathways involving a nucleotide, ACSL3 Any process that negative the frequency, rate or extent of 1 ACSL3 Any process that negative the frequency, rate or extent of 1 ACSL3 Any process that activates the frequency, rate or ethB2 The chemical reactions and pathways involving an phosphol ACSL3 Any process that activates or increases the frequency, rate or PHB2 A process that activates or increases the frequency, rate or PHB2 A process that activates or increases the frequency, rate or PHB2 The chemical reactions and pathways resulting in the formati FASN The process in	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.29 1/347 0.29 1/347 0.29 1/347 0.29 1/347 0.28 1/357 0.21 1/364 0.27 1/364 0.27 1/364 0.21 1/361 0.21 1/361 0.26 1/382 0.26 1/382 0.26 1/382 0.26 1/382 0.26 1/383 0.26 1/382 0.26 1/383 0.26 1/386 0.26 1/386 0.26 1/386 0.26 1/386 0.26 1/386 0.26 1/386 0.26 1/386 0.26 1/386 0.26 1/386 0.25 1/398 0.25 1/398 0.25 1/404 0.25 1/404 0.25 1/404 0.25 1/404 0.25 1/404 0.25 1/404 0.24 1/420 0.26 1/420 0.23 1/437 0.23 1/437 0.23 1/437 0.23 1/434 0.22 1/464 0.22 1/463 0.21 1/477	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,317959 0,3217928 0,3217928 0,3217928 0,3227928 0,3227928 0,3328304 0,3328304 0,3328304 0,3332316 0,3332316 0,3335216 0,3335216 0,33394535 0,3394535 0,339845 0,3398845 0,342209 0,342209 0,342250 0,342250 0,342250 0,34266 0,342209 0,34226 0,342209 0,342250 0,34266 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,34226 0,34226 0,342209 0,34226 0,34226 0,342209 0,34226 0,34226 0,34226 0,34226 0,34226 0,342209 0,34226 0,342209 0,34226 0,342209 0,342220 0,34226 0,342209 0,34226 0,3
G0:1903131 G0:0071396 G0:0051674 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0072503 G0:0051919 G0:0061919 G0:0061919 G0:0061919 G0:0061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:00061919 G0:0000710 G0:00051040 G0:00051046 G0:00051347 G0:00051347 G0:00051347 G0:00051347 G0:00051347 G0:00051640 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000521 G0:000522 G0:0003893 G0:000252 G0:0007257	mononuclar cell differentiation cellular response to lipid localization of cell ion transport purine-containing compound metabolic process cellular divalent inorganic cation homeostasis establishment of protein localization to organelle divalent inorganic cation homeostasis positive regulation of kinase activity animal organ development transmembrane transport process utilizing autophagic mechanism cellular response to organic cyclic compound autophagy generation of precursor metabolites and energy regulation of transmembrane transport tissue development cell cycle phase transition organic hydroxy compound metabolic process positive regulation of organelle organization morphogenesis of an epithelium nucleotide metabolic process positive regulation of nydrolase activity behavior positive regulation of hydrolase activity small molecule biosynthetic process positive regulation of hydrolase activity small molecule biosynthetic process organelle localization regulation of ion transport immune effector process reganese to lipid brain development epithelial cell differentiation protein localization to membrane	Any process that results in a change in state or activity of a c PH82 Any process in which a cell is transported to, and/or maintair NDRG4 PH82 The directed movement of charged atoms or small charged r ATP13A3 PH82 The chemical reactions and pathways involving a purine-cont ACSL3 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PH82 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PH82 Any process involved in the maintenance of an internal stead ATP13A3 The directed movement of a protein to a specific location on PH82 Any process involved in the maintenance of an internal stead ATP13A3 Any process involved in the maintenance of an internal stead ATP13A3 Any process in which a solute is transported across a lipid bil. ATP13A3 PH82 A cellular process involving delivery of a portion of the cytop PH82 Any process that results in a change in state or activity of a c PH82 Any process that results in a change in state or activity of a c PH82 The chemical reactions and pathways resulting in the formati PH82 The chemical reactions and pathways resulting in the formati PH82 The cellular catabolic process in which cells digest parts of th PH82 The cleude rocess by which a cell commits to entering the PH82 The chemical reactions and pathways roubving organic hydrs SQLE Any process that increases the frequency, rate or extent of a SURF4 The process whose specific outcome is the progression of the NDRG4 Any process that increases the frequency, rate or extent of ACSL3 Any process that results in a change in state or activity of a c PH82 A process that results in a change in state or activity of a c PH82 A process that toward responses (actions or inactions) of NDRG4 Any process that activates or increases the frequency, rate or PH82 The chemical reactions and pathways resulting in the formati FASN Any process that activates or increases the frequency, rate or PH82 T	8.33 1/12 8.33 1/12 16.67 2/12 8.33 1/12 8.33	0.15 2/1350 0.29 1/349 0.29 1/347 0.15 2/1350 0.15 2/1347 0.29 1/347 0.29 1/347 0.29 1/347 0.21 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.27 1/364 0.26 1/382 0.26 1/382 0.25 1/388 0.25 1/398 0.25 1/398 0.25 1/404 0.25 1/404 0.24 1/421 0.24 1/421 0.24 1/421 0.24 1/421 0.24 1/421 0.24 1/421 0.24 1/43 0.23 1/433 0.23 1/443 0.23 1/443 0.23 1/443 0.23 1/443 0.22 1/464 0.22 1/464 0.22 1/464 0.21 1/473	0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,314588 0,317928 0,3217928 0,3217928 0,3227928 0,3227928 0,3292 0,3328304 0,3328304 0,3328304 0,3332316 0,3334535 0,3398455 0,3398845 0,339845 0,339845 0,349226 0,349226 0,349226 0,349226 0,349226 0,359387 0,359

GO:0048729	tissue morphogenesis	The process in which the anatomical structures of a tissue an PHB2	8.33 1/12		0,3816918
GO:0065008 GO:0009725	regulation of biological quality	Any process that modulates a qualitative or quantitative trait ATP13A3 PHB2 SURF4	25.00 3/12 8.33 1/12	0.10 3/2959 0.20 1/488	0,3816918 0.3821825
GO:0009725 GO:0055065	response to hormone metal ion homeostasis	Any process that results in a change in state or activity of a cr PHB2 Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12 8.33 1/12	0.20 1/488	0.3821825
GO:0030003	cellular cation homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.20 1/491	0,383239
GO:0045859	regulation of protein kinase activity	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.20 1/496	0,383239
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	A series of molecular signals initiated by the binding of an ex NDRG4	8.33 1/12	0.20 1/496	0,383239
GO:0014070 GO:0006873	response to organic cyclic compound cellular ion homeostasis	Any process that results in a change in state or activity of a cr PHB2 Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12 8.33 1/12	0.20 1/495 0.20 1/504	0,383239 0,385975
GO:0006935	chemotaxis	The directed movement of a motile cell or organism, or the c CMTM8	8.33 1/12	0.20 1/504	0,385975
GO:0060322	head development	The biological process whose specific outcome is the progres NDRG4	8.33 1/12	0.20 1/503	0,385975
GO:0042330	taxis	The directed movement of a motile cell or organism in respo CMTM8	8.33 1/12	0.20 1/506	0,3864328
GO:0048522 GO:0006928	positive regulation of cellular process	Any process that activates or increases the frequency, rate or ACSL3 NDRG4 PHB2 SURF4		0.09 4/4480	0,393603
GO:0006928 GO:0048519	movement of cell or subcellular component negative regulation of biological process	The directed, self-propelled movement of a cell or subcellula NDRG4 PHB2 Any process that stops, prevents, or reduces the frequency, r ANKRD13A NDRG4 PHB2 VAT1	16.67 2/12 33 33 4/12	0.12 2/1707 0.09 4/4543	0,3958285 0,405219
GO:0055080	cation homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.18 1/556	0,4153099
GO:0045087	innate immune response	Innate immune responses are defense responses mediated b PHB2	8.33 1/12	0.18 1/558	0,4156599
GO:0098771	inorganic ion homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.18 1/565	0,4191672
GO:0000226	microtubule cytoskeleton organization positive regulation of transport	A process that is carried out at the cellular level which result: CUL9	8.33 1/12 8.33 1/12	0.18 1/569 0.17 1/576	0,4207582
GO:0051050 GO:0044248	cellular catabolic process	Any process that activates or increases the frequency, rate or ACSL3 The chemical reactions and pathways resulting in the breakd CUL9 PHB2		0.17 1/578	0,4242116 0,4250981
GO:0050793	regulation of developmental process	Any process that modulates the frequency, rate or extent of PHB2 VAT1		0.11 2/1822	0,4258722
GO:0001934	positive regulation of protein phosphorylation	Any process that activates or increases the frequency, rate or PHB2	8.33 1/12	0.17 1/583	0,4258722
GO:0006511	ubiquitin-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakd CUL9	8.33 1/12	0.17 1/589	0,4266619
GO:0055082 GO:0043549	cellular chemical homeostasis regulation of kinase activity	Any biological process involved in the maintenance of an inte ATP13A3 Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12 8.33 1/12	0.17 1/586 0.17 1/588	0,4266619 0,4266619
GO:0071310	cellular response to organic substance	Any process that modulates the requery, face of extent of FHB2 Any process that results in a change in state or activity of a cr FASN PHB2		0.11 2/1848	0,430665
GO:0050801	ion homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.17 1/602	0,4323745
GO:0019941	modification-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakd CUL9	8.33 1/12	0.17 1/603	0,4323745
GO:0046649 GO:0043632	lymphocyte activation modification-dependent macromolecule catabolic process	A change in morphology and behavior of a lymphocyte result PHB2 The chemical reactions and pathways resulting in the breakdi CUL9	8.33 1/12	0.17 1/605	0,4326457 0,4353083
GO:0043632 GO:0050776	regulation of immune response	Any process that modulates the frequency, rate or extent of 1 PHB2	8.33 1/12 8.33 1/12	0.16 1/611 0.16 1/616	0,4353085
GO:0043066	negative regulation of apoptotic process	Any process that stops, prevents, or reduces the frequency, r PHB2	8.33 1/12	0.15 1/646	0,4511908
GO:0035239	tube morphogenesis	The process in which the anatomical structures of a tube are PHB2	8.33 1/12	0.15 1/646	0,4511908
GO:0032501	multicellular organismal process	Any biological process, occurring at the level of a multicellula ACSL3 CMTM8 FASN NDRG4 PHB2		0.08 5/6399	0,4511908
GO:0007417	central nervous system development	The process whose specific outcome is the progression of the NDRG4 Any process that activates or increases the frequency, rate or PHB2	8.33 1/12	0.15 1/649	0,4511908
GO:0042327 GO:0051093	positive regulation of phosphorylation negative regulation of developmental process	Any process that activates of increases the requercy, rate of Phb2 Any process that stops, prevents or reduces the rate or exten VAT1	8.33 1/12 8.33 1/12	0.15 1/647 0.15 1/651	0,4511908 0,4511908
GO:0046903	secretion	The controlled release of a substance by a cell or a tissue. ACSL3	8.33 1/12	0.16 1/645	0,4511908
GO:0071345	cellular response to cytokine stimulus	Any process that results in a change in state or activity of a cr FASN	8.33 1/12	0.15 1/660	0,4544275
GO:0019725	cellular homeostasis	Any process involved in the maintenance of an internal stead ATP13A3	8.33 1/12	0.15 1/660	0,4544275
GO:0043069 GO:0003006	negative regulation of programmed cell death developmental process involved in reproduction	Any process that stops, prevents, or reduces the frequency, r PHB2 A developmental process in which a progressive change in th PHB2	8.33 1/12 8.33 1/12	0.15 1/663 0.15 1/666	0,4551756 0,4559176
GO:0030097	hemopoiesis	The process whose specific outcome is the progression of the FASN	8.33 1/12	0.15 1/600	0,4572163
GO:0098662	inorganic cation transmembrane transport	A process in which an inorganic cation is transported from or PHB2	8.33 1/12	0.15 1/673	0,4579443
GO:0002684	positive regulation of immune system process	Any process that activates or increases the frequency, rate, o PHB2	8.33 1/12	0.15 1/677	0,4582698
GO:0051338	regulation of transferase activity	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.15 1/676	0,4582698
GO:0009605 GO:0048518	response to external stimulus positive regulation of biological process	Any process that results in a change in state or activity of a cr CMTM8 PHB2 Any process that activates or increases the frequency, rate or ACSL3 NDRG4 PHB2 SURF4		0.10 2/2004 0.08 4/4958	0,4603966 0,4603966
GO:0051241	negative regulation of multicellular organismal process	Any process that activates of increases the requerty, rate of Actes Norder Fibe Softer Any process that stops, prevents, or reduces the frequency, r PHB2	8.33 1/12	0.15 1/686	0,4603966
GO:0030334	regulation of cell migration	Any process that modulates the frequency, rate or extent of INDRG4	8.33 1/12	0.14 1/697	0,4641036
GO:0051603	proteolysis involved in cellular protein catabolic process	The hydrolysis of a peptide bond or bonds within a protein a: CUL9	8.33 1/12	0.14 1/696	0,4641036
GO:0009628	response to abiotic stimulus	Any process that results in a change in state or activity of a cr NDRG4	8.33 1/12	0.14 1/698	0,4641036
GO:0031324 GO:0016567	negative regulation of cellular metabolic process protein ubiquitination	Any process that stops, prevents, or reduces the frequency, r ANKRD13A PHB2 The process in which one or more ubiquitin groups are addec CUL9	16.67 2/12 8.33 1/12	0.10 2/2035 0.14 1/702	0,4643665 0,4643678
GO:0048534	hematopoietic or lymphoid organ development	The process whose specific outcome is the progression of any FASN	8.33 1/12	0.14 1/705	0,4645733
GO:0002376	immune system process	Any process involved in the development or functioning of the FASN PHB2	16.67 2/12	0.10 2/2045	0,4645733
GO:0045321	leukocyte activation	A change in morphology and behavior of a leukocyte resultin PHB2	8.33 1/12	0.14 1/713	0,4664732
GO:0034097 GO:0060548	response to cytokine negative regulation of cell death	Any process that results in a change in state or activity of a cr FASN Any process that decreases the rate or frequency of cell deat PHB2	8.33 1/12 8.33 1/12	0.14 1/713 0.14 1/719	0,4664732 0,4687105
GO:0000348 GO:0044257	cellular protein catabolic process	The chemical reactions and pathways resulting in the breakd ₂ CUL9	8.33 1/12	0.14 1/732	0,4087103
GO:0035556	intracellular signal transduction	The process in which a signal is passed on to downstream cor NDRG4 PHB2		0.10 2/2097	0,4747833
GO:0098660	inorganic ion transmembrane transport	The process in which an inorganic ion is transported across a PHB2	8.33 1/12	0.14 1/736	0,4747833
GO:0009056	catabolic process	The chemical reactions and pathways resulting in the breakd CUL9 PHB2		0.09 2/2106	0,4750372
GO:2000145 GO:0009653	regulation of cell motility anatomical structure morphogenesis	Any process that modulates the frequency, rate or extent of INDRG4 The process in which anatomical structures are generated an PHB2 VAT1	8.33 1/12 16.67 2/12	0.13 1/742 0.09 2/2107	0,4750372 0,4750372
GO:0002520	immune system development	The process whose specific outcome is the progression of an FASN	8.33 1/12	0.13 1/758	0,4813342
GO:0032446	protein modification by small protein conjugation	A protein modification process in which one or more groups CUL9	8.33 1/12	0.13 1/758	0,4813342
GO:0051130	positive regulation of cellular component organization	Any process that activates or increases the frequency, rate or SURF4	8.33 1/12	0.13 1/763	0,4829162
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the formati ACSL3 FASN PHB2 SQLE		0.08 4/5165 0.13 1/774	0,4833261
GO:0031401 GO:0040012	positive regulation of protein modification process regulation of locomotion	Any process that activates or increases the frequency, rate or PHB2 Any process that modulates the frequency, rate or extent of NDRG4	8.33 1/12 8.33 1/12	0.13 1/773	0,4855804 0,4855804
GO:0007167	enzyme linked receptor protein signaling pathway	Any process that modulates the neglectly, rate of extent of monor Any series of molecular signals initiated by the binding of an NDRG4	8.33 1/12	0.13 1/778	0,4855804
GO:0070925	organelle assembly	The aggregation, arrangement and bonding together of a set SQLE	8.33 1/12	0.13 1/786	0,4896355
GO:0051270	regulation of cellular component movement	Any process that modulates the frequency, rate or extent of INDRG4	8.33 1/12	0.13 1/788	0,4896622
GO:0009058 GO:0001775	biosynthetic process cell activation	The chemical reactions and pathways resulting in the formati ACSL3 FASN PHB2 SQLE A change in the morphology or behavior of a cell resulting frc PHB2	33.33 4/12 8.33 1/12	0.08 4/5231 0.13 1/793	0,4902026 0,4902026
GO:0001775 GO:0072359	circulatory system development	The process whose specific outcome is the progression of the NDRG4	8.33 1/12	0.12 1/804	0,4902028
GO:0035295	tube development	The process whose specific outcome is the progression of a t PHB2	8.33 1/12	0.12 1/804	0,493651
GO:0007017	microtubule-based process	Any cellular process that depends upon or alters the microtul CUL9	8.33 1/12	0.12 1/809	0,4941496
GO:0010033	response to organic substance	Any process that results in a change in state or activity of a cr FASN PHB2		0.09 2/2222	0,4941496
GO:0098542 GO:0051336	defense response to other organism regulation of hydrolase activity	Reactions triggered in response to the presence of another o PHB2 Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12 8.33 1/12	0.12 1/812 0.12 1/819	0,4946353 0,4951148
GO:0009887	animal organ morphogenesis	Morphogenesis of an animal organ. An organ is defined as a 1 PHB2	8.33 1/12	0.12 1/817	0,4951148
GO:0044092	negative regulation of molecular function	Any process that stops or reduces the rate or extent of a mol PHB2	8.33 1/12	0.12 1/816	0,4951148
GO:0007166	cell surface receptor signaling pathway	A series of molecular signals initiated by activation of a recer, NDRG4 PHB2		0.09 2/2259	0,499612
GO:0043085	positive regulation of catalytic activity	Any process that activates or increases the activity of an enzy PHB2	8.33 1/12	0.12 1/845	0,5044835
GO:0009966 GO:0030163	regulation of signal transduction protein catabolic process	Any process that modulates the frequency, rate or extent of : NDRG4 PHB2 The chemical reactions and pathways resulting in the breakd CUL9	8.33 1/12	0.09 2/2282 0.12 1/855	0,5044835 0,5081131
GO:0010628	positive regulation of gene expression	Any process that increases the frequency, rate or extent of gr PHB2	8.33 1/12	0.12 1/857	0,5081131
GO:0001932	regulation of protein phosphorylation	Any process that modulates the frequency, rate or extent of i PHB2	8.33 1/12	0.12 1/867	0,5117368
GO:1901135	carbohydrate derivative metabolic process	The chemical reactions and pathways involving carbohydrate ACSL3	8.33 1/12	0.11 1/870	0,5121337
GO:0070647	protein modification by small protein conjugation or removal	A protein modification process in which one or more groups CUL9	8.33 1/12	0.11 1/877	0,5143428
GO:0051276 GO:0009987	chromosome organization cellular process	A process that is carried out at the cellular level that results i PHB2 Any process that is carried out at the cellular level, but not ni ACSL3 ANKRD13A AP2B1 ATP13A3 CMTM8 CI	8.33 1/12 . 100.00 12/1	0.11 1/881 2 0.06 12/1870	0,5151772 0,5186106
GO:0070887	cellular response to chemical stimulus	Any process that results in a change in state or activity of a cr FASN PHB2		0.08 2/2376	0,52229
GO:0006796	phosphate-containing compound metabolic process	The chemical reactions and pathways involving the phosphat ACSL3 PHB2	16.67 2/12	0.08 2/2404	0,5288993
GO:0006793	phosphorus metabolic process	The chemical reactions and pathways involving the nonmetal ACSL3 PHB2		0.08 2/2425	0,5335686
GO:0051173 GO:0042221	positive regulation of nitrogen compound metabolic process response to chemical	Any process that activates or increases the frequency, rate or ACSL3 PHB2 Any process that results in a change in state or activity of a cr CMTM8 FASN PHB2		0.08 2/2473 0.07 3/4056	0,5454193 0,5482549
GO:0042221 GO:0071495	cellular response to endogenous stimulus	Any process that results in a change in state or activity of a crowing rASN PHB2	8.33 1/12	0.10 1/988	0,5526274
GO:0042325	regulation of phosphorylation	Any process that modulates the frequency, rate or extent of i PHB2	8.33 1/12	0.10 1/986	0,5526274
GO:0044265	cellular macromolecule catabolic process	The chemical reactions and pathways resulting in the breakd CUL9	8.33 1/12	0.10 1/985	0,5526274
GO:0010646	regulation of cell communication	Any process that modulates the frequency, rate or extent of INDRG4 PHB2		0.08 2/2562	0,5613355
GO:0000003 GO:0010605	reproduction negative regulation of macromolecule metabolic process	The production of new individuals that contain some portion PHB2 Any process that decreases the frequency, rate or extent of t ANKRD13A PHB2	8.33 1/12	0.10 1/1024 0.08 2/2563	0,5613355 0,5613355
GO:0010605 GO:0023051	regulation of signaling	Any process that decreases the frequency, rate or extent of t ANKRUI3A PHB2 Any process that modulates the frequency, rate or extent of i NDRG4 PHB2		0.08 2/2563	0,5613355
GO:0020001			8.33 1/12	0.10 1/1022	0,5613355
	neuron differentiation	The process in which a relatively unspecialized cell acquires s ACSL3	0.00 -/	0.10 1/1022	
GO:0022414	neuron differentiation reproductive process	A biological process that directly contributes to the process c PHB2	8.33 1/12	0.10 1/1021	0,5613355

