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## 1 Low-redundancy sequencing of the entire Lactococcus lactis

## 2 **IL1403 genome**

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6

### 7 Abstract

8 Lactococcus lactis is an AT-rich gram positive bacterium phylogenetically close to the genus 9 Streptococcus. Various strains of L. lactis are used in dairy industry as starters for cheese making. L. 10 lactis is also one of the well characterized laboratory microorganisms, widely used for studies on 11 physiology of lactic acid bacteria. We describe here a low redundancy sequence of the genome of the 12 strain L. lactis IL1403. The strategy which we followed to determine the sequence consists of two main 13 steps. First, a limited number of plasmids and -phages that carryrandom segments of the genome were 14 sequenced. Second, sequences of the inserts were used for production of novel sequencing templates by 15 applying Multiplex Long Accurate PCR protocols. Using of these PCR product sallowed to determine 16 the sequence of the entire 2.35 Mb genome with a very low redundancy, close to 2. The error rate of the 17 sequence is estimated to be below 1%. The correctness of the sequence assembly was confirmed by PCR 18 amplification of the entire L. lactis IL1403 genome, using a set of 266 oligonucleotides. Anotation of 19 the sequence was undertaken by using automatic gene prediction computer tools. This allowed to 20 identify 1495protein-encoding genes, to locate them on the genome map and to classify their functions 21 on the basis of homology to known proteins. The function of about 700 genes expected to encode 22 proteins that lack homologs in data bases cannot be reliably predicted in this way. The approach which 23 we used eliminates high redundancy sequencing and mapping efforts, needed to obtain detailed and 24 comprehensive genetic and physical maps of a bacterium.

Availability of detailed genetic and physical maps of the L. lactis IL1403 genome provides many entries to study metabolism and physiology of bacteria from this group. The presence of 42 copies of five different IS elements in the IL1403 genome confirms the importance of these elements for genetic exchange in Lactococci. These include two previously unknown elements, present at seven and fifteen 29 copies and designated IS1077 and IS983, respectively. Five potential or rudimentary prophages were 30 identified in the genome by detecting clusters of phage-related genes. The metabolic and regulatory 31 potential of L. lactis was evaluated by inspecting gene sets classified into different functional categories. 32 L. lactis has the genetic potential to synthesise 20 standard amino acids, purine and pyrimidine 33 nucleotides and at least four cofactors. Some of these metabolites, which are usually present in 34 chemically defined media, can probably be omitted. About twenty compounds can be used by L. lactis 35 as a sole carbon source. Some 83 regulators were revealed, indicating a regulatory potential close to that 36 of Haemophilus influenzae, a bacterium with a similar genome size. Unexpectedly, L. lactis has a 37 complete set of late competence genes, which may have concerted transcriptional regulation and 38 unleadered polycistronic mRNAs. These findings open new possibilities for developing genetic tools, 39 useful for studies of gene regulation in AT-rich gram positive bacteria and for engineering of new strains 40 for the diary industry.

41

#### 42 Introduction

43 Lactococcus lactis is probably the best characterised lactic acid bacterium, with highly developed 44 knowledge on physiology and genetics. It is therefore an obvious target for genome sequencing, since 45 the availability of the full sequence would greatly improve the efficiency of numerous studies that are 46 currently being conducted with this organism, or are planned in the near future. We decided to undertake the L. lactis genome sequencing project in an academic setting, with resources of a single laboratory, 47 48 which obviates the need to raise a rather large amount of funding which would be required for sequence 49 determination by a private company, or by a consortium of academic laboratories. For this purpose, we 50 developed an aproach that allowed us to determine the genome sequence with a redundancy much lower 51 than generally used, and at a commensurately lower cost. Due to the low redundancy, the sequence is of 52 a so-called diagnostic quality, allowing to detect essentially all genes that have homologs in other 53 organisms, but not the genes which may be present in the Lactococcus genome only.

The approach most often used for sequencing of an entire bacterial genome is based on a highthroughput random clone sequencing (Fleischmann et al. 1995). This method is most efficient if the facilities to produce raw reading data are not limiting. However, the speed of accumulation of new sequencing data decreases exponentially with the linear increase of the number of randomly sequenced 58 templates (Lander & Waterman 1988). This becomes a limiting factor, in particular for relatively large 59 bacterial genomes. Furthermore, the assembly becomes exceedingly difficult if the genome contains 60 numerous repeated elements. The chromosome of L. lactis IL1403 was estimated to have a size of about 61 2.4 Mb (Le Bourgeois et al. 1992). Application of the whole-genome random sequencing and assembly 62 method (Fleischmann et al.1995) would require producing of 30,000 random gel readings, 63 corresponding to six-fold coverage, and the sequence would be distributed in about 80 contigs. We 64 considered an alternative strategy that would consist in a much less massive random sequencing 65 followed by primer walking on templates generated by Long Range PCR (LR PCR, Cheng et al. 1994). 66 If sequence acquisition and assembly were carried out in parallel, template synthesis can be conducted 67 in such a way that the re-sequencing of the regions that were sequenced already is kept at a minimum. 68 We estimated that such approach may allow to sequence the whole L. lactis genome with a coverage of 69 only about two. Some 10,000 sequencing reactions instead of 30,000would therefore be required. We 70 report here the L.lactis genome sequence determined by this approach.