GO:0045892	negative regulation of transcription, DNA-templated	Any process that stops, prevents, or reduces the frequency, r PHB2	8.33 1/12	0.10 1/1044	0,5655129
GO:0042981	regulation of apoptotic process	Any process that modulates the occurrence or rate of cell de PHB2	8.33 1/12	0.10 1/1039	0,5655129
GO:1902679	negative regulation of RNA biosynthetic process negative regulation of nucleic acid-templated transcription	Any process that stops, prevents or reduces the frequency, rc PHB2 Any process that stops, prevents or reduces the frequency, rc PHB2	8.33 1/12	0.10 1/1045	0,5655129 0,5655129
GO:1903507 GO:0031325	positive regulation of cellular metabolic process	Any process that stops, prevents or reduces the frequency, rate or ACSL3 PHB2 Any process that activates or increases the frequency, rate or ACSL3 PHB2	8.33 1/12	0.10 1/1045 0.08 2/2631	0,5655129
GO:0043067	regulation of programmed cell death	Any process that modulates the frequency, rate or extent of LPHB2	8.33 1/12	0.09 1/1065	0,5704055
GO:0043207	response to external biotic stimulus	Any process that results in a change in state or activity of a cr PHB2	8.33 1/12	0.09 1/1068	0,5704059
GO:0051707	response to other organism	Any process that results in a change in state or activity of a cr PHB2	8.33 1/12	0.09 1/1066	0,5704059
GO:0009719	response to endogenous stimulus	Any process that results in a change in state or activity of a ci PHB2	8.33 1/12	0.09 1/1076	0,5707868
GO:0002682 GO:0032270	regulation of immune system process positive regulation of cellular protein metabolic process	Any process that modulates the frequency, rate, or extent of PHB2 Any process that activates or increases the frequency, rate or PHB2	8.33 1/12 8.33 1/12	0.09 1/1077 0.09 1/1072	0,5707868 0,5707868
GO:0009607	response to biotic stimulus	Any process that results in a change in state or activity of a ci PHB2	8.33 1/12	0.09 1/1098	0,5777702
GO:0043603	cellular amide metabolic process	The chemical reactions and pathways involving an amide, an ACSL3	8.33 1/12	0.09 1/1112	0,580964
GO:0009892	negative regulation of metabolic process	Any process that stops, prevents, or reduces the frequency, r ANKRD13A PHB2	16.67 2/12	0.07 2/2707	0,580964
GO:0051253	negative regulation of RNA metabolic process	Any process that stops, prevents, or reduces the frequency, r PHB2	8.33 1/12	0.09 1/1131 0.09 1/1129	0,5859421
GO:1901565 GO:0009057	organonitrogen compound catabolic process macromolecule catabolic process	The chemical reactions and pathways resulting in the breakd CUL9 The chemical reactions and pathways resulting in the breakd CUL9	8.33 1/12 8.33 1/12	0.09 1/1129	0,5859421 0,5872562
GO:0010941	regulation of cell death	Any process that modulates the rate or frequency of cell dear PHB2	8.33 1/12	0.09 1/1142	0,5872562
GO:0051247	positive regulation of protein metabolic process	Any process that activates or increases the frequency, rate or PHB2	8.33 1/12	0.09 1/1145	0,5872562
GO:0048699	generation of neurons	The process in which nerve cells are generated. This includes ACSL3	8.33 1/12	0.09 1/1146	0,5872562
GO:0044093	positive regulation of molecular function	Any process that activates or increases the rate or extent of a PHB2	8.33 1/12	0.09 1/1149	0,5873028
GO:0044419 GO:0006952	biological process involved in interspecies interaction between organ defense response	Reactions, triggered in response to the presence of a foreign PHB2	8.33 1/12 8.33 1/12	0.09 1/1167 0.09 1/1172	0,592739 0,5934754
GO:0031399	regulation of protein modification process	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.08 1/1192	0,5994992
GO:0010558	negative regulation of macromolecule biosynthetic process	Any process that decreases the rate, frequency or extent of t PHB2	8.33 1/12	0.08 1/1221	0,6081521
GO:0045934	negative regulation of nucleobase-containing compound metabolic p		8.33 1/12	0.08 1/1223	0,6081521
GO:0022008	neurogenesis	Generation of cells within the nervous system. ACSL3	8.33 1/12 8.33 1/12	0.08 1/1245 0.08 1/1245	0,6135148
GO:0007010 GO:0031327	cytoskeleton organization negative regulation of cellular biosynthetic process	A process that is carried out at the cellular level which result: CUL9 Any process that stops, prevents, or reduces the frequency, r PHB2	8.33 1/12	0.08 1/1245	0,6135148 0,6171524
GO:0009890	negative regulation of biosynthetic process	Any process that stops, prevents, or reduces the rate of the c PHB2	8.33 1/12	0.08 1/1277	0,6220644
GO:0006955	immune response	Any immune system process that functions in the calibrated PHB2	8.33 1/12	0.08 1/1288	0,6246035
GO:0048583	regulation of response to stimulus	Any process that modulates the frequency, rate or extent of NDRG4 PHB2		0.07 2/2982	0,625435
GO:0006915 GO:0009893	apoptotic process	A programmed cell death process which begins when a cell n PHB2	8.33 1/12	0.08 1/1299 0.07 2/3040	0,6260218 0,6360302
GO:0009895 GO:0012501	positive regulation of metabolic process programmed cell death	Any process that activates or increases the frequency, rate or ACSL3 PHB2 A process which begins when a cell receives an internal or ex PHB2	8.33 1/12	0.07 2/3040	0.6368246
GO:0006468	protein phosphorylation	The process of introducing a phosphate group on to a proteir PHB2	8.33 1/12	0.07 1/1340	0,6368246
GO:0030154	cell differentiation	The process in which relatively unspecialized cells, e.g. embry ACSL3 FASN	16.67 2/12	0.06 2/3098	0,6452496
GO:0048869	cellular developmental process	A biological process whose specific outcome is the progressic ACSL3 FASN		0.06 2/3162	0,6576973
GO:0008219 GO:0006464	cell death cellular protein modification process	Any biological process that results in permanent cessation of PHB2 The covalent alteration of one or more amino acids occurring CUL9 PHB2	8.33 1/12	0.07 1/1432 0.06 2/3236	0,6607283 0,6696226
GO:0006464 GO:0036211	protein modification process	The covalent alteration of one or more amino acids occurring CUL9 PHB2		0.06 2/3236	0,6696226
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent of ACSL3 ANKRD13A PHB2		0.06 3/5027	0,6811726
GO:0044249	cellular biosynthetic process	The chemical reactions and pathways resulting in the formati ACSL3 FASN PHB2		0.06 3/5094	0,6914526
GO:1901566	organonitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formati ACSL3	8.33 1/12	0.06 1/1575	0,6947104
GO:0031326 GO:0031328	regulation of cellular biosynthetic process positive regulation of cellular biosynthetic process	Any process that modulates the frequency, rate or extent of I ACSL3 PHB2 Any process that activates or increases the frequency, rate or ACSL3	16.67 2/12 8.33 1/12	0.06 2/3385 0.06 1/1596	0,6947104 0,6965817
GO:0031328 GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units in a CUL9 PHB2		0.06 2/3413	0,6965817
GO:0048468	cell development	The process whose specific outcome is the progression of the FASN	8.33 1/12	0.06 1/1592	0,6965817
GO:0009889	regulation of biosynthetic process	Any process that modulates the frequency, rate or extent of I ACSL3 PHB2		0.06 2/3433	0,6968717
GO:0016310	phosphorylation	The process of introducing a phosphate group into a molecul PHB2	8.33 1/12	0.06 1/1608	0,6968717
GO:0051716 GO:0009891	cellular response to stimulus positive regulation of biosynthetic process	Any process that results in a change in state or activity of a cr CMTM8 FASN NDRG4 PHB2 Any process that activates or increases the frequency, rate or ACSL3	33.33 4/12 8.33 1/12	0.06 4/6878 0.06 1/1617	0,6968717 0,6972951
GO:0006508	proteolysis	The hydrolysis of proteins into smaller polypeptides and/or a CUL9	8.33 1/12	0.06 1/1674	0,7107193
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromolecL ANKRD13A CUL9 PHB2		0.06 3/5305	0,7130572
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the formati PHB2 SQLE		0.06 2/3552	0,7142344
GO:1901575	organic substance catabolic process	The chemical reactions and pathways resulting in the breakd CUL9	8.33 1/12	0.06 1/1742	0,723849
GO:0022607 GO:0050877	cellular component assembly nervous system process	The aggregation, arrangement and bonding together of a cell ACSL3 SQLE A organ system process carried out by any of the organs or ti NDRG4	8.33 1/12	0.05 2/3663 0.05 1/1827	0,7315838 0.7413014
GO:0050790	regulation of catalytic activity	Any process that modulates the activity of an enzyme. PHB2	8.33 1/12	0.05 1/1868	0,7492779
GO:0032268	regulation of cellular protein metabolic process	Any process that modulates the frequency, rate or extent of 1 PHB2	8.33 1/12	0.05 1/1884	0,7515615
GO:0007165	signal transduction	The cellular process in which a signal is conveyed to trigger a CMTM8 NDRG4 PHB2		0.05 3/5642	0,7556332
GO:0051172	negative regulation of nitrogen compound metabolic process	Any process that stops, prevents, or reduces the frequency, r PHB2	8.33 1/12	0.05 1/1924	0,7577161
GO:0051239 GO:0044085	regulation of multicellular organismal process cellular component biogenesis	Any process that modulates the frequency, rate or extent of : PHB2 A process that results in the biosynthesis of constituent macr ACSL3 SQLE	8.33 1/12	0.05 1/1943 0.05 2/3907	0,7604901 0.7635171
GO:0051246	regulation of protein metabolic process	Any process that modulates the frequency, rate or extent of 1PHB2		0.05 1/2025	0,7747789
GO:1901564	organonitrogen compound metabolic process	The chemical reactions and pathways involving organonitrog ACSL3 CUL9 PHB2		0.05 3/5915	0,787099
GO:0019222	regulation of metabolic process	Any process that modulates the frequency, rate or extent of I ACSL3 ANKRD13A PHB2		0.05 3/5976	0,7938144
GO:0023052	signaling	The entirety of a process in which information is transmitted CMTM8 NDRG4 PHB2		0.05 3/6020 0.05 3/6065	0,7981898 0.802601
GO:0007154 GO:0050896	cell communication response to stimulus	Any process that mediates interactions between a cell and it: CMTM8 NDRG4 PHB2 Any process that results in a change in state or activity of a ci CMTM8 FASN NDRG4 PHB2		0.05 3/6065	0,802601
GO:0003008	system process	A multicellular organismal process carried out by any of the c NDRG4	8.33 1/12	0.04 1/2314	0,8195921
GO:0044267	cellular protein metabolic process	The chemical reactions and pathways involving a specific pro CUL9 PHB2	16.67 2/12	0.04 2/4461	0,8317141
GO:0065009	regulation of molecular function	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.04 1/2439	0,8367886
GO:0065003 GO:0051171	protein-containing complex assembly regulation of nitrogen compound metabolic process	The aggregation, arrangement and bonding together of a set ACSL3 Any process that modulates the frequency, rate or extent of I ACSL3 PHB2	8.33 1/12	0.04 1/2520 0.04 2/4722	0,84748 0,8586797
GO:0051171 GO:0043933	protein-containing complex organization	Any process in which macromolecules aggregate, disaggregal ACSL3	8.33 1/12	0.04 2/4/22	0,8664832
GO:0080090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent of LACSL3 PHB2		0.04 2/4857	0,8705709
GO:0010604	positive regulation of macromolecule metabolic process	Any process that increases the frequency, rate or extent of th PHB2	8.33 1/12	0.04 1/2795	0,8784046
GO:0006950	response to stress	Any process that results in a change in state or activity of a cr PHB2	8.33 1/12	0.04 1/2809	0,8786781
GO:0006355 GO:1903506	regulation of transcription, DNA-templated regulation of nucleic acid-templated transcription	Any process that modulates the frequency, rate or extent of I PHB2 Any process that modulates the frequency, rate or extent of I PHB2	8.33 1/12 8.33 1/12	0.03 1/2881 0.03 1/2881	0,8831973 0,8831973
GO:2001141	regulation of RNA biosynthetic process	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.03 1/2881	0,8831973
GO:0019538	protein metabolic process	The chemical reactions and pathways involving a protein. Inc CUL9 PHB2		0.04 2/5108	0,8869735
GO:1901360	organic cyclic compound metabolic process	The chemical reactions and pathways involving organic cyclic ACSL3 PHB2 SQLE		0.04 3/7066	0,8877152
GO:0097659	nucleic acid-templated transcription	The cellular synthesis of RNA on a template of nucleic acid (C PHB2	8.33 1/12	0.03 1/3019	0,8919133
GO:0006351 GO:0032774	transcription, DNA-templated RNA biosynthetic process	The cellular synthesis of RNA on a template of DNA. PHB2 The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12 8.33 1/12	0.03 1/3019 0.03 1/3030	0,8919133 0,8919133
GO:0032774 GO:0071704	organic substance metabolic process	The chemical reactions and pathways resulting in the format PHB2 The chemical reactions and pathways involving an organic su ACSL3 ANKRD13A CUL9 FASN PHB2 SQLE	50.00 6/12	0.05 6/12360	
GO:0051252	regulation of RNA metabolic process	Any process that modulates the frequency, rate or extent of I PHB2	8.33 1/12	0.03 1/3134	0,8993919
GO:0010556	regulation of macromolecule biosynthetic process	Any process that modulates the rate, frequency or extent of 1 PHB2	8.33 1/12	0.03 1/3278	0,9111134
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent of LANKRD13A PHB2		0.04 2/5552	0,9124633
GO:0019219 GO:0034654	regulation of nucleobase-containing compound metabolic process nucleobase-containing compound biosynthetic process	Any cellular process that modulates the frequency, rate or ex PHB2 The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12 8.33 1/12	0.03 1/3342 0.03 1/3364	0,9136827 0,9140608
GO:0034634 GO:0019438	aromatic compound biosynthetic process	The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12	0.03 1/3364	0,9140808
GO:0018130	heterocycle biosynthetic process	The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12	0.03 1/3434	0,9173246
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism ar ACSL3 ANKRD13A CUL9 FASN PHB2 SQLE		0.05 6/12915	
GO:0044238	primary metabolic process	The chemical reactions and pathways involving those compol ACSL3 CUL9 FASN PHB2 SQLE	41.67 5/12	0.04 5/11429	0,93122
GO:0044237 GO:0044271	cellular metabolic process cellular nitrogen compound biosynthetic process	The chemical reactions and pathways by which individual cel ACSL3 ANKRD13A CUL9 FASN PHB2 The chemical reactions and pathways resulting in the formati PHB2	41.67 5/12 8.33 1/12	0.04 5/11581 0.02 1/4213	0,9383581 0,9580875
GO:00044271 GO:0006139	nucleobase-containing compound metabolic process	Any cellular metabolic process involving nucleobases, nucleo ACSL3 PHB2		0.02 1/4213	0,9599763
GO:0010468	regulation of gene expression	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	0.02 1/4340	0,9599763
GO:0009059	macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formati PHB2	8.33 1/12	0.02 1/4337	0,9599763
GO:0046483	heterocycle metabolic process	The chemical reactions and pathways involving heterocyclic (ACSL3 PHB2 The chemical reactions and pathways involving accentic core ACSL3 PHB2		0.03 2/6828	0,9624271
GO:0006725 GO:0034641	cellular aromatic compound metabolic process cellular nitrogen compound metabolic process	The chemical reactions and pathways involving aromatic corr ACSL3 PHB2 The chemical reactions and pathways involving various organ ACSL3 PHB2		0.03 2/6891 0.03 2/7596	0,9631377 0,9811064
GO:0016070	RNA metabolic process	The cellular chemical reactions and pathways involving NA, PHB2	8.33 1/12	0.02 1/5843	0,9913437
GO:0006807	nitrogen compound metabolic process	The chemical reactions and pathways involving organic or inc ACSL3 CUL9 PHB2	25.00 3/12	0.03 3/10926	0,9941861
GO:0090304	nucleic acid metabolic process	Any cellular metabolic process involving nucleic acids. PHB2	8.33 1/12	0.02 1/6311	0,9941861
GO:0043170	macromolecule metabolic process	The chemical reactions and pathways involving macromolect ANKRD13A CUL9 PHB2	25.00 3/12	0.03 3/10935	0,9941861

GO:0010467 gene expression GO:0008150 biological_process
 The process in which a gene's sequence is converted into a rr PHB2
 8.33 1/12
 0.01 1/7489
 0,9977989

 A biological process represents a specific objective that the o ACSL3 ANKRD13A AP2B1 ATP13A3 CMTM8 CL 100.00 12/12 0.06 12/2011
 1

Diet	animal	A0A3Q1M3L(P	IGR	CUL9 S	QLE C	D5L	PPIA	HID1	A0A3Q1LRW K	RT10	RAB2A	TMC4	GP2 L	.BP	AUP1	GNG12	ACSS2	ALPL
HL	c8	3226518	18491661	55721	267138	643807	4010575	150009	4893882	883223	10535572	1392806	4238810	423454	7645294	769263	2114252	8423425
HL	c6	2621250	17827237	42068	333860	592909	2290016	369420	5780402	963247	3997409	1674433	7983325	250048	7533428	514114	1577784	5029499
HL	c5	4618716	16234862	57630	222873	562089	3584617	149259	4249250	1133275	7852213	2569959	6800899	120660	7454262	879234	2816705	7231044
HL	c3	4488714	56889382	12035	348292	266766	6517901	308098	9587083	391108	4848207	1110141	7208158	126822	6136405	596975	4387306	4136854
HL	c4	3744970	24959346	63371	513451	338739	4244459	341137	1750842	584185	7005446	1160836	5478408	145365	6756025	948293	4059671	2849111
HL	c1	4456646	13957555	155657	176116	337455	2079380	135199	5222401	748431	4912477	938296	6206673	106415	7592812	1372805	4092851	3978422
HL	c7	3369445	22436490	32947	265883	131201	4202181	186125	9810590	913247	11433758	1818823	5097694	143527	7761627	813274	2617173	10412417
HL	c2	4974398	24789977	24046	319247	310142	6021004	185060	6730173	1961319	9508143	1839859	10608024	227590	3795844	2282752	2284696	4162687
LL	c8	2228555	6311510	106520	492317	127599	3740351	414099	1070669	194422	7763388	1386477	2424584	39144	6607011	1951921	4289839	2338748
LL	c6	1349347	16559764	228090	1316786	26711	8048892	946040	1817993	127432	9786634	671131	3124936	168252	10030098	2157106	6310487	403245
LL	c5	1586230	5968660	731736	1651682	80848	6802231	652788	1951621	142178	10670042	780583	1604835	91116	11771302	1636973	10846871	2313361
LL	c3	2537017	10893410	91953	620758	104284	6978896	336053	2026944	406512	6609125	794407	2466313	79247	8395895	1337010	6608888	1715647
LL	c4	2647998	16724980	263421	482820	129637	4898127	359689	2145015	386029	12262340	807036	4036523	55110	9106829	1375231	4509270	4935284
LL	c1	1919380	9122168	136179	269110	207537	8894368	236875	1817171	943935	18548596	1223767	3978824	38138	7854526	3103622	2152739	3497869
LL	c7	2153799	7368834	78939	337201	127133	7140479	380311	2387631	241266	12715467	1257034	2995935	32871	7614252	2503532	2854309	3559427
LL	c2	1202398	17332069	66437	1060616	226291	12533023	435730	4305990	361512	15876310	514567	4722875	96054	13062908	1936831	9948758	1783223
	Moy HL	. 3937582	24448314	55434	305857	397889	4118767	228038	6003078	947255	7511653	1563144	6702749	192985	6834462	1022089	2993805	5777932
	ET HL	. 820307	13699246	44184	101893	180727	1567416	95400	2697027	470424	2805219	528410	1983806	106494	1346504	571266	1051570	2625892
	Moy LL	. 1953090	11285174	212910	778911	128755	7379546	470198	2190379	350411	11778988	929375	3169353	74991	9305352	2000278	5940145	2568350
	ET LL	. 535030	4886573	221425	504298	64400	2652578	225777	935964	263530	3996034	315560	1024651	45090	2198626	593319	3147948	1393739
	Ratio HL/LL	. 2,0	2,2		0,4	3,1	0,6	0,5	2,7	2,7	0,6	1,7	2,1	2,6		0,5	0,5	2,2
	Ratio LL/HL	. 0,5	0,5	3,8	2,5	0,3	1,8	2,1	0,4	0,4	1,6	0,6	0,5	0,4	1,4	2,0	2,0	0,4

PSEN1	KRT7	CNTFR	APOA4	F1MH40	SELENOF	MARCKS	RAB3GAP2	SLC6A8	LSS	CSTB	C4BPA	ATP13A3	ALB	ZDHHC18	FAF2	FASN	SEC22B	RAB13
521189	348587	4635077	3104310	1730907	239484	1356703	819917	924262	40183899	1170879	384050	2184290	552810	59117	3354205	4144732	352640	608319
470865	683041	1967503	1776546	1772626	187035	1200599	684956	1028849	32772747	758225	498445	2756134	512617	17238	4056370	3426255	309229	261969
302372	415822	1984517	302598	1371175	500675	853963	841835	1354651	36866579	778259	288435	2924505	891593	76560	3685925	5003815	381666	786305
1005377	326480	1919417	459812	776731	638425	385107	456899	892850	44694265	2115827	66578	2993222	498733	72388	3287263	12529573	329112	272913
251318	350165	2108630	393613	263100	202178	570318	1248151	531101	31218702	957953	10100	2740416	648380	47171	2264581	22749906	671157	448751
870944	185141	2407122	511824	960929	325442	899710	384583	805669	19000071	722954	465844	3158768	876041	24136	1312724	18893801	221413	422625
869947	216983	3502870	1920270	1278585	449553	938623	852648	1032097	40310361	1490040	297912	2080695	918869	28068	3433115	3743940	533578	744490
593459	479894	2446000	606006	1693129	793840	658359	748010	853460	24919069	931657	85171	2177796	1342093	76055	2683479	9727860	1192359	696952
708107	147272	930868	323928	280019	482354	628734	2727916	602041	45001505	1206587	36782	3893128	393748	111961	3526532	15144389	621532	551656
1510679	224216	528658	259873	432583	903434	63997	682038	298207	79828774	1049224	129449	10147833	511213	38027	4356340	80382645	931684	637171
1229433	99932	360485	122680	334921	806062	116997	1227056	556840	113957118	1509295	69469	6705968	759848	76692	5737916	39515881	755999	727681
1757367	253901	796890	55187	512970	491656	129379	1113708	547517	61645104	1753080	15268	4910873	246604	42220	2979207	16972339	275161	354147
540016	203872	3732271	376609	1446930	791788	376576	1389198	568751	37061194	1613617	20536	3032263	488320	70203	3157992	18101400	1084932	942710
892899	184163	1873800	179461	717647	786618	921401	1421875	903711	34428648	2093182	48367	2236400	674346	81234	2982014	19271271	1466128	1449530
580572	273669	2069573	155496	1189429	526637	465689	1540285	950536	32278390	1484308	29628	2576470	347039	136189	3688504	5895740	1564941	1101374
2039818	180670	667784	134563	396489	2228024	48188	695999	446262	67655057	4203706	228893	3629961	211724	129260	6214712	16435192	437020	1057936
610684	375764	2621392	1134372	1230898	417079	857923	754625	927867	33745712	1115724	262067	2626978	780142	50092	3009708	10027485	498894	530290
278463	156861	963437	1019315	533837	219749	320843	266060	233708	8592617	477806	187942	419382	286968	24495	883916	7461568	313665	207629
1157361	195962	1370041	200975	663873	877072	343870	1349759	609233	58981974	1864125	72299	4641612	454105	85723	4080402	26464857	892175	852776
567493	56343	1137975	109388	430215	569889	314832	642140	218680	28109712	997696	73078	2642403	193954	37111	1259765	23727909	462974	352447
0,5	1,9	1,9	5,6	1,9	0,5	2,5	0,6	1,5	0,6	0,6		0,6	1,7	0,6	0,7	0,4	0,6	0,6
1,9	0,5	0,5	0,2	0,5	2,1	0,4	1,8	0,7	1,7	1,7	0,3	1,8	0,6	1,7	1,4	2,6	1,8	1,6

SACM1L	MUC15	ANKRD22	SCAMP2	CSN1S1	STK26	REEP6	ARF4	FABP3	FGG	PGD	SEC14L1	ІММТ	PFN1	TC2N	TMEM120B	IDH1	АСТВ	PHB2
326960	25843723	2291745	8378051	161025009	518338	401554	12389670	120510636	2805032	10054736	159418	20233	471111	57289	633832	1960074	9387976	24101
262467	7 15816447	904395	7153414	44936046	640270	314594	4717871	89246663	1921266	6641776	93606	6714	258068	42467	558013	1789382	11076102	63091
217194	13939732	2172792	1983184	46322973	504866	173301	7849047	150313686	1828229	12415049	135498	10030	613479	106359	646845	1668287	7641346	1674
450825	5 5291420	681096	1526808	111661782	1738375	130999	7445385	125251540	548270	8789050	85439	41886	416788	11735	706073	705714	6466282	120489
486318	3 15021924	2157662	2980145	36995023	372233	239592	7546355	77807444	485152	20652379	259066	219950	396919	58920	782901	2304733	11028798	163133
287094	12135382	1502431	5224795	37737358	425815	131499	6926538	183975063	1151472	10897343	179623	46374	361165	106406	587792	2194203	7383537	20708
611780	13836104	3209587	6514626	76215672	184188	208868	12784481	228480112	7546779	12661578	158798	71597	846161	75919	1284593	2217150	11784602	59706
594868	3 12234034	1952154	1663009	52489829	362193	319564	13513925	220308398	1453435	15311257	140695	94989	973792	37261	1337892	2093191	12667531	136018
626100) 12185499	2119462	947656	20555789	422672	479905	7465823	124709129	546856	4665172	185468	20052	875670	41379	953628	1279630	9287169	37510
398469	689047	2630031	246255	43708857	1426413	385261	9261434	144277778	1105455	13169664	183872	99555	974451	8087	1375209	390133	880221	392101
1748787	4159545	2829724	3360519	30167063	2125087	265245	8443344	183334593	2008564	17590860	290153	26173	624776	6771	1591442	451894	1493721	39418
814410	5562389	2308755	1206023	63020894	1805481	158140	9353538	184228358	504073	5952254	124066	144090	435757	11576	975275	631123	5333149	81226
556407	9853067	6982344	2750893	37541099	523826	616112	19118788	295301610	814441	10182792	155439	224086	1056945	73992	1125357	1516842	9539225	516736
440818	3 11253964	2478720	4753553	33671378	473108	488483	20588024	512545569	581835	5153470	251223	107735	1020348	24937	1530180	3017134	9371053	39482
357876	5 12111773	4652210	3950952	52384591	474466	535379	19832858	310699131	805344	6726724	129365	185653	1025505	53519	897881	1786878	8998890	165170
575303	3874178	2803099	1170866	52396524	5342356	306931	14817677	277180804	296796	7591456	236408	142857	1455522	15177	2156269	666095	5725931	1012445
404688	3 14264846	1858983	4428004	70922961	593285	239996	9146659	149486693	2217454	12177896	151518	63972	542185	62045	817242	1866592	9679522	73615
152643	5688607	813595	2729604	44205190	481745	97882	3262472	56870198	2283270	4312863	54203	69947	250468	33134	312947	517576	2298016	59564
689771	7461183	3350543	2298339	41680774	1574176	404432	13610186	254034621	832921	8879049	194499	118775	933622	29430	1325655	1217466	6328670	285511
451819	4428610	1661985	1629723	13882315	1666002	153354	5614964	125880069	534250	4511857	59818	71311	. 305154	24553	429140	892422	3582960	344771
0,6	5 1,9	0,6	1,9	1,7	0,4	0,6	0,7	0,6	2,7	1,4	0,8	0,5	0,6	2,1	0,6	1,5	1,5	0,3
1,7	0,5	1,8	0,5	0,6	2,7	1,7	1,5	1,7	0,4	0,7	1,3	1,9	1,7	0,5	1,6	0,7	0,7	3,9

ALG1	ATP13A4	ACSL3	SLC39A8	RAB3GAP1	UBA1	RAB3D	GPAM	G5E513	DGKD	ARL1	SSR4	BSPRY	G5E5T5	CHP1	Q3ZC78	RNH1	KRT1	RACK1
283061	11301660	10970286	39827879	540560	273060	1884006	10929563	19033541	325786	28304	73165	2603496	275850	2553243	384360	1780243	840334	687339
190849	17431189	9600273	49597974	365804	274384	759378	16147365	23036916	267298	98878	128637	977136	395094	2146141	108718	1057732	564739	280690
248658	10039576	15584159	46462100	382879	157084	1582352	11576359	30939797	442505	139888	142304	1294897	1826588	3812724	127835	1665154	824825	76821
166397	37907607	17631092	32248307	459335	172117	3393771	19521772	49477999	976442	303395	228682	1001547	964891	1574298	110635	693359	374332	740057
274814	13228619	8916733	32306141	669911	449520	1027487	16217480	22155140	338529	70112	226760	1744865	343250	4200723	112657	1810069	580871	290168
252561	23050734	8645180	38176620	698710	110861	862387	11640787	20557234	172945	131509	150741	724930	426722	3713656	412938	1024037	604052	111840
455966	12129888	10191715	49590814	457234	196528	1921571	14336045	23502086	291913	33129	187570	3807036	266075	7288614	551312	1871270	406581	673797
217948	10911521	8924628	39781710	410208	315133	1480311	12911469	46776018	190298	150325	590834	1263800	548859	2871096	187739	1789602	930043	469158
138538	14897056	12679894	31850057	1274081	454241	1038555	19624499	9177365	376220	98541	. 268760	665228	181523	2824948	387792	1531308	345046	297874
443816	46385969	24335161	5058191	472865	438996	2044450	56683811	58483052	543537	497425	460091	51885	452720	2178195	401344	2374688	62326	620871
271809	44070442	48193756	14768271	1240601	348356	3748496	28776539	19444731	1615914	282695	191669	137041	1193891	4121978	100053	3525612	293226	876437
344802	48814806	21521470	29966372	988401	285284	3350960	20606123	18244026	715445	207570	98481	547652	244244	2669685	204383	2010586	449041	715176
424717	16243829	8633362	51150168	867857	401517	1629244	16724728	18977867	394362	125304	472872	2436890	265675	9113256	663209	2112486	461258	984408
243969	15643876	9786557	25408522	736963	241697	1338772	8795682	13158740	304655	229757	472785	506567	132523	6013110	243859	1161833	761826	393153
353104	11872096	10582010	36322096	1166341	192039	2305639	16250200	11500995	331011	163196	464423	1538631	27307	6559770	349759	1217596	267928	473354
514535	31600251	20307125	25017637	282998	285953	2539981	31798545	20641626	681998	1128077	837856	503908	307305	7613262	419447	3062571	480632	414743
261282	17000099	11308008	40998943	498080	243586	1613908	14160105	29434841	375714	119442	216087	1677213	630916	3520062	249524	1461433	640722	416234
88347	9485740	3402367	6975126	127191	108078	844585	2975582	12076148	257317	87805	160049	1039868	532802	1765461	174207	460524	204915	264473
341911	28691041	19504917	27442664	878763	331010	2249512	24907516	21203550	620393	341570	408367	798475	350649	5136775	346231	2124585	390160	597002
121327	15862708	13038006	13827548	362893	95266	946445	14736248	15631336	431599	341103	227114	799980	363049	2562152	169797	846833	203080	245601
0,8	0,6	,		0,6	0,7	0,7	0,6	1,4	0,6	0,3	,		1,8	0,7	0,7	0,7	1,6	0,7
1,3	1,7	1,7	0,7	1,8	1,4	1,4	1,8	0,7	1,7	2,9	1,9	0,5	0,6	1,5	1,4	1,5	0,6	1,4

ESYT2	A0A3Q1MAC	CD36	CALR	ESYT1	ABCG2	A0A3Q1LSB7 0	SNB2	KPNB1	CSN1S2	RAP2B	CLU	R	ALA	TMC5	RAB9A	STK38	RPL27	ANXA7	NDRG4
252726	1414293	143997448	523566	347326	424107538	512996	40399240	81326	68732759	340528		288187	2319529	2112956	204756	142392	43557	1529932	101213
172319	476607	149497712	931652	580287	461975398	402973	23310644	182891	31098216	95591		76744	1073963	1884604	118524	214231	49334	1369942	103263
143362	1372027	182819900	890090	513852	668353352	622600	30192318	109470	41767609	188510) :	265258	999288	1644183	437663	352131	20118	1369675	31975
73471	2854271	83497265	506204	572999	488077770	316503	23220382	259132	161472957	255029		405674	1371778	564614	155676	119747	113972	1447517	703719
198040	373019	97663915	1333057	498439	479930166	99962	23274841	185854	20987921	92890		292720	751487	928720	137264	235029	195814	1518536	46246
124239	855774	83961123	401319	340351	486354649	126843	25213570	198606	28320301	126794	. :	367063	758656	1488567	40271	147636	34023	1217346	206094
228712	528278	100327738	807130	163441	418876367	285278	37696047	285029	39679872	191976		143813	1360987	2025285	102645	155020	87870	1548335	49559
244149	1013709	82265905	1857495	883319	423358218	377126	25947838	241734	29867499	173925		223661	1203761	1704571	260923	307738	389209	1860894	92051
337043	624914	99143455	1357902	802442	690853813	468454	16629770	189836	10305392	227064		55493	703850	1144658	142924	277404	165507	1173251	61904
345377	2595561	61634168	130628	1133274	1158483830	269096	8605381	500764	15672696	383963		79907	1464020	509800	223822	424892	240162	454663	905120
370038	1246285	115136234	146462	1533512	1051269989	259263	11997878	436592	15127098	231484	. :	127540	3368133	451640	272606	666730	69842	600472	484582
339694	2045653	54075464	226906	701471	832837543	415424	18469106	406919	50720013	279424	. :	139680	1329147	798961	96323	227751	46689	1114488	840211
321314	439518	77953662	759699	309018	477209303	901794	31729017	276931	24510735	192541		32435	1090928	1228386	195225	201154	492780	1390209	119490
192705	1819953	110618413	551179	588742	419380640	548339	27465899	103418	29665800	222668		152802	1918756	1128225	404524	198329	292201	1271622	163691
237160	1474259	103384136	1100984	528497	482422490	488485	31008681	222706	30454229	333280) :	247781	1426424	1483802	378151	235595	313085	1225384	141667
121413	3321064	35028991	587882	468217	513711745	1710821	15251271	311477	39601644	717266		113589	2528991	820244	545616	213024	194816	790708	447577
179627	1110997	115503876	906314	487502	481379182	343035	28656860	193005	52740892	183156		257890	1229931	1544187	182215	209241	116737	1482772	166765
63201	807143	38119403	486856	213716	81029667	177949	6847800	70560	46237923	83765		108853	500534	540901	122601	84534	123872	188222	223673
283093	1695901	82121815	607705	758147	703271169	632709	20144625	306081	27007201	323461	. :	118653	1728781	945715	282399	305610	226885	1002600	395530
88990	968434	29484329	450106	398981	283263657	479363	8819273	134970	13599676	171477		66880	857110	361295	150509	163615	143677	342413	332472
0,6	0,7	1,4	1,5	0,6	0,7	0,5	1,4	0,6	2,0	0,6		2,2	0,7	1,6	0,6	0,7	0,5	1,5	0,4
1,6	1,5	0,7	0,7	1,6	1,5	1,8	0,7	1,6	0,5	1,8		0,5	1,4	0,6	1,5	1,5	1,9	0,7	2,4

ATP5F1A	STX3	GSN	RDH11	PSMD6	RHEB	XYLB	RTN4	RAB1A	SURF4	DENND3	GLYCAM1	A0A3Q1LUE9 TLR	4	MYO6	FLOT1	LRATD2	SERPINB1	HDLBP
121706	7210758	2067625	1043871	40571	2380743	53699	247792	14940887	117251	39488	640784409	2644865	160478	10037	2196855	404112	120431	1569
177294	7375898	2999108	589269	87418	1437415	140234	124823	9712159	119801	70264	242453861	754844	183403	36362	2122085	425610	204428	8500
261886	8748547	1296172	729724	34102	2265168	47949	295099	7951142	176909	110654	86826587	853854	228006	51343	1457094	588836	38950	21257
1711626	5303185	1043635	392841	17438	1667086	222436	113434	10677674	221837	12484	87166125	2186592	106237	38681	1257120	316533	23599	27533
1653075	5933924	2821905	839921	183269	1701305	140692	316306	12095728	301517	116151	53667656	1657844	250525	126248	1118278	398223	197351	77523
253816	9480739	2544757	744151	100301	2230678	62876	219166	12704576	242422	89540	77562767	1675448	174774	38441	1964580	338138	67724	11207
471179	10677219	3860350	1271219	108902	3003353	50632	240349	17995602	176613	81965	586199525	1209995	127766	84672	2694993	300993	779375	1087
1258790	8954598	2576334	948898	289243	3087500	111240	469420	14063890	508244	134694	44722289	2546179	260131	73291	905866	476470	104698	47539
300185	4475666	2307605	872171	78429	1801138	117543	287262	11940108	263762	67434	63050707	379475	460603	68853	1196429	357354	62872	87557
1879162	762761	336645	1193689	30111	1465418	344329	476120	29309739	470282	4160	23829553	453927	507700	51807	688761	57484	90506	217640
858949	1912742	697902	871779	2598	2733390	175150	323432	19392814	507171	36761	27257874	310222	965086	135122	1503148	160508	43994	43219
1253484	5025278	1130886	505683	8830	2349452	125250	196951	16287264	485828	19186	22508319	707284	372129	52344	1176841	285475	56616	27968
1213581	8691792	2563257	1876601	69989	3889256	98612	408224	14941060	348935	95669	145525320	2832810	96261	74541	1525996	342439	92014	39762
782053	9591049	1799801	873333	55934	4033726	51628	389383	10903186	224167	102169	128982789	1937601	262055	66021	2426115	375874	24480	23359
1383566	9093376	3296721	1063431	230717	5235709	109363	460577	15066166	317948	94591	68494225	1542230	256146	83872	843140	517911	81284	27224
3598483	4678745	991957	1885348	83966	3496704	177452	520065	38407563	368502	914	69182238	449475	220370	52634	1237744	161509	55039	14275
738671	7960608	2401236	819987	107656	2221656	103720	253299	12517707	233074	81905	227422902	1691202	186415	57385	1714609	406114	192069	24527
684841	1827299	917312	272641	90401	607262	62048	113299	3175647	127169	40705	246484447	726706	56010	36191	621924	94476	246450	26373
1408683	5528926	1640597	1142754	70072	3125599	149916	382752	19530988	373324	52610	68603878	1076628	392544	73149	1324772	282319	63351	60125
1000214	3318537	1023565	496265	71883	1268564	88467	107890	9528547	105498	42562	46953987	928372	267040	27610	530185	148080	23546	67437
0,5	1,4	1,5	0,7	1,5	0,7	0,7	0,7	0,6	0,6	1,6			0,5		1,3	1,4	3,0	0,4
1,9	0,7	0,7	1,4	0,7	1,4	1,4	1,5	1,6	1,6	0,6	0,3	0,6	2,1	1,3	0,8	0,7	0,3	2,5

RAB23	PRDX5	ткт	ANKRD13A	GPC1	GOLGA7	RAB26	DENND2D	SH3YL1	STX19	PLIN3	GNA13	MARCKSL1	FGB	DHDDS	PDXK	SDC2	F1N647	NSDHL
500542	340574	209182	519344	485916	947646	161174	71074	907923	3828347	32280411	16278876	289266	1034499	276697	2457007	455212	6343805	24169884
101029	227004	292677	581017	473572	666227	235850	153783	562947	2366125	33982030	14217482	349559	823341	291111	3291746	416237	5384548	19651208
212222	258731	129892	378113	372440	852003	125151	154501	427045	2439429	28701724	17257914	265223	843464	358534	2746430	379602	7994487	25683347
93537	68562	123294	893732	272496	845599	20896	120902	1039315	1141314	9481570	7165632	45403	122246	758436	901539	153620	2343877	33739170
199398	246892	384939	462972	388935	811846	125027	220772	437571	1909137	10800805	10600935	205010	129581	290931	2984866	472827	27096882	23890793
250073	166897	214666	448416	368220	702891	63844	176421	604473	3221951	16603809	13524458	302786	343169	517221	6988500	621689	14995535	20018493
709665	436131	305124	409824	867623	1238811	209473	117990	958450	2981171	44578771	14913602	158752	3461117	95986	6121051	395570	7336711	22542889
291320	431683	183141	506996	816994	1259535	149828	149413	426234	3060404	7996695	16412466	172783	540492	312007	3116123	553437	11784053	16802076
187317	373428	229630	571214	309868	1011604	149754	167737	548349	1339322	14203313	8966526	384397	132729	454158	1390050	248855	21894506	21794291
323184	296688	17514	1675867	249384	694390	37753	537824	1378049	864736	9171467	3695555	11158	905105	3285128	199859	52127	16040376	69614069
498487	230150	26791	1735123	378606	732416	10110	307252	818808	912557	11643365	5116959	73272	1546809	1374270	350028	146785	20685331	58232331
221829	161448	150783	1140098	101973	863795	32979	169354	1371408	905172	13055652	5128256	28886	73612	820556	805641	137179	6017149	30503505
507317	569433	232777	331211	552167	1571765	215039	147686	542812	2116524	11915010	14166120	54641	237632	99453	5736861	459480	39034625	23097801
233977	609873	166914	507913	83227	1676718	67056	159115	349999	3300412	16573889	20774540	483383	65796	359121	2963651	437595	23755405	20454811
259495	541697	239208	472645	284686	2158893	177152	169426	675506	3194500	12481725	16737467	215261	225215	301906	5890834	505045	13152755	25930674
699311	333361	55588	859738	108966	1539000	27039	101026	1293101	864374	9936007	5923403	38605	414569	1224345	297865	206585	4301034	62497121
294723	272059	230364	525052	505775	915570	136405	145607	670495	2618485	23053227	13796421	223598	912239	362615	3575908	431024	10409987	23312232
210588	126720	90907	162134	218434	223902	70595	44220	257579	839704	13640486	3394661	97883	1083845	197078	1994895	138741	7778160	5107968
366365	389510	139900	911726	258610	1281073	89610	219927	872254	1687199	12372554	10063603	161200	450183	989867	2204349	274206	18110147	39015575
182027	166273	94316	551045	161092	530510	78970	141204	415737	1051861	2342350	6367541	181532	520568	1031683	2401071	170652	11061178	20684897
0,8	0,7	1,6	0,6	2,0	0,7	1,5	0,7	0,8	1,6	1,9	1,4	1,4	2,0	0,4	1,6	1,6	0,6	0,6
1,2	1,4	0,6	1,7	0,5	1,4	0,7	1,5	1,3	0,6	0,5	0,7	0,7	0,5	2,7	0,6	0,6	1,7	1,7

SLC7A4	UQCRC2	TUBA4A	APOE	CMTM8	MICALL2	SDHA	STXBP2	SIRT2	GSTM3	INPP5A	SELENBP1	SLC1A2	FERMT2	FGR	GNAI1	ALOX15	G3MYK6	ARL15
25223615	4773	588859	13748865	88956	461981	2605	4054254	927585	1001450	263340	9776895	126469	137698	6120610	323860	2174792	163480	2395654
37964137	67436	1010508	5625880	226500	667860	19084	4451862	808541	241378	177199	9926574	173714	103452	6952135	521368	3930796	35747	2363790
19233095	66840	659014	11954768	106486	668829	11388	2029059	442946	448729	346572	2229867	173607	173493	14187891	445607	2009879	432674	2027140
24177642	825992	440858	4008162	1230897	232350	18668	2235943	326967	741248	131277	2421743	110825	90886	4223641	1418556	2387425	221844	1082544
33556536	759368	1455352	6083109	90493	887124	187389	5525779	946021	415349	256275	5058559	128950	231851	8837368	589757	3515277	143187	1392692
20099670	69011	932122	4986925	142552	654627	13155	4040743	971216	623578	309077	4492427	152462	145494	6616310	1520796	1685146	148825	968736
30897255	271146	581053	9082569	14509	732247	53364	4022576	780906	1122663	126440	7252831	87946	78517	6258043	299026	2235020	347343	2620773
44699868	320730	1325079	3543134	201463	803946	77281	5726599	591149	857684	251518	4191776	333202	198122	6470083	574647	2622905	248590	1944480
21929177	59220	929266	3304198	109424	501466	38431	3816512	512204	840941	165220	6995236	75749	382541	10597130	442257	5264626	97579	1449870
11320834	170757	642424	2604502	992816	73383	57157	1870031	207413	856641	42903	5803778	21611	205859	3086429	2789335	6948884	206411	1176698
12385278	198782	484508	3811198	1149724	155746	34149	2469318	476424	1092684	73364	1650338	15576	161746	11640203	2197748	3977529	111021	1190792
18877015	676294	333724	2933654	660626	202138	55257	3293017	407992	1049478	146188	4012829	133320	259707	7783530	1495118	3661055	331300	1156246
40047583	554661	851406	4229353	217536	652964	97185	3772571	390248	615509	161345	3825984	195029	109718	11323497	340110	4588021	281348	2642501
13762609	233346	949138	5718625	245108	704707	26821	2699685	666404	945031	219791	5565690	83482	77886	10172703	461961	2411678	879576	2573302
38348174	435239	916070	4335363	86556	783146	107660	4665076	874145	756688	306783	3687680	373810	186520	10674532	541464	2218614	634679	3352329
16948873	1790133	569602	5019579	1732033	158252	110546	1877907	195943	1053648	59743	2685111	24703	215702	7125732	2243657	1642964	606779	3053159
29481477	298162	874106	7379177	262732	638621	47867	4010852	724416	681510	232712	5668834	160897	144939	7458260	711702	2570155	217711	1849476
8956029	324673	371177	3797860	396907	205681	61676	1337054	243931	305587	80451	3019501	75707	53858	2995807	480429	769652	125547	629156
21702443	514804	709517	3994559	649228	403975	65901	3058014	466347	901328	146917	4278331	115410	199960	9050469	1313956	3839171	393587	2074362
11350794	556196	234348	1053046	597471	287287	34217	1000193	226112	165587	88833	1749879	121312	94017	2904234	991814	1764780	282524	924460
1,4	0,6	1,2	1,8	0,4	1,6	0,7	1,3	1,6	0,8	1,6	1,3	1,4	0,7	0,8	0,5	0,7	0,6	0,9
0,7	1,7	0,8	0,5	2,5	0,6	1,4	0,8	0,6	1,3	0,6	0,8	0,7	1,4	1,2	1,8	1,5	1,8	1,1

GNAI3	APOA1	CNP I	PARK7	SH3GLB2	RPN1	FGA	COPB1	EEF1A1	PRKAA2	TPRG1L	ACTN1	GPX4	TBC1D24	A0A0A0MPA	ANXA2	CANX	MELTF	TMCO4
2368901	13946364	1253189	525352	252623	274628	1162652	53475	215216457	68197	3546593	530621	1628370	375847	34641	10998032	152377	809505	103109
1795272	4838576	1244795	221632	348154	620148	417219	75970	137618376	79556	2384652	875156	1244502	438867	30150	6521406	415563	54071	49699
1635343	3586474	1152208	84059	316273	246058	321102	62219	120797101	94542	2440162	226098	1196636	323336	10894	9225836	536907	74760	55946
3885368	3736069	305209	240364	114516	329935	35740	141463	106756877	33251	4004585	761647	295762	865782	27007	4045465	266950	150999	37360
1756668	2879454	702365	254354	293313	950186	103920	343005	185143076	166108	1494247	643257	914755	508481	139987	6385136	868591	44509	97911
2409988	4374234	732093	377975	583752	233800	105310	211898	158814188	42010	2915596	565853	864085	115670	32743	7364266	559993	151586	44926
2240896	10652807	1021783	1074901	248279	391650	3898346	42397	251558921	27763	6128790	880590	1877287	325145	82929	13242106	146802	146542	161810
2102046	4682469	511600	209013	535443	1272988	309869	474038	154729579	86512	2189501	742017	1799777	409965	238312	10157105	811071	94599	66183
1742458	1171033	1310668	96561	247615	999182	174584	261164	125109688	126095	2338464	858705	1539932	410742	94481	5895738	919279	180422	126999
7942804	3846005	136064	12486	65454	2744369	248729	443788	35434343	145019	16351548	372443	785390	395662	104348	1714534	465996	405	45156
4391313	2186233	327892	18186	112761	797707	819838	286956	38072623	86226	6290093	402375	1395462	749495	20243	5380451	733906	38905	104328
3460764	1247671	363868	513210	84459	266715	45557	140645	96784381	30789	6465232	271928	819868	981717	21002	3466061	295586	63825	75578
2575034	4047976	411431	284737	251516	972580	309395	192208	307158946	73925	1774903	544470	2570101	449887	285877	9675035	459076	98903	110011
2451715	4922640	745973	291933	457707	584607	87625	161167	171739984	99155	2384320	329271	3042912	240350	202086	8849687	705618	251384	72776
1642277	4598667	662405	547872	510148	611043	88467	230789	162146596	119317	2379185	500926	2569271	511164	259349	8266358	574174	71151	45794
5029675	4254443	473539	80724	57875	593233	30952	156607	70490490	75925	12583712	204173	686895	579096	194978	6284617	569288	14527	132589
2274310	6087056	865405	373456	336544	539924	794270	175558	166329322	74742	3138016	653155	1227647	420387	74583	8492419	469782	190821	77118
713078	3984773	355442	311874	154558	383343	1303748	158119	48763867	44632	1442631	215735	535814	213780	78189	2964561	277054	253741	41777
3654505	3284333	553980	230714	223442	946180	225643	234165	125867131	94556	6320932	435537	1676229	539764	147796	6191560	590365	89940	89154
2110449	1515214	360535	213924	178242	764230	259512	99513	89511498	36023	5443452	204200	931012	232014	102651	2718487	193604	85919	34336
0,6	1,9	1,6	1,6	1,5		3,5	0,7	1,3	0,8	0,5		0,7	0,8		1,4	0,8		0,9
1,6	0,5	0,6	0,6	0,7	1,8	0,3	1,3	0,8	1,3	2,0	0,7	1,4	1,3	2,0	0,7	1,3	0,5	1,2

TXNDC5	ZW10	RAB7A	OSBPL9	SLC29A1	RHPN2	GOLPH3	NUP155	LPL	DDX3X	VPS4A	SFT2D2	DNAJB9	LRRC47	ZDHHC9	GPD1	EHD3	SLC34A2	RPS20
536003	234761	7388429	1876188	694370	73081	1856989	65969	45131818	23318	826829	2080625	473424	78062	972463	2650714	388266	236827348	53703
444914	163262	2911712	1636604	637600	69972	1130089	115944	22847767	68795	844869	1068752	496464	124726	805326	2440579	373334	264178040	45418
731413	225368	5109179	2064111	1174429	130143	572663	89125	7187396	41559	159295	1375136	574656	37706	1122859	4094920	823949	326263369	49147
642012	375936	2146192	1077032	597091	164054	880790	41444	10134553	57777	34403	2965373	926670	198586	489086	1539737	402997	152179283	21633
1386506	526895	3471770	2496570	1018246	161556	1300402	80776	6435015	79798	237278	1376708	470104	277719	711827	3258004	480448	174927907	226525
733597	681014	2720806	1843618	775790	38206	1261917	127940	7962983	42730	72876	653270	369705	58316	1020538	5307256	269928	205031360	32185
866988	334689	6366472	2428092	773644	107782	668294	42141	15727714	43673	374211	2132566	955479	106420	1433248	2123351	436708	221108685	80825
1335869	352741	4589272	3133709	856207	61523	2182337	47323	7242363	61449	239781	2001051	814908	194579	866737	3038443	396840	198664912	552194
1116928	550210	3867841	1681219	530771	97067	1563214	109677	6280426	104621	203805	1197879	426795	229163	591398	1670288	381803	269477265	271703
3343514	667382	5389077	1123951	1608978	320260	1527115	201939	16324052	311007	143079	1754243	609703	132068	121120	1092902	180416	52990663	141263
1310041	1211303	4266396	2866147	1131294	141740	934217	468825	12960547	62812	56734	2189602	450443	199395	270324	1139512	172987	132256718	26627
590508	830467	3271934	1667393	519424	153098	799803	170009	6537403	35447	55427	3320316	916910	329797	960953	1548186	371462	142303132	78854
1371660	367855	6314539	1710952	698444	89850	732888	53556	6920828	57308	267780	1727979	642064	283366	1636794	2009825	394255	254054352	503340
737490	246489	6925502	1302443	711731	70522	753436	151023	5626937	46811	194848	1930019	1070165	92214	860818	4674866	301959	235955165	369633
884398	407015	7799347	2215774	800663	89932	593137	37849	2969959	51764	211781	992610	1652413	193696	975602	4810394	491493	178840270	588528
1167076	685121	5111146	1031319	278707	155106	944983	65793	6415555	35771	31126	5869917	1264608	94184	368151	1662555	208385	122697477	517646
834663	361833	4337979	2069491	815922	100790	1231685	76333	15333701	52388	348693	1706685	635176	134514	927760	3056626	446559	222397613	132704
349668	170855	1862474	621557	196012	47481	558768	33276	13292971	17981	318581	729736	228866	82350	283338	1189268	163880	54500842	181560
1315202	620730	5368223	1699900	785001	139697	981099	157334	8004464	88192	145572	2372821	879138	194235	723145	2326066	312845	173571881	312199
863799	305600	1565572	605271	414636	79811	365926	138829	4368731	92647	88042	1578471	431220	86066	490605	1520937	116412	75030863	215559
0,6	0,6	0,8	1,2	1,0	0,7	1,3	0,5	1,9	0,6	2,4	0,7	0,7	0,7	1,3	1,3	1,4	1,3	0,4
1,6	1,7	1,2	0,8	1,0	1,4	0,8	2,1	0,5	1,7	0,4	1,4	1,4	1,4	0,8	0,8	0,7	0,8	2,4

AP2B1	ACO1	F1MPK7	С3	PDIA3	BAG5	SCCPDH	PLSCR2	REEP5	ARHGDIA	VAT1	SLC25A5	KARS1	GNAQ	MFGE8	JAK2	GNAS	VPS35	LOC508879
89733	5236061	17859227	6728540	547516	438172	1449379	968816	15017	3545652	10683860	364375	400994	4594396	1807715376	260198	21084159	1674657	3270466
92852	5930019	19548280	3322776	1237351	451076	832315	890374	13248	1968444	11383993	539780	1118513	4226714	1464682655	479129	15160228	2403559	4814507
71691	4579988	20691620	4891430	776943	436828	1538013	785301	69335	1353978	25566700	974434	743484	6873066	1032113700	561701	19932104	1588423	5046585
325738	4653283	11960517	3608629	438247	559754	1003695	529104	14239	4235984	22451491	427704	318825	1947814	3330843349	193854	35071183	4496673	1623347
218915	6168644	14147042	6512458	1617207	415341	959205	498366	30585	1379554	10202879	1878378	1158356	4445113	1802404868	542150	15594337	3372195	8149796
131727	5873107	27374865	5408736	788404	738319	740794	1041543	144779	1397954	9543991	1222199	1128843	6461293	1571095540	476332	15177219	2571700	7563720
45657	6097265	16568307	8298953	1004802	419470	999799	1269158	24212	3224491	10160930	1294868	616816	4620980	1836718502	170066	20121086	2606410	4652539
151768	5334314	16805477	2624170	2615387	326362	1045294	1106113	134361	2119936	11011629	1963788	466341	6431487	1139725437	544992	16224557	2108498	4111958
176539	7482555	14841569	6175490	1506315	725838	890523	765365	24360	3530288	12772956	606459	667562	3149972	1237389842	496301	12843660	2516700	7294153
453444	27110242	4936340	1075971	467421	1327022	387647	443522	3415	1317391	19477049	561916	255026	1985573	2981670009	118129	29582469	4102247	6330672
279422	7730289	16915539	1303389	369818	1359468	583034	1308440	318473	4091810	45692138	844783	113082	1794414	1785543040	405342	23613590	6006971	6743299
426343	8151194	9511297	1305611	263689	750837	699722	783408	14927	3809350	28826269	1043525	311365	1821387	2755876345	246409	28182029	6702151	5380471
168785	5095960	19609325	15867058	1641596	500416	1173098	925692	37645	2339273	10048573	2076412	790585	5037695	1801897921	124267	18579977	2607912	5192421
74954	4677056	22693939	3137885	930938	314293	888230	2495199	279249	4232623	12874906	1875274	794724	5784925	1160338996	377473	20152080	2571872	4385015
123723	4385329	18216028	3504853	1441347	278323	896274	2004299	433198	2155949	10628221	6359310	942427	6844290	1430965956	535998	16095891	2114870	7614948
266445	6345141	5501633	3620283	388235	916519	861527	1912983	78696	3348550	17344947	2663217	188168	1772543	2402746864	191653	24529970	4357828	6203017
141010	5484085	18119417	5174462	1128232	473165	1071062	886097	55722	2403249	13875684	1083191	744022	4950108	1748162428	403553	19795609	2602764	4904115
91995	630915	4663431	1945228	710137	124565	280315	271005	54912	1119139	6334439	623972	348825	1612579	708503926	166593	6636990	952751	2130034
246207	8872221	14028209	4498817	876170	771590	797507	1329864	148745	3103154	19708133	2003862	507867	3523850	1944553622	311946	21697458	3872569	6143000
137367	7509597	6639136	4895818	578430	414660	237652	728951	168397	1046366	12156647	1916997	324514	2066467	693673091	164211	5828402	1734914	1099774
0,6	0,6	1,3	1,2	1,3	0,6	1,3	0,7	0,4	0,8	0,7	0,5	1,5	1,4	0,9	1,3	0,9	0,7	0,8
1,7	1,6	0,8	0,9	0,8	1,6	0,7	1,5	2,7	1,3	1,4	1,8	0,7	0,7	1,1	0,8	1,1	1,5	1,3

NRAS	UBE4A	ANXA11	EIF5	FAM83F	A0A3Q1LLH1 NP	TN	RASAL1	ACAP2	STOML1	GIPC1	FLOT2	МҮН9	FCGR2B	ANXA5	NAPA	PGLS	VDAC2	SLC5A9
2682940) 19364	4 211466	87832	682599	86075	449957	2309013	271190	75833	387432	2380852	177287	11052162	13195648	2810925	234556	74478	3368735
1543656	5 25007	5 236161	151226	1635705	102971	860296	1510912	414706	92223	470827	2200792	316550	2233687	6092051	1867567	99953	188207	3355511
1429853	35860	4 75980	194312	156176	83271	675515	2325345	556870	107195	1040538	898329	97675	2485288	8933596	3562338	291014	139289	6004460
1832535	5 50306	8 34923	148557	551227	191144	412317	1392469	136664	161774	378534	944843	90412	1669942	4932989	1289745	63921	407913	1060345
1343744	36882	2 216863	259144	1307626	350771	463975	2064227	407801	206179	481578	751818	611496	1985562	10015976	1496409	176612	809766	2795337
1064054	\$ 52532	3 17133	108349	498712	111768	652823	1859592	293433	147933	953543	714755	170802	4196682	7631467	2909201	173601	84206	3389908
2457544	1 24334	6 221993	110429	1570645	155988	320945	2762977	272418	107836	527344	2677846	273185	2272822	8132045	2854346	180297	791787	3706915
1923018	3 24663	4 160647	331759	489451	445277	679940	1709027	530473	50060	558280	747766	277588	6720757	20399137	2308121	161953	610566	2640027
1505098	61723	3 245901	316793	874989	160283	323480	2395714	454628	208818	297042	1108403	107153	9223405	3209101	1538034	94028	122064	2898400
3200305	5 134419	1 21388	103071	1315810	211416	296325	1764372	26687	805729	72322	307399	312035	232981	6676038	436830	48524	438790	1261759
1904262	2 83856	2 23046	105786	1973756	115689	125374	2657297	104495	203117	159673	559027	92935	410062	5407506	1758097	20520	394743	2047990
1523229	77990	7 21189	151750	909448	105754	282990	1722932	114698	170463	339096	442221	. 120904	1056561	4561266	1108957	45819	437918	883008
1342563	3 16793	3 276040	310159	1547084	315133	522411	1011355	349286	83441	522953	1544272	311927	2136419	10607811	. 1705971	173309	1127000	3312032
1955872	2 29095	8 84758	360829	411962	144422	747955	845065	391569	77819	547100	1458039	157104	1494340	5658814	2916148	320505	527932	2476218
1970253	3 20730	1 123323	320362	366453	242639	485178	1745466	366682	109772	877432	634237	190094	4890220	8857657	2192256	174922	1240971	2276753
5442598	3 58851	1 9976	150908	1867358	273817	64165	1030778	61775	250517	231976	443682	238362	741218	4220032	1589731	101098	268058	859426
1784668				861518	190908	564471	1991695		118629				4077113					
557900) 12510	7 90449	84085	560243	135252	179941	462868	142910	50516	253836	845870	167592	3273511	4920539	786074	70851	312415	1373270
2355523	60432	4 100703	227457	1158358	196144	355985	1646622	233727	238710	380949	812160	191314	2523151	6149778	1655753	122341	569685	2001948
1373083	39275	2 106548	108961	617591	76710	222426	658720	172397	237573	258972	487567	88014	3087778	2483387	726282	98239	399895	
0,8				0,7	1,0	1,6							1,6			1,4		
1,3	3 1,	8 0,7	1,3	1,3	1,0	0,6	0,8	0,6	2,0	0,6	0,6	0,8	0,6	0,6	0,7	0,7	1,5	0,6

PARVA	MOB1A	CIDEA	SYPL1	TAX1BP1	RNPEP	PDCD10	GDI2	CLIC4	LOC1003374! R	RBP1	CADPS2	C4A	LAP3	AKR1A1	KRT14	DYNC1H1 L	TF	ADAM9
220150	637739	254221616	3140724	376309	85621	1308150	5259054	716320	207092	159902	53027	150069	48982	416475	686361	58024	4168335	72553
71368	218889	89732855	2044049	323683	294912	529158	4515261	514966	3981215	614816	34514	139371	38551	416412	488307	21429	2643051	1281
75355	335285	117581919	1788271	562483	221567	716889	1315036	1141488	3059184	467004	97538	352314	35270	206961	611359	21898	1156651	1218360
351692	113863	73887543	2124580	159893	412503	437578	6401667	643879	1081630	162189	46428	84126	41048	144224	560198	53511	5284606	1110054
106232	407195	112245315	2106227	474670	363663	568518	7814903	667654	575638	807162	237903	50321	103306	300532	807411	438593	1026528	476090
42911	314721	97707817	2007548	714155	217055	407265	3803855	929933	1971493	469213	203104	122325	65568	378973	282768	257612	842460	455184
206506	786573	285878442	3505816	689623	118006	624285	4923081	618531	1249024	352380	69408	188042	58644	695763	807046	248831	5251915	30189
143524	448489	163126554	3255214	207747	290800	873293	3370085	1477478	6788053	1196113	197450	87149	14794	309000	1372127	152617	1063843	373722
73655	326264	149748471	2395637	632967	255110	249841	3596017	466812	325822	692321	280328	97739	27383	217541	487779	225706	647901	458641
161641	276633	113752545	1923435	132471	974834	88715	8325308	171262	943632	62894	51703	405989	16379	95580	256205	252773	3430734	2118172
324537	304196	159733476	1527258	489528	558015	273822	3317223	295961	1053212	92849	528462	1297906	3910	37013	499295	148621	2259074	499738
284798	327918	97898627	2509897	466026	458393	324807	7926111	347101	933520	112259	127191	116019	80284	148197	678328	80212	2216261	1369367
194644	362543	266576901	2661144	628883	150827	734407	2756353	635551	479366	618510	106605	157512	30001	374081	471465	510466	877979	63558
102601	1055834	145161392	1406183	556109	164321	969662	1894332	1334857	3805604	595996	67741	62940	36962	604627	496652	475159	412168	1322772
118712	984169	262873708	2739706	551752	258993	1019784	2158919	1343912	4401199	859309	180434	156871	17376	428915	388621	124755	428348	616045
344702	376949	215963443	1274759	454319	272554	302023	2857906	523278	571990	162643	94788	537690	15178	189158	97837	29876	6023158	370383
152217	407844	149297758	2496554	438570	250516	683142	4675368	838781	2364166	528597	117421	146714	50770	358543	701947	156564	2679674	467179
102772	218438	79399094	680903	208274	112974	293903	1964674	325907	2189687	346239	81961	93653	26248	167148	320982	148808	1951494	470603
200661	501813	176463570	2054752	489007	386631	495383	4104021	639842	1564293	399598	179657	354083	28434	261889	422023	230946	2036953	852334
105012	321916	64615242	595790	159275	275716	358232	2545021	454474	1595142	322865	158560	416086	23328	191373	176356	177071	1942538	684583
0,8	0,8	0,8	1,2	0,9	0,6	1,4	1,1	1,3	1,5	1,3	0,7	0,4	1,8	1,4	1,7	0,7	1,3	0,5
1,3	1,2	1,2	0,8	1,1	1,5	0,7	0,9	0,8	0,7	0,8	1,5	2,4	0,6	0,7	0,6	1,5	0,8	1,8

SPHK2	P4HB	ARHGAP1	PTPRJ	GALM	СҮВ5А	EIF3H E	ZR	мук	RDH14	WDR1	YWHAE	GAPDH	AACS	PRDX1	GPAT4	WARS1	YWHAQ	RAB21
20165	5 757019	103338	2121873	2155125	123300	21589	746908	36816	171181	. 263755	3426483	1735669	1028030	1934709	7329314	955311	496456	4269504
10714	7 1184551	114434	2538274	1906724	73846	51671	394763	72235	218426	583423	2112376	705252	1033128	807439	6548366	1208735	284010	2669470
435459	908435	179349	2960369	2163833	246463	5652	502947	57363	177016	214718	2346892	1046240	1522822	936085	12856352	681372	590079	1855555
125890	552323	50213	619779	624998	91673	123876	168099	13941	56551	. 264100	1140915	575491	306951	574787	6338846	337407	236620	939244
254788	8 1274873	208056	1662603	2226785	294420	115409	318630	171026	145583	561300	2591909	774839	2317461	1202437	11345946	1665677	405244	1533810
217699	9 686640	172562	3063373	3245281	191047	0	247212	59958	160532	92647	2671535	527800	1001822	727298	9123932	1246558	394443	1540699
14611:	1 1310318	87625	2056944	1862554	281304	7	569383	56896	225421	462881	4327958	1461664	961745	2429135	9899607	1393198	763064	4081923
294243	1 2790518	180553	1744437	2963621	439769	201869	568751	96108	152868	395682	4077090	1156006	1736724	2440444	5901378	1097585	677170	2473018
21132	7 837129	110716	1884802	2271767	178510	57847	516535	25346	100600	622974	2088479	996678	2367948	1738087	10157908	897146	284862	2322875
31217:	1 246976	50417	483142	711414	77835	3254	97215	4553	52591	. 250140	331204	136466	978777	700931	6626837	112496	61420	2133850
22967	5 451406	57397	1175193	2683539	81766	20288	94541	20242	22016	144155	535800	110968	1965317	571219	13119993	197086	189372	4738884
155928	8 813814	68619	983494	1411791	77868	19498	176975	3301	47296	58369	1036323	454513	926314	996490	7614234	464308	190366	2322450
42088	3 1415290	116814	1496263	1777157	471800	73874	470819	111190	168622	272819	4084237	1183960	1873902	2794102	12936811	1291040	664313	3436102
113333	807366	124636	2460533	1420004	939427	1234	586452	57387	225217	414401	4243732	1282043	2148430	3893387	8841076	1651961	709997	3180766
156062	2 1150948	190967	3256487	2643868	729317	110415	507452	156313	202411	. 309117	4850493	1335076	2016876	3150882	7227995	1920220	733154	2373607
97493	1 466915	33881	913118	958486	749321	803	76489	49542	90758	21984	1405166	946455	510725	1456290	15135326	333336	353208	1071172
222874	4 1183085	137016	2095957	2143615	217728	65009	439586	70543	163447	354813	2836895	997870	1238585	1381542	8667968	1073230	480886	2420403
107219	708090	55570	790244	786933	123214	74426	192482	47157	52063	174490	1058146	434501	607112	771243	2557971	415978	185910	1214051
164760	773731	94181	1581629	1734753	413231	35901	315810	53484	113689	261745	2321929	805770	1598536	1912673	10207522	858449	398337	2697463
84924	4 384735	51601	914437	743548	355186	40511	222834	54437	76129	196020	1808459	501479	686508	1229360	3173741	693911	266008	1088569
1,4				1,2	0,5	1,8	1,4	1,3	1,4	1,4	1,2	,	,	0,7	0,8	1,3	1,2	0,9
0,7	7 0,7	0,7	0,8	0,8	1,9	0,6	0,7	0,8	0,7	0,7	0,8	0,8	1,3	1,4	1,2	0,8	0,8	1,1

FKBP4	NT5E	PALS1	VCP	ABHD4	A0A3Q1MQ9	CSN3	SPPL2A	ENPP3	PLIN2	LOC782884	SLC5A1	SYT4	PYCR3	UBXN6	ATL3	CKAP4	F1MZQ4	SLC16A1
24789	4243928	20403	1061286	309460	890995	47148359	18021	16859508	3320453595	117378	6665715	1861486	132526	242671	227119	25907	8641352	5605344
31058	2385241	76119	1286799	224704	986857	30412557	185924	13819687	3170644059	3650	4901714	1873431	115511	580515	282151	73147	6634432	4966618
89046	11254490	147911	510414	496260	506725	41321917	241668	29087672	2322576722	11710	11225281	2551187	59453	885259	261322	25547	1146288	6925547
24952	7071548	123324	880626	361458	318779	117699649	506231	31269029	4541495610	53628	9047344	1625530	21755	455211	102667	80960	729871	1535135
77311	3252225	158414	1096980	487154	170695	39154554	173152	14986517	2404907347	2712	7921977	2081646	83242	672854	314103	71386	8209046	3036553
163605	5009836	83740	811035	390922	1031090	53771033	254724	25036971	2245905773	24723	5706859	2057834	111259	334627	100179	114264	6794326	4212299
55167	11961192	47437	1111561	384696	122735	88484445	30778	15763760	2835317002	59114	5575202	2372014	113178	197200	303898	56295	1137136	5908878
52433	5690714	207236	734010	409802	506581	35487387	272514	15858877	2277998048	96845	9741337	3073017	131201	630603	345889	81575	2151752	4152466
42445	1490580	49518	1868138	331291	1124895	16038459	303979	21252691	2195808929	21731	6225515	1882269	72119	527061	397388	74050	9116541	5916135
2384	681090	233059	2798644	462124	893169	28703738	242159	74176507	6350759763	0	2916786	589337	5342	165078	227084	60812	2055057	517022
16966	7982956	339825		238523	1170084	50796962	357552	54778235	4353991487	40053	4150599	731006	21285	340684	281091	28961	3155260	2527484
22603	5877164	145116		321245	478209	53400384		32639309	3754120600	8871	8816407	1416712	12440	322245	126279	20112	1329236	1236596
44346	7989894	36517		307721	357765	30309807	35239	12727895	2854750807	0	6824252	2496184		142852		71210	7317347	4917209
152864	8245212	160482		248885	1485830	21038012	220616	16496263	1743488392	2387427	8316539	2771991	339267	753689	107398	141841	3139222	5504892
78595	7032739	149815		431221	458937	35097057	192427	14530595	2287868285			3929984		654309	303589	63064	10979446	4898356
6289	6293246	82769		403283	282530	72532227	300010	33491221	3254647525	29631	3994024	1340362		199512	69662	19476	1956588	1509889
64795	6358647	108073	936589	383057	566807	56684988		20335252	2889912270	46220	7598179	2187018	96016		242166	66135	4430525	4542855
46414	3546453	62293	249599	88954	362523	30510775		6993235	787506655	43434	2260337	462787	38716	235767	93775	29794	3442867	1708328
45812	5699110	149638		343037	781427	38489581	257403	32511590	3349429474	315452	6383155	1894731	132259	388179	287386	59941	4881087	3378448
49810	2976138	100399		82146		18956703		21813197	1486673810			1125540	154436	231723	230218	40050	3707748	2159050
1,4	1,1	0,7	,	1,1	0,7	1,5	0,8	0,6		0,1	1,2	1,2	0,7	1,3	0,8	1,1	0,9	1,3
0,7	0,9	1,4	1,5	0,9	1,4	0,7	1,2	1,6	1,2	6,8	0,8	0,9	1,4	0,8	1,2	0,9	1,1	0,7

DNAJB2	PAK6	LYN	DNAJA2	TMEM30A	SEC23B	MROH6	RPL8	/APB	RPL18	NDRG1	YWHAB	ANXA4	MYO1C	RPL4	ATP2B2	AZU1	A0A3Q1M58 (SBPL10
217888	181306	1981523	824820	609763	73134	10051	154894	349727	29631	1375195	1089141	225423	852127	273106	1816583	354	234820	541593
143746	190975	1158525	1008853	434018	117989	32427	144645	95078	63394	1000759	656148	89208	868865	414242	2649842	47892	861385	332080
345770	169532	1960883	1023074	637305	75445	15677	156296	200437	85477	1223182	1289887	131080	987446	325270	1647297	5562	199173	1082105
94889	104077	824080	332828	494838	134147	12165	77428	118529	93889	2827323	389105	82784	322778	578463	4855848	14299	324296	461549
169246	177646	1162780	967021	978193	274324	45543	227810	268524	254267	1652561	948259	191829	985405	1389707	1736805	7905	624285	774981
178210	126016	739253	1267523	488004	137933	35694	299441	373327	14932	2628271	935249	70734	767737	583095	1827257	1410	120927	922942
174983	232199	936299	439795	379555	113270	21664	283282	442807	53041	1542422	1715704	162431	1012381	335969	565354	321597	4437917	772661
252780	300733	1320093	841476	517195	180389	22985	410312	462357	454444	1393787	1592363	316152	1181523	1243814	2082049	5313	448780	1057246
150320	225971	1134146	760329	568213	273992	60975	206569	160843	177852	936259	606720	51539	1047165	698080	1552601	0	34070	669208
50409	150800	1284359	90973	78431	377507	11994	26275	129575	43071	2742518	75045	67871	283304	1490632	5645133	96767	249957	96431
68047	146657	620119	326929	144008	184873	42470	47258	145447	54641	2610219	397944	20653	296186	269655	3313724	0	13605	474106
80966	138656	782700	270961	444100	297758	69239	35033	172638	5167	4525181	349574	31449	359860	382992	4045983	1727	271235	369480
144100	262407	916942	632641	1248816	184284	21634	550544	701982	184455	909093	1600872	172410	967473	1019701	1594532	49785	2110094	457419
280193	303849	757986	1145527	505704	109015	12332	335635	1235039	220821	1856084	1586896	197481	1279058	687728	1614218	1567	278126	1103624
302984	345332	1120555	1270410	728808	134752	36682	372694	986834	561944	1891984	1978573	305335	1111295	831350	1331404	10529	552106	1340495
141106	77818	778441	283089	246075	59755	16784	154071	384648	521253	1640000	445941	84948	265081	816913	1720929	255942	1235442	289230
197189	185310	1260429	838174	567359	138329	24526	219263	288848	131134	1705437	1076982	158705	872283	642958	2147629	50541	906448	743145
76112	60935	478267	311340	186164	64948	12422	107500	141137	150074	662781	448170	84047	254845	432711	1237850	110590	1447641	276885
152266	206436	924406	597607	495519	202742	34014	216010	489626	221150	2138917	880196	116461	701178	774632	2602315	52040	593079	599999
93982	92660	231072	433614	376005	106342	22205	189709	433532	212304	1172875	722198	99530	437212	377873	1573664	89283	725499	421941
1,3	0,9	1,4	1,4	1,1	0,7	0,7	1,0	0,6	0,6	0,8	1,2	1,4	1,2	0,8	0,8	1,0	1,5	1,2
0,8	1,1	0,7	0,7	0,9	1,5	1,4	1,0	1,7	1,7	1,3	0,8	0,7	0,8	1,2	1,2	1,0	0,7	0,8

PNP	ELMOD2	KRT6A	TMEM43	EEF1D	ASAP3	FRK	LRRC8C	GFUS	RPS9	INPP5B	HSPA1B	SLC7A8	PRKCH	ABHD5	LRATD1	RAB1B	GOLPH3L	CNNM3
84079	157083	244853	302607	287156	54238	499	2 898720	1 107717	148083	130455	1601916	288069	1187404	128100	128786	2931030	1565718	1077884
19604	107342	31707	367253	344821	70504	393	4 9242699	9 192241	70304	126270	1371376	185696	1138957	242204	116101	1142091	827981	905895
59378	443249	298069	379725	307316	170977	539	6 8846242	2 103937	17820	94920	1876003	386623	1209542	219494	134176	2602037	981815	689993
201749	746952	285459	887189	209184	32453	129	7 22096903	3 78530	21804	145488	700347	116293	564779	104783	15621	1313001	2244341	306999
42648	180750	432738	455246	801745	132317	791	0 9506393	1 209406	215527	159894	1352462	139555	1303424	279575	53979	1895323	1477568	856773
249896	633550	79553	460530	370983	70909	31	672804	7 143426	38473	91903	900125	354301	726763	157602	31817	1918133	1774472	375802
82477	183452	86104	602790	345030	49916	162	1110341	5 90491	179315	121505	694484	216480	1190745	207060	45734	3211462	1292330	1694754
78759	550768	753886	633427	610244	105613	406	613740	5 153759	425463	122221	1401270	242889	773684	304114	181983	2638486	1639223	1021932
81404	142633	109863	456102	223583	76497	881	0 1170823	7 112164	220387	166794	2111315	239249	997500	200806	90602	1355772	1246630	773540
240333	831273	161629	469976	125408	8831	159	0 2350966	5 47791	131559	261334	547440	106337	188212	104231	110814	1481812	3554343	394756
423022	114457	379957	566037	96806	35947	90	8 1801607	60579	35407	230036	718786	274444	282704	429915	159608	2372936	2534271	406272
225019	776473	709289	590279	97883	31410	267	3 1986817	5 93874	30300	242423	728155	38919	543407	97314	29699	1495974	2342337	240401
31752	165913	109307	836357	611213	83475	794	9 9462428	3 126993	482865	69980	848800	163716	1838958	389483	106025	3461535	1477326	1483226
158813	734743	90324	380194	665479	92159	447	3 1101398	5 172230	321616	56879	1638971	262407	552035	192900	99357	4530849	1184270	794868
64004	380594	38546	412207	898022	141404	605	590163	7 108966	415206	82594	1607648	197809	1341301	307754	109579	4825124	1114635	1090788
263891	758566	206592	1072325	239867	27541	306	5 22266962	2 24873	50895	187917	366297	241010	498511	370415	19203	3543662	2655321	227939
102323	375393	276546	511096	409560	85866	369	.3 1033103	3 134938	139599	124082	1237248	241238	1011912	205367	88525	2206445	1475431	866254
80350	249084	235680	189703	196219	46900	250	9 500678	5 47980	137771	22935	430227	96927	277989	70898	59468	754912	449127	437766
186030	488081	225689	597935	369783	62158	444	4 1521839	5 93434	211030	162245	1070926	190486	780329	261602	90611	2883458	2013642	676474
129326	318306	221179	239453	309649	43939	291	0 6522558	8 47495	178631	82360	627299	82787	569267	130288	45751	1400928	889351	445559
0,6	0,8	1,2	0,9	1,1	1,4	(,8 0,1	7 1,4	0,7	0,8	1,2	1,3	1,3	0,8	1,0	0,8	0,7	1,3
1,8	1,3	0,8	1,2	0,9	0,7	:	,2 1,5	5 0,7	1,5	1,3	0,9	0,8	0,8	1,3	1,0	1,3	1,4	0,8

ERLIN2	CHMP6	DHRS3	LRRC8A	PCBP2	CARMIL1	CEMIP2	ASNS	PNPLA2	TOM1L1	MAPK13	TMEM63A	RP2	CHMP7	NCSTN	SNX9	ІТСН	RPL12	HSD17B12
511341	431935	7355212	3101283	343792	48775	643306	705043	3011037	706070	968187	168836	2662179	597289	710934	430682	84157	34126	71265
511856	374567	3304955	2694355	217411	240458	591511	882389	3532769	811580	811913	237737	3048154	1153600	608373	581075	122723	32202	98971
415864	529266	3081445	1721895	373015	138913	582491	975750	2395467	315890	914154	423525	4611882	488726	927554	442893	153392	14828	69154
164387	247420	1083571	2310617	405435	955907	399490	274863	352697	744687	341797	79887	1183261	206140	1397805	1077067	41918	26652	26318
256060	398233	2769045	3831847	465414	568197	406151	1415487	1050195	640185	653854	290365	3242550	512983	405069	622040	87873	98506	253948
559721	352738	864777	2194458	392060	78529	410708	622329	1701234	229595	559780	364817	3285045	481807	590173	528809	164027	49991	99432
516709	425226	6336392	4104028	355272	67071	202037	1033421	3545251	613206	975546	392753	3077082	1058043	1259397	411839	169614	136175	352028
358533	442378	4120168	2521656	594113	446320	759960	1306495	758703	455717	799397	339155	4232105	766405	401980	597469	87833	265041	283615
340478	246810	2781260	3653899	290779	358415	859364	1013541	1300822	702051	642834	225401	1996615	1289409	546273	609460	80413	79042	151730
45373			3292744	274531	317582	288301	421775	1032894		369556		812435	740534	955878		11499	188338	57325
72730		1297842	4116490	281000	356820	169261	436088	606766		346212	87628	1700868	1291862	1746305	821430	38493	4270	97226
127516			3263449	342514	419463	160131	308480	494695		531476		1250684	697627	2561913	890746	35507	20269	35109
540899				598298	308297	329667	1687107	1940568		907742		3147671	1080154	729400		140696		610499
266587	420075		2597524	314106	179420	532595		1339258	141230	651523		3834301	658528	647946		72268	144798	293118
305099			2681827	389780	355975	705832	1080508	2147901	491358	1025929	439292	4998354	536603	788430		99003	230972	397010
131176			1923321	368287	211627	76687	289137	898017	728364	269151	125713	1413434	158810	303636		9456	250696	258034
411809				393314	318021	499457	901972	2043419		753079		3167782	658124	787661	586484	113942	82190	156841
141990				107518	320015	176860		1261887	209578	221578		1031922	317580	375412		45790	84585	120885
228732		2776966		357412	313450	390230		1220115		593053		2394295	806691	1034972	777997	60917	147989	237506
166870				105855	80468	281348		590615		270421	133406	1455704	391720	748467	462073	45612	103241	195866
1,8		1,3	0,9	1,1	1,0	1,3	1,2			1,3	1,4	1,3	0,8	0,8	0,8	1,9	0,6	0,7
0,6	0,7	0,8	1,1	0,9	1,0	0,8	0,8	0,6	1,1	0,8	0,7	0,8	1,2	1,3	1,3	0,5	1,8	1,5

UBTD1	SRPRA	RAB18	GNAI2	PABPC1	GC	PTBP1	A0A3Q1LQD(FB	XL20	PSMD5	ALDH3A2	PLPP1	ATP5F1B	MAP2K2	STK38L	LOC1019027(I	MAP2K1	RPSA	SH3GLB1
1208316	878980	86889952	2610103	14624	193888	12873	123765	692766	18844	140353	584146	428718	1340658	344610	32063131	216322	123439	35428
794827	859229	41644239	1561623	23819	61756	85483	91205	603649	77801	163984	324914	985397	1646129	497765	25420589	417698	163295	16871
480485	687500	55294414	2278230	51213	76868	26997	22623	614787	66359	57028	1141752	744464	2746069	658496	38960640	859034	119487	285946
129138	107658	37893521	3871594	35007	154352	8471	37530	171952	8457	44422	308658	1002386	662909	549027	14941353	265268	134956	11726
521642	926286	51988411	4039050	182128	115559	144844	189149	481754	160446	266463	499778	3306460	718161	398430	26841077	763784	247196	70659
423591	534638	52538875	2657625	23627	106845	102093	8970	650119	50034	188110	509295	524057	3112468	290815	23084397	405863	137331	30375
1129702	645249	82784605	2447274	2224	35442	109196	227469	733836	43606	185744	672983	1514109	2596888	398337	29532599	264121	160176	93528
975505	857997	70450944	2949237	157358	188439	169919	260678	365601	123992	323442	794543	2758033	568109	403362	27352362	456611	628860	58277
828027	1277436	60094696	4022541	39049	88795	108385	103486	379850	80773	181127	608335	915406	873793	451384	31394633	351107	241397	11365
272306	227777	33160127	6783303	91722	148108	52783	35424	177311	41071	75240	72522	832516	640855	650063	5122200	140052	294522	321
846262	195688	48793998	4129759	0	143711	10880	1509	155480	18684	325693	238545	540749	3281537	228354	22610205	116578	180576	20772
540525	170633	44029210	4466256	5379	216517	4138	23011	149428	2635	173148	148140	1381678	744503	568658	14672450	244224	86011	8932
1301811	1028977	98665403	4106389	111105	12598	139534	394443	822700	3653	390086	709589	3390757	1899490	371401	33838597	333306	374046	51866
776017	914551	107225748	2016788	105809	39253	35264	20525	760801	132031	99861	819171	1809383	3408710	254147	39439830	570272	202551	17177
1003845	895834	118876544	2731777	146361	79076	161562	400968	772149	131087	214723	1058023	3137438	692228	437143	40000537	889421	219380	137605
202912	125633	42672067	4668808	15632	33565	18262	19893	271052	9070	96305	338910	1610202	938980	231369	13591545	91068	321559	14392
707901	687192	59935620	2801842	61250	116644	82485	120173	539308	68692	171193	604509	1407953	1673924	442605	27274519	456088	214342	75351
379795	270874	18201349	818742	68777	58345	60996	96788	189715	51625	94764	271394	1066486	1024072	118967	6947664	236580	172352	89506
721463	604566	69189724	4115703	64382	95203	66351	124908	436096	52376	194523	499155	1702266	1560012	399065	25083750	342004	240005	32804
368360	469138	33631213	1407864	56076	69615	61642	171072	299076	55205	112967	352495	1052764	1172062	158105	13039117	271520	89973	44975
1,0	1,1	0,9	0,7	1,0	1,2	1,2	1,0	1,2	1,3	0,9	1,2	0,8	1,1	1,1	1,1	1,3	0,9	2,3
1,0	0,9	1,2	1,5	1,1	0,8	0,8	1,0	0,8	0,8	1,1	0,8	1,2	0,9	0,9	0,9	0,7	1,1	0,4

PKN1	LPO	CD47	PRDX6	MSRA	ACACA	EIF3L	IST1	LOC1008487(0	CAB39L	ATP5F1C	GNAO1	CAPG	DHRS1	GK5	TMEM263	COASY	LRRC26	HSP90AA1
51332	79975	1 4126832	387499	167940	20454389	3583	9061	1563686	136921	4946	8565907	215195	4002119	885881	4365100	21913	326635	1937635
87194	75190	2 5466289	156460	7441	39590692	29838	89826	1995186	122863	8321	5069006	217069	1061026	813651	2776695	75815	174593	1722759
84417	77746	8 6775698	291026	74223	22588704	45502	16800	964482	121081	19534	7276419	206219	2369728	573714	2439239	38538	137979	2072921
55309	124544	0 9060640	162015	101721	8165981	6051	62329	75236	16255	1675	4364126	192291	3314348	1714239	1699710	18784	203269	739589
313068	142744	5 2162107	149295	50547	48701261	46092	13766	1056287	115579	70365	5880222	644624	4137221	1051665	1684194	147496	598702	3109930
140825	5 79409	7 2104076	164945	30752	51716730	23496	69434	1847226	61388	16472	3769010	318870	5111220	1831005	2387345	52472	432356	1837118
62616	238912	5 4527530	219399	77976	26388899	9439	0	347025	117121	60313	8352418	233987	4974180	1248348	4822262	44116	542942	1658066
213707	182883	5 2577275	413213	101326	23409615	63591	28669	1154033	140550	76250	7049364	511108	5967995	1552208	2858689	108370	522597	4094833
248868	8 83018	4 4359214	199078	13105	22234935	36927	40066	2471067	58785	19113	6492314	285343	4334056	1033541	3065403	91278	149805	2977991
104754				53966	34940222	5201	38111	1441159	39821				6839259		2881585			546055
48477				86016	21825629	2513	31367	1210484	53425			65095	3730257	1658108	2961243		36228	1385644
111478				60269	8468522	9910	4534	203920	35202				4531327	1727776	2196388			630653
232393					32663474	25847	13142		148196			402490	2643759	892988	4163800		603233	3747236
60697	70390	2 3523605	377796	122171	28016578	45610	107193	2252619	97816	80128	11139010	276548	7727021	424095	5083917	39965	157288	2343857
138614					21805362	40644	10643		156874	143411	8240092	555740	6964703		4118984	51381		3023382
16086					6691112	8079	23873		58113				6354844		1810357	91176		1075135
126058				76491	30127034	28449	36235		103970					1208839	2879154			2146606
93145					15082863	21860	33050		42909						1149474	44832		1018856
120171					22080729	21841	33616		81029						3285209			1966244
83939					10246201	17502	32443		47997	63895			1817437	617924	1094098	29589		1218172
1,0	,			0,8	1,4	1,3	1,1	,	1,3			,	,		0,9			1,1
1,0) 1,	2 1,2	1,3	1,2	0,7	0,8	0,9	1,2	0,8	1,7	0,9	0,8	1,4	1,2	1,1	1,2	0,8	0,9

OSMR	ACTA1	ZDHHC20	RPN2	TSG101	RPL10	GIPC2	RPS2	TTC39C	СОРА	EIF5A	PAK4	STXBP1	PSMD3	STOM	AIFM2	RAB25	CYB5R3	COPG1
164731	13544638	551885	526441	656273	274831	24156575	66272	6828	109388	2037412	722137	79266	113075	60373522	140791	5047864	48945774	11533
283606	18355798	309176	986431	418514	215779	18731553	64431	20401	141755	1684866	540243	247073	156298	91349651	313468	1783318	22467884	41491
238046	8733833	355325	290805	136968	271668	20683868	51362	84733	86453	1481287	644082	128278	80040	45803924	202998	3110348	24836033	66704
165856	14172765	321219	1227796	179476	173178	9702983	19798	16547	122843	928981	253066	154547	280821	43134514	75011	1868010	12809855	87039
201750	18661697	155605	1062458	341710	460338	13178444	168852	79683	569718	2187940	446464	390088	511390	39847355	271145	2112387	15500960	294607
51483	22708149			316171	185417	15738149	30718			1668968								
207227	17045928		956911	634837	398478	23520110	85331			1778909					225860	4357330	44437268	
160098	19785706		1581004	353776	768417	20193277	242330			2361375								
168637	13167254			385280	347318	13428170	101640				535008							
271266				510092	303035	5699257	178548											
299063				382486		12742010	62056		381540	792417	136196							
298064	18712412		1083130	407463	153118	9841077	39129			776689								
238344	10109555		1623092	462706	896783	26400686	193035			3052732						4922255	29385753	
31847	10950581	470197	432264	303094	606945	18034936	125812				701998					3521649	21111300	
227994				238658	929757	29829476	191307			3758783								
316985				299903	685518	10688852	289971			1520208								
184100	16626064			379716	343513	18238120	91137			1766217	584317			67916975				
68169				188321	199075	5038056	76145		219472		172966						13423532	
231525	15635134			373710	508323	15833058	147687		321842	2067462						2707536		
93927	4396933			89876	315441	8390653	81830					78743						
0,8	1,1			1,0	0,7	1,2	0,6		,	0,9			-				1,3	
1,3	0,9	0,8	1,3	1,0	1,5	0,9	1,6	0,7	1,3	1,2	0,8	0,7	1,1	0,8	0,8	0,9	0,8	0,9

SAR1A	LOC10029918 H	ISPA8	PI4KA	TLR5	CIB1	ACTR1A	CNDP2	OS9	IMPDH2	RPL3	TMBIM1	ARRDC1	EPB41L4A	НР	РНВ	SPCS2	EFR3A	LOC523126
6168849	1531101	14052058	112336	656318	265167	191938	1282737	45008	76659	33139	3370472	280237	27676	20091	11874	4 135671	l 178347	1065745
3370327	2346252	11078066	45241	385818	183733	107710	894065	67773	164622	257138	3089234	244679	29560	285530	20584	4 159671	l 118961	1477946
5310904	1064929	11955207	103300	1274207	417259	232921	806696	58630	31652	130663	5843183	357735	93351	0	1839	9 117867	295706	646204
805108	1373230	6117322	81442	427366	428224	252069	481506	11090	38016	54578	6582117	85660	24527	22740	(0 15647	257086	196696
2583967	2252867	14415107	179310	857929	248885	452020	2155611	151594	639270	779114	3440695	267558	39395	83954	6622	7 39631	357917	1989193
1740227	3462122	6326820	61323	349742	354553	135794	685300	5891	10468	273887	4106714	317503	56816	2843	17803	3 325063	3 174148	1739839
7634330	349561	11445384	185851	440053	631412	183952	1067291	39569	81030	59626	3422831	. 409323	13149	743480	10670	0 0	268779	407895
4739220	958416	12064999	161970	1433580	571397	262743	1620978	218347	796480	724769	3065683	189169	29033	3290	118644	4 143388	3 405775	620399
4901527	1177477	17909468	175769	706510	297206	308385	956320	90686	276784	336010	3264034	206970	6631	0	10659	9 131922	332612	855817
2012760	2324857	3651884	129863	313342	666838	249434	1397613	13223	40862	15209	4091763	80911	3299	144280	4938	B 907	281574	191091
1896708	1421763	4215081	359770	684928	143540	165431	821232	6389	6508	59783	10676616	94130	95426	0	188	5 53421	490639	227373
1508192	1063437	10563883	203565	336954	478809	108231	751984	18021	11796	29794	5215582	108331	. 67610	3744	905	5 16593	568182	221424
7998505	2569770	14311828	144380	661733	422136	173004	1272702	166857	574528	301483	2099299	273063	21765	88792	19451	8 3589	216912	2969060
9629022	3413401	14816749	31431	754843	499323	120645	855639	108513	237172	339901	4647436	391600	92212	0	47652	2 223570	103423	1651339
8519503	1223265	12424865	44482	1552446	790716	224291	1746161	143356	219263	636034	2161232	301144	46755	10667	18065	1 163739	9 157656	748959
2941069	800798	3998545	264051	112707	1026173	213771	824225	5305	4392	194924	5113864	61788	23792	718876	77754	4 37337	199377	103564
4044116	1667310	10931871	116347	728126	387579	227393	1124273	74738	229775	289114	4115116	268983	39188	145241	42959	9 117117	257090	1017990
2326161	980676	3136676	53938	422859	157045	105698	547518	73436	307705	299869	1347735	100444	25258	260088	47762	2 104269	97145	656961
4925911	1749346	10236538	169164	640433	540593	195399	1078234	69044	171413	239142	4658728	189742	44686	120795	65889	9 78884	293797	871078
3332899	914542	5604644	109045	435765	280491	67022	356043	66358	199223	210117	2719956	5 122114	36812	247525	7953	5 83625	5 162697	993791
0,8	1,0	1,1	0,7	1,1	0,7	1,2	1,0	1,1	1,3	1,2	2 0,9	1,4	0,9	1,2		-	5 0,9	1,2
1,2	1,0	0,9	1,5	0,9	1,4	0,9	1,0	0,9	0,7	0,8	3 1,1	. 0,7	1,1	0,8	1,!	5 0,7	7 1,1	0,9

SCD	DNAJC5	A0A3Q1LYA8 SI	MAD5	MUC1	PSMC1	OSBP	TUBB2B	PSMC5	LOC782057	MYH1	ACSL1	DNAJA1	GRTP1	DCTN1	BSCL2	SYTL2	HSP90AB1	PSMD2
3630632	1308176	2201329	340383	32937354	59095	1646903	681639	18156	589526	219688	92232224	3466014	448727	130694	2679941	89064	2165964	82766
2946491	L 984098	2714295	505609	12212498	89539	2377610	872258	67535	1029517	308099	105966818	3488045	216549	62027	3367688	163110	2656053	162162
5747437	7 832374	2773410	684289	12342770	54810	2174433	957848	49881	535552	84714	78487739	967006	242263	61723	4161972	195946	2799471	158205
1492075	367905	2002752	1028252	10262314	61317	658696	1086801	43	258840	43202	123208931	735815	79668	14415	1891451	13144	1343856	71007
5180964	858664	3894743	415659	36385894	124732	2271451	1636525	191671	721975	221273	70911409	2052796	228427	201754	3656691	173887	4322433	463441
3113087	7 1291355	4953606	172371	29800963	107824	993770	1024024	95938	872046	257751	86602355	726195	121464	88971	3671687	89647	2075867	40064
4626246	5 1474264	3081049	443834	15946485	160777	2314284	1027509	12560	761289	140525	97695277	3160813	220258	119593	2867332	124358	3825603	161964
7881150	972871	2639453	334296	13838021	234246	2038215	1341839	208420	494787	150592	42901902	1999955	457108	140183	3335340	113923	4976140	910576
4043073	681640	1939456	513613	8006172	154404	2124947	1151152	137921	521161	280402	94441569	3058838	8 287997	207501	3045523	157282	6162502	395577
1727600	58893	7800893	297640	16694669	198816	270630	2741698	89870	183042	74573	227854949	380588	121730	37106	1754831	142829	2218059	49597
2442522	431983	8487524	713664	30610284	247658	1177295	1459779	60778	246167	84034	109786938	1309565	115806	35706	4229038	55231	4335561	87125
2836704	1 329303	3852569	1057811	14781640	107550	761870	1292178	13177	297012	98772	132747080	308439	114901	23110	2460065	162103	1235108	100279
8153637	7 1742903	2708286	600635	54134426	216988	3048370	854334	98196	733106	357329	57151521	3569657	342954	246947	4409893	172904	6363572	440528
8443483	3 1889869	783261	260854	16145773	14011	2170336	886810	104504	876485	161677	56516954	2080061	433123	84366	3728225	91504	3574515	185191
8810477	7 2496823	2423449	668248	31338311	156556	2951380	794909	99262	840218	174831	44491906	2265210	517048	128207	2046348	113761	3578425	450104
2158846	5 483664	4186404	371562	16658913	146183	560370	1347549	53798	263016	92328	146211325	238723	189416	13400	776452	74609	1408769	67204
4327260	0 1011213	3032580	490587	20465788	111542	1809420	1078555	80525	657941	178231	87250832	2074580	251808	102420	3204013	120385	3020673	256273
1977355	5 348955	964407	262646	10681745	61695	653850	293006	80216	240313	89382	24166655	1192660	136499	58065	706721	58409	1241147	295097
4827043	3 1014385	4022730	560503	23546273	155271	1633150	1316051	82188	495026	165493	108650280	1651385	265372	97043	2806297	121278	3609564	221950
3093783	8 895123	2761581	262073	14705258	72267	1085308	626886	38243	286440	103381	60816731	1295714	155575	89140	1277617	44039	1965748	176458
0,9	9 1,0	0,8	0,9	0,9	0,7	1,1	0,8	1,0	1,3	1,1	0,8	1,3	s 0,9	1,1	1,1	1,0	0,8	1,2
1,1	L 1,0	1,3	1,1	1,2	1,4	0,9	1,2	1,0	0,8	0,9	1,2	0,8	3 1,1	0,9	0,9	1,0	1,2	0,9

PPA1	LIFR	WBP2	GNA11	EIF3F	ABHD14B	TMED4	METTL9	PTP4A2	VPS37B	RHOA	EEF1G	CSNK1G3	SQSTM1	RALB	ANXA1	ARF2	DCTN2	RPL13
41568	8 803	14 261250	9231667	95198	494414	763787	3713559	563233	163797	9007613	480627	48721	729260	1352498	811366	838085	194442	215655
7860	0 1823	19 148292	2 5623221	229111	202528	800943	1734740	231016	75320	2094431	855513	106741	615425	407678	1455216	1787873	285525	166744
86278	3 1377	62 342326	5 9390527	11596	198543	474037	2108129	306735	154212	3871108	802553	73195	1042975	526221	400520	1059829	170277	281849
41249	9 684	47 70697	7 17653929	66360	25550	684733	667701	384929	42180	2831882	780845	83812	200782	210060	1291154	714753	98716	575558
213498					310280		2395410		92066			156274		390626	1066584			613284
283072					300221		1592340	462597	136297						382265			235244
53469					463073		4978480	1448922	16202					561780	4694573			143688
104013					591464		2754483		149988						792913			679708
49540					406555		2661607	198355	78464		1047386				206252			348312
281129					301688				8951						3788864			
43734					194495		2312600		34623		447287				932980			117169
186330					172564				31343				123575		740594			
4068					597399		4998346		101379				908422	1019645	1420121			598449
145724					256183		3418642		232099						151405			658411
13992:					910275		3271728		127544					680788	465353			
27462 103870					146706 323259				43887 103758					114478 572900	4186541 1361824			321015 363966
95620					185255		1342240		55741					352770	1361824			220179
109738					373233		2622187		82286						1399919			444352
9514					262440		1256462		72300					319937	1486514			272372
0,9		72 90304 L,5 1,3			202440				1,3						0,9			0,8
0,: 1,:		1,5 1,5),7 0,8			0,9	1,0	1,0	0,7	0,8	,	0,9		0,9		0,9 1,1	0,9	0,9 1,1	0,8 1,2
1,.	L	<i>,,</i> 0,0	J 1,0	1,2	1,2	1,0	1,1	0,7	0,8	0,7	0,9	1,1	0,9	0,9	1,1	1,1	1,1	1,2

RPL23	OLA1	ABCE1	PGK1	NBR1	QARS1	EHD4	NAPG	LYPLA2	HSPA5	EIF4A1	VAPA	CAPN6	LMAN1	EPHB4	ALDOC	EHD1	CEACAM19	RAB5A
205423	204674	1966	7 64886	725055	9125	20782693	3109396	133861	572346	548097	178971	9421357	1019399	62003	294489	472442	80191	3115387
156713	150110	3656	6 109210	423251	17771	25265097	2270925	82438	346232	1098919	130463	9327532	2209016	26439	255725	751860	62369	1354030
48648	173984	2257	7 34133	827888	21113	19100907	2121419	94761	573653	768564	277847	21992351	437660	63411	110672	1153038	541125	1892520
104326	259423	123	1 77255	129377	16657	8939703	802806	68519	895422	562083	73129	8510289	182709	15340	302863	600971	37566	747012
288197	520722	6572	9 183540	363285	392414	23245075	2935738	168048	964068	1416528	178945	2847652	924559	90882	506334	744703	116481	1308026
386139	157134	2171	0 30151	1459334	8406	16082108	2105415	154098	566072	777638	300340	1779080	1615876	39863	368105	470674	133248	910916
2690124	198615	2989	6 151309	493895	40495	20009907	2308264	202149	412065	707458	163803	2319491	1082359	34012	246247	283198	258103	3292361
713347	493076	7318	5 75846	273242	177775	17368036	3388547	186544	2126841	1335992	236805	1589652	911079	50250	296909	679234	122835	1958250
491479	302142	18915	1 113644	736727	154189	23239360	1741199	124630	499580	1150066	150646	14297110	984176	98053	362698	546653	71753	2111636
247233	215928		0 130237	75683	43624	10527622	1066506	133529	1377908	631810	52763	4303160	128320	28880	382851	793411	5153	261155
109906	151903		0 28558	177415	16094	21946354	708769	43497	824625	912882	189999	30605756	734779	77943	241463	787700	237968	503270
192173	427437	173	3 75044	460163	14723	12926388	1811629	96780	386661	376135	115539	16206766	273637	63871	422968	610511	46132	800937
917804	319609	21522	6 36491	303598	217939	21811025	2189561	142859	692921	1478776	308993	3661400	1849892	45680	190030	317755	127386	2531574
312708	170072	4173	1 68298	825400	57496	11648266	5264303	206606	703074	634533	777450	3085590	1621569	19568	118613	737550	297094	4128671
525596	315580	6796	2 56537	712589	110372	20294485	4025204	326373	680818	1109567	544498	2607850	915736	91158	264872	869415	188152	2953947
165267	151118	770	4 54502	311098	3247	9475827	674711	102646	686967	827065	136026	1182414	277342	27983	269578	438904	106242	987443
574114	269717	3382	0 90791	586916	85470	18849191	2380314	136302	807087	901910	192538	7223426	1047832	47775	297668	644515	168990	1822313
880011	150442	2427	9 54207	419429	136269	4981182	802218	49874	574495	338858	75749	6903535	635573	24114	112066	260120	164367	950728
370271	256724	6543	8 70414	450334	77210	16483666	2185235	147115	731569	890104	284489	9493756	848181	56642	281634	637737	134985	1784829
266886	99955	8804	7 35500	279626	76957	5843226	1643868	85881	294246	351114	251379	10228606	633768	30470	102677	193214	99531	1367621
1,6	1,1	0,	5 1,3	1,3	1,1	1,1	1,1	0,9	1,1	1,0	0,7	0,8	1,2	0,8	1,1	1,0	1,3	1,0
0,6	1,0	1,	9 0,8	0,8	0,9	0,9	0,9	1,1	0,9	1,0	1,5	1,3	0,8	1,2	0,9	1,0	0,8	1,0

SND1	PDIA6	EEF2	RHOG	DARS1	PBXIP1	PTGR2	GLIPR2	NDRG2	OSBPL2	SUSD2	HINT3	STXBP3	BMP1	PRKCI	TMEM214	SNAP23	CMPK1	NSF
942955	5 160215	7183725	1254600	27316	29341	544989	141033	2333883	32349	58551	219539	160725	66958	103502	4177	5635039	1125244	54974
2133009	436321	11073785	368131	93996	71834	693297	161777	682471	374619	195537	201209	305100	60412	192313	6362	2962044	596455	81617
2008000	225664	8917337	542606	41923	91420	383030	386839	1393652	250156	347221	434973	132936	95830	104102	13160	5496460	1316237	140568
1455160	849714	4414080	591257	74142	182268	172473	36081	171935	144199	280605	139148	56564	14067	268296	21602	3220168	483015	37598
2916953	351756	14781514	447326	312847	100253	946078	133448	833607	177377	846752	335674	100523	126131	113938	70236	2939193	820209	135405
1716543	310769	5831716	511550	56223	147240	287700	54638	837400	122468	556197	437000	183203	21561	234838	8546	3113544	825639	87283
997474	177599	9421023	918334	46981	20845	797223	227819	1734455	30986	80794	103143	39490	101184	113392	3696	5632162	1320489	75086
2434240	599070	11144934	975324	277443	90650	820865	97279	114999	171947	183068	389797	65944	109824	102955	71197	4761244	1318510	139627
2936626		13042671	528647	150630	122127	682592	201858	2028388	136336	110795	270610	192979	55064	241154	28354	2848559	772124	115425
988732		4797582		134112	25139	509093	76665		249397	751923			12551		71521	1991414		3761
628475		5294546			68967	269110			149173						0	3153270		50602
1290278		5303297	759617	53982	112129	582592	23681		149985						9631	3155983		40325
2025929		13935176			80233	714746	196681		25209						32381	4754673		171927
2162604		9690355			36145	1154935	569137		88888						56696			103212
1981271		14420427	1601750		74241	711861	68684		313314						29117	7723499		116182
1005702		3619512			182893	248653	497167		75283				7784					11782
1825542		9096014		116359	91731	580707	154864		163013						24872			94020
686943		3312425		112591	54334	278667	111678		112858									40045
1627452		8762946		109399	87734	609198	228473		148448						28463	4291614		76652
773718		4537356		53571	50714	288166	200599		93816						25751	1991948		59001
1,1		1,0	,	1,1	1,0	1,0	0,7		1,1			,			0,9			1,2
0,9	9 1,3	1,0	1,4	0,9	1,0	1,0	1,5	0,7	0,9	0,7	1,2	0,8	0,6	1,2	1,1	1,0	0,9	0,8

PCDHGA3	BTN1A1	DHRS12	LANCL2	RAB10	ECHDC1	RETSAT	RRAS2	TBC1D9B	YWHAZ	GK	R	AB43	MDH1	ENG	LOC521224	SNX3	SNAP29	ERGIC1	G3N0S9
295705	23855104	31436	437356	2517363	419891	23081	2741323	45371	2798671		67728	791780	244939	344426	478878	8121	3865041	36175	817105
22171	30476236	158335	446958	1620866	250109	242591	990606	58930	1926326		36274	490001	209534	597720	105466	3980	2847702	104828	90012
238006	33642721	177439	414240	2818424	278907	223142	2271980	156802	2484904		12562	651421	236543	318736	96514	8740	1999560	231925	121416
484890	9601544	18184	907155	802049	182138	111365	688917	17417	1805951		3112	205050	97465	832466	18636	1502	646371	. 37023	42479
222996	25590865	192237	661142	1829274	604808	172421	1109513	110323	3176037		44804	388318	375100	383772	353905	5438	1881200	298555	32318
168269	12476234	188002	915640	2033900	428155	137323	1325179	213128	2594787		6130	557607	362242	570628	20113	6962	816867	236697	20972
109037	14429006	23123	559646	2474059	786045	93929	3143845	68138	3668015		95229	733671	349548	400056	280787	8606	4787441	. 11888	551920
274675	22677516	252307	710054	3199170	401083	21742	2314053	69461	3916035		29228	446795	177802	315105	303974	9306	3315317	516088	106752
224702	38693052	159299	744277	1777649	307388	97741	1232406	107464	2316213		42162	481652	158091	385809	532258	4923	2922785	196932	27982
153833	21363211	21589	1340277	276385	164584	10440	447457	14398	2805288		11954	84128	105591	2153397	38451	4365	428001	. 112711	87583
907333	15328410	58128	919434	963052	159046	91752	867922	73412	2528040		52014	201891	145162	613432	322937	2140	1456492	72153	25466
202618	9191386	37591	1116700	894774	314325	112030	602520	27254	1953337		19360	264686	208699	566092	63805	1660	648661	40607	24510
259681	14773589	121796	262090	2692080	406623	213787	2000524	5594	4257735		94762	736038	312422	297657	341056	12379	3779502	145035	108116
246998	20692618	254150	562165	4984169	714886	199944	3910900	289054	3766574		14140	1044985	435970	207687	266666	24574	3866978	207911	39791
183797	21159283	301663	477632	4519566	473729	74471	3318367	94815	4947371		23114	966638	358336	182310	207439	20512	4980381	. 333148	85810
139229	6420978	62510	529013	2017678	425423	123870	1116200	29583	3843039		30932	466431	284229	825449	69652	5810	964713	43604	578168
226969	21593653	130133	631524	2161888	418892	128199	1823177	92446	2796341		36883	533080	256647	470364	207284	6582	2519937	184147	222872
137818	8657096	91722	202796	755899	197812	82790	907633	64491	759052		31971	192587	98654	182361	170407	2740	1453096	5 172306	295787
289774	18452816	127091	743948	2265669	370751	115504	1687037	80197	3302200		36055	530806	251063	653979	230283	9545	2380939	144012	122178
253072	9887344	104028	360100	1710689	180409	65980	1288482	92493	1053269		27444	354871	115498	644488	170799	8728	1727510	99696	187158
0,8	1,2	1,0	0,8	1,0	1,1	1,1	1,1	1,2	0,8		1,0	1,0	1,0	0,7	0,9	0,	' 1,1	1,3	1,8
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РКМ	MYO1D	RPL7A	A0A3Q1MBN C	SNK1G1	CDC42	CPNE3	RAB14	CYRIA	HSD17B7	MPO	SLC1A1	RAB33B	EPRS1	BSG	GSTM2	СНМРЗ	LDAH	сстз
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97051	1241404	139807	336584	100447	2500532	31086	545780	1933182	6128516	25313	4396202	181125	2253	1896139	321291	723362	717586	46812
94245	636448	106496	233942	8320	1012253	58583	92522	572840	2206093	0	3186340	23192	79729	502689	212354	348624	124126	7944
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289976	795602	471547	8892989	2033	4135801	77097	537925	494971	3637504	951076	3037712	370756	1934	2129458	332968	1029538	276093	92556
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358627	1100105	305388	211272	3335	1938440	332496	974139	612951	3020610	2352	4401816	223536	20851	2212628	294864	645600	255448	112663
148425	712253	170836	1989644	40528	597471	39393	277543	482816	649793	256193	7935890	24720	77326	1114246	251288	212735	298263	44908
233003	981609	101781	62946	47551	936132	164126	429444	1143939	2087957	0	5829210	72041	23394	2029907	153178	362652	669797	22673
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218792	1435321	476210	965530	146709	5881261	112518	1922231	1466821	5495813	0	1917516	538581	42545	2073633	619870	839617	1043458	48493
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STXBP6	AGPAT1	AIDA	S100A9	JAK1	UGP2	RAB11B	CYSTM1	TMED10	PAEP	MVP	CD109	TLR2	CSNK1A1	PRKG2	VAMP8	TOLLIP	A0A3Q1LP69 H	SPB1
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870236	175389	290038	56048	973148	1537530	3296956	1014398	456692	3721792	539989	510277	13435903	86673	13844379	682223	1949392	53445	1610890
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945136	107986	424045	3763616	212914	3147189	5663562	1211465	813363	3555265	469073	377130	12512239	186957	11487872	1311602	2719967	25720	2366542
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750802	58527	101570	32165	576231	4364206	3053292	648065	488259	312923	991610	1941227	13322024	105554	16583144	632410	1129835	42601	1915783
238498	31593	375082	1473632	103895	2227383	1765824	92395	375417	960248	1178480	1637747	18600191	73244	4294769	135028	1349735	11525	1081269
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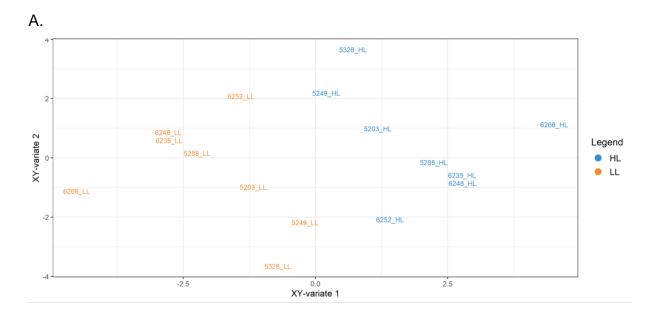
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565002	270293	305280	261369	24964240	1993093885	38338	22050	5615964	1157454	72995644	439433	18182	907426	186168	3 250712	633316	315761	478263
1113148	246117	157589	116118	17968802	1223964723	75867	5294	7398919	228280	124281671	164183	14399	1271873	99195	133633	645274	126758	240601
461454	27952	126143	99180	13598227	3182385413	52345	0	3539345	566393	36590295	177553	5956	333318	55660	180723	1072746	49241	512626
504571	229751	436072	436882	11086771	1762899098	82550	73971	4849853	7201655	70145107	162690	80567	994427	78266	237494	476738	310788	2267689
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441503	231067	230524		14002471	1799861198	17764	0	10634895	70527	48294567	146514	152985	1588174	125870) 441792	331244	516800	1206959
596105		417142			1472825717	93438		9036721	105086	68826645						369591		1265348
613685				13727045	1822115781	66470	12208		136340	89889042						377278		
669395	129112	333569	141365	27342802	3103167193	188562		4582285	907416	57815418			250822	131741		2182461		814012
732427	216608			20406826	2088722702	47713		4300828	379761	80335095	96587	7199	594694	84480		750876		221667
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234533			1147617	9955868	1335881001	25884		9939178	5438518	52722908						144027	173262	1356782
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217388		145134		5997124	594158743	39941	52004		2420796	26130811						265698		
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176250				8346545	713746463	65499		3021260	1799353	18204208						619816		555007
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1,1	1,1	1,0	1,2	1,0	1,1	1,2	0,6	1,0	0,9	1,0	0,9	1,1	. 1,1	0,8	3 0,9	1,3	0,7	1,1

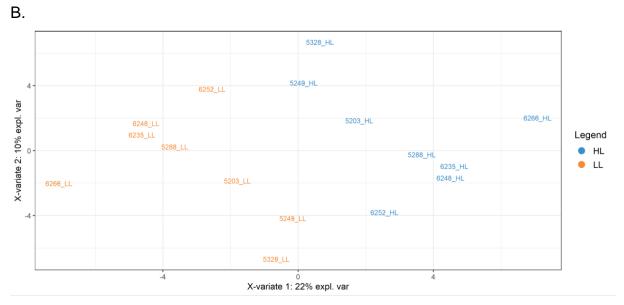
A0A3Q	1LP69 CAB	39	GALE	PGRMC2	HRAS	IQGAP1	RASA3	HSP90B1	LASP1	GANAB	RPL6	PRXL2B	RAC1	ССТ8	RIT1	ALDOA	RHOF	PSMD12	PTPN6
29	2622	684473	320420	34917	410253	131747	27329	324613	1 119759	139449	387265	6248782	9740900	21417	1109904	295743	3375029	0	56719
14	1514	246652	372030	3755	189053	186543	44426	554279	9 111410	186525	335045	2637485	2437959	23113	645398	506708	1583328	0	92241
72	0866	452742	221721	110523	359557	93591	18150	649159	264082	83304	406913	3800557	3411918	58958	1326735	78493	2845201	5989	121019
99	2525	235328	370036	11905	166697	519818	7423	357148	8 81575	230058	331498	1846621	3591959	5414	256724	191423	1265063	8137	45654
31	6867	221095	539211	41522	570103	480190	17708	981346	5 273862	203364	999404	2124678	2734789	60276	537245	467996	1674675	37584	132961
79	6311	104893	319069	43927	292610	166164	28970	403395	5 150272	78014	369817	3839946	3567453	45169	765463	130242	1679069	8671	79947
27	4160	787744	468201	28922	401637	288076	65589	471066	5 231530	153500	687478	6912701	9582643	26916	2125604	460598	2320999	0	40000
26	6025	374600	296443	56056	437495	479448	8335	1319702	326496	323274	1096756	4065851	4841092	64857	954201	304904	3660585	40453	188034
17	7304	246067	472684	5679	261525	425476	18117	1049493	l 155931	263977	816912	2409100	2526178	24490	586207	415221	. 1680545	3648	99206
107	6566	178320	895673	44316	257619	804512	898	250192	2 45056	224245	279599	488719	1834414	5589	219290	192709	1058245	11323	117571
81	1060	173100	623137	11914	143754	355905	7723	257522	1 70018	362232	91580	989879	1728057	10221	. 783076	73116	1135924	0	31737
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25	7698	395802	713483	26410	501192	215985	88563	771545	5 176529	249835	1330441	7099213	7436962	39776	1162747	402306	3317892	0	
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15	1494	553261	289607	114449	530861	130530	56153	967063	3 581560	102580	1078816	9887084	9057722	66439	1427861	246143	5341940	36834	155068
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ATP8B1	GFPT1	TPT1	OXSR1	A0A3Q1LJQ7 RP	S16	RAB35	RPL14	EIF3A	BLVRB	PRKCD	IL1R1	SULT1A1	ҮКТ6	BZW1	RPLP0	APMAP	DNAJC12	PATJ
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277805	5 117881	. 311146	219305	144102	32932	3558884	73115	37585	448480	85209	215630	1018439	6914050	120406	139643	175274	553009	11964
525850) 185983	486583	76397	52609	49158	5514725	143426	9630	711736	117088	380301	430070	8486935	139277	48168	419612	779233	110349
1319248	3 59506	238400	140033	480607	37092	1795402	163139	3629	252787	24109	58361	575273	2737061	55345	39881	152248	227975	159947
521579	341457	427007	162147	207999	144561	3570426	279116	130891	442653	254761	397289	647941	6564642	149227	433943	602221	614119	201602
416568	3 239019	512377	47550	262939	64666	3573476	179708	744	319550	170066	106366	1286626	5951974	186162	59372	287990	679631	274898
239745	5 40198	481505	200694	268729	84890	5403875	148641	16844	637190	74863	388639	2074483	15605423	20106	209528	88349	828853	27756
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410222		409937	75929	98333	9204	2974771	44637	5240	270789	31966	5 155919			25890	21019	165899	402774	258921
764338			38196		24551	1946661	81970			47749				41632	25863	189745		203180
405337			176839	172199	439754	5908627	294250	79087	660097	184726					361377	173762		875
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481997	7 172901		152296	277774	189731	4886926		26550		125098				85459	201976	260438	627448	140234
121988				173178	188453	3063320		-							128368	178111	334819	
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0,9	9 1,0) 1,0	1,1	1,3	1,8	1,1	1,2	0,6	1,0	1,0	0,9	0,9	1,1	0,8	1,1	0,9	1,0	1,2

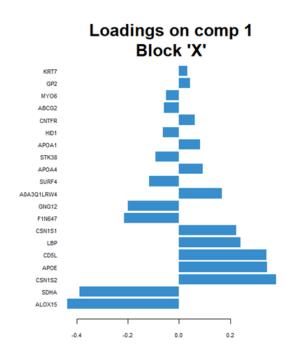
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150835	48798	56223	2825800	89265	1951235	133620	79096	488671	239472	6350325	0	713822	3618902	607706	1712767	272461	203069	71568
192186	302245	18204	8542255	45748	3290180	21600	162031	163354	236689	3721216	2837	231671	5775701	3690883	1294217	368495	353024	18492
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80876	168320	113430	6574516	44339	4462594	118952	56368	432012	443996	3200357	23644	603745	8860684	2430393	1936809	80707	273763	85785
70440	413274	129843	4420679	16748	4360721	77205	2815256	73672	148753	11837650	399	258749	7115658	3505470	1483855	558267	568317	80000
113171	278892	6947	6006347	20518	4194046	65897	78481	321817	641194	3958086	0	312838	4150534	1317051	761848	58462	110203	80296
181484	265141	7645	11217777	40239	2815376	25149	79623	181032	153347	10175430	8512	430740	3881072	1752733	697729	342889	452856	63561
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198635	248070	73269	3924586	15721	2141884	97201	4475751	356075	84606	11061551	5804	364542	4036194	1497001	1038071	3480476	154633	16317
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G5E554	PSMC2	DDOST	ARCN1	RAB22A	PSAT1	NIBAN2	PCBP1	SPTLC1	NAPRT	
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15400107	15709	108693	119247	159602	156080	1254262	1230730	142391	45777	
1015592	33818	98704	44273	21279	116223	986809	932879	24067	250927	
2941278	169754	258141	234543	103915	524678	1226313	1399949	172365	82458	
7128657	26723	68664	83092	56065	181109	1632583	1434999	232817	42776	
4638224	19832	54090	66364	272525	52626	638203	1245714	63842	0	
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6639682	9801	44904	24489	14464	52925	1520525	1062392	134511	238539	
2174398	6150	72910	23190	41777	150437	1442623	991519	23838	130442	
3010860	126389	157183	223152	237571	241532	729229	1439026	116656	0	
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5487718	62252	134075	134686	125771	233013	1116249	1188818	136332	62388	
4521591	70410	99494	131091	85544	245587	296068	213421	72585	80011	
5739511	78046	124656	135152	124994	190190	1281992	1094642	137722	80156	
5689053	63881	77156	93674	126125	146746	726410	236780	83491	77749	
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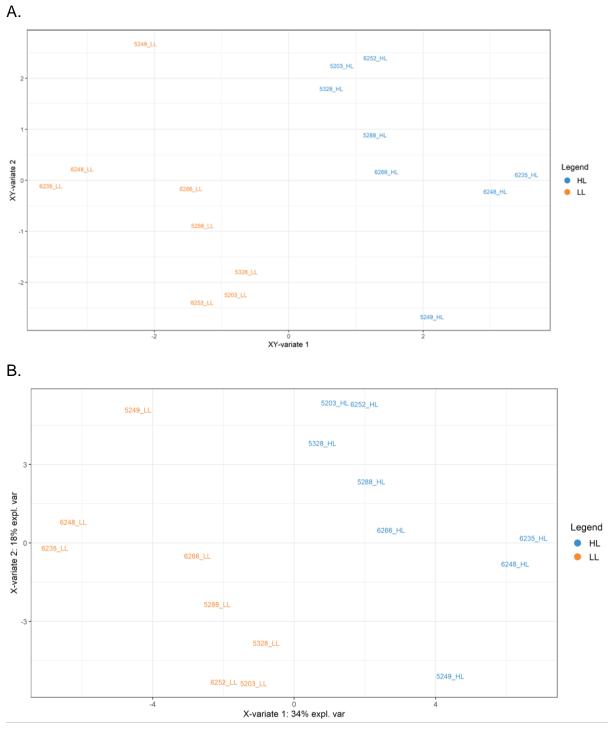




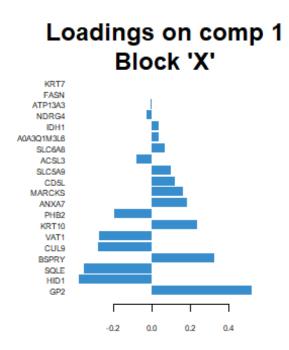
C.



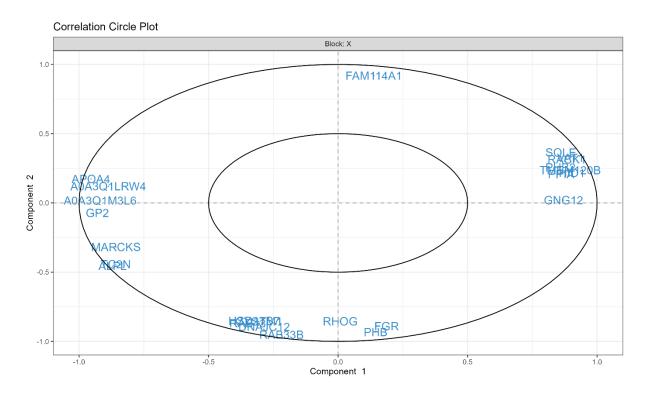
Supplementary Figure S1: sPLS - lipolysis results: A. Plot of the XY space, B. Plot of the X space, C. Loadings on component 1 of Block X.



C.



Supplementary Figure S2: sPLs – milk LPL activity results: A. Plot of the XY space, B. Plot of the X space, C. Loadings on component 1 of Block X.



Supplementary Figure S3: Correlation circle plot representing the proteins selected by sPLS-DA with a cut-off at r > 0.85. Only the proteins selected by sPLS-DA (corresponding to 20% of the total protein dataset) are shown in components 1 and 2 (details of sPLS-DA analysis not shown).