71

## 72 Low-redundancy genome sequencing

73 The strategy of low-redundancy L. lactis genome sequencing is presented in Table 1. This strategy is a 74 compromise between completely random and directed approaches. Its objective was to reduce time and 75 effort or obtaining complete information about gene content and genome organisation. In the first stage, 76 a limited number of randomly chosen clones is sequenced, so that the speed of new sequence 77 accumulation keeps approximately constant. We estimated that this condition is fulfilled up to the 78 genome coverage of about one. A large number of small contigs, separated by sequencing gaps, is 79 present at the end of the first stage. In the second stage randomly chosen clones carrying large inserts 80 are sequenced by primer walking. This allows to close some sequencing gaps and extend the contigs, as 81 verified by sequence assembly, which is carried out in parallel with the acquisition of new sequence. 82 The redundancy is kept low by selecting the primers that correspond to the ends of the extended contigs 83 for the next round of primer walking. This stage is carried out until the rate of acquisition of the new 84 sequence is above about 1 new base for 3 sequenced bases. Finishing of the sequence is achieved by 85 applying another directed procedure, which was designated Multiplex Long Accurate PCR (MLA PCR) 86 and tested in the course of our participation in the Bacillus subtilis sequencing project (Sorokin et al. 87 1996; Bolotin et al. 1997; Lapidus et al. 1997). It involves mixing a large number of primers that 88 correspond to the ends of contigs. A product will be obtained each time when the distance between two 89 sites on the genome, corresponding to two contig ends, is less than the maximalsize that can be 90 synthesised by LR PCR. The probability of producing such pruducts, as a function of the genome size 91 and the number of primers present in LRPCR reaction is shown in Figure 1. For the genome of L. lactis 92 size this probability is between 0.5 and 1 if some 20 primers are mixed (that is at least half of PCR 93 reactions containing 20 randomly chosen primers will give an amplification product). It should be noted 94 that the efficiency of gap closure is expected to increase with the progression of the sequencing project, 95 since the number of contigs continuously decreases. This is in sharp contrast with the fully random 96 approach, where the efficiency of gap closure decreases exponentially with sequence acquisition. We 97 now believe that the long-insert library construction can be omitted.

Some statistical data of application of this strategy for the L. lactis sequencing are presented in Table 2. A library consisting of 2854 clones with insert sizes in the range from 1 to 2 kb, was constructed by using pBluescript II KS+ (Stratagene) or pSGMU2 (Errington1986) vectors. 2625 clones were sequenced by forward (M13-21) and 2168 by reverse (M13RP1) primers with successful sequencing rate of about 90%. After accumulating about 2100 kb of sequence 23570ligonucleotides were synthesised to fill the gaps between the forward and reverse sequences. A total of about 3.3 Mb of sequence was thus acquired.

105 -FIXII vector (Stratagene) was used to construct along insert library. L. lactis chromosome was 106 partially digested with Sau3A, fractionated by centrifugation in sucrose gradient, treated with Klenow 107 polymerase in the presence of dGTP and dATP, and ligated with -FIXII arms cut by XhoI and treated 108 with Klenow in the presence of dCTP and dTTP. 262 phages were chosen at random and the ends of 109 inserts sequenced by the T7primer (Stratagene). Of these, 122 phages which had a unique sequence 110 obtained by the T7 primer, were sequenced by the T3 primer (Stratagene). These 122 clones appeared 111 to constitute a nonredundant set and their inserts were sequenced by primer walking (see Table 2). Some 112 250 kb of sequence were obtained in this way.

MLA PCR was used to obtain new sequencing substrates. A critical step in the procedure is to identify in the mixture the two primers that give a product useful for sequencing. The previously developed protocol (Sorokin et al. 1996), where two steps were required for the identification, was modified here

116 so that only a single step is required. The principle of the modification is illustrated in Figure 2A. In this 117 theoretical example each reaction contains 8 different primers. A total of 16 primers is used (labelled 1– 118 16 on the left) and there are 16 reactions (labelled 1-16 on the top). To obtain a different primer 119 combination in each reaction one primer is replaced at a time with a new primer (for instance, reaction 120 8 contains primers 1–8, reaction 9 contains primers 2–9, etc). The primer couples which give a useful 121 product can be identified unambigously, by simply identifying the reaction mixtures in which the 122 product is synthesized, as illustrated in the three lower rows. For instance, if a product were found only 123 in the reaction 8, primers 1 and 8 would be required for it, since only the reaction 8 contains these two 124 primers together. Alternatively, if a product were found in reactions 4 to 10, primers 3 and 4 would be 125 required. A general correlation between positive reactions and primer couples is given in the legend of 126 Figure 2. An example of application of this protocol to the IL1403 genome, using 32 oligonucleotides 127 in each reaction, is shown on Figure 2B (the analysis of 36 reactions out of a total of 96 that were 128 routinely run together is displayed). There are 4 different products in the reaction mixtures, ranging 129 between 1 and 10kb. The largest product appears in reactions 7 to 34, identifying that the primers 7 and 130 3 are required for its synthesis (see legend, Figure 2). The primers identified in this way were used to 131 sequence the ends of the PCR products and thus confirm the identification and to extend the sequence. 132 In total 1641 such sequencing reactions on the products with sizes from 1 to 20 kb were performed and 133 about 0.77 Mb of sequence was read (Table 2). This step allowed to finish the entire chromosome 134 assembling, giving a contig of 2.34 Mb. The total redundancy was close to 2 (Table 2).

To test the correctness of the assembling we carried out LR PCR amplification of the entire genome using266 oligonucleotides, predicted to be separated by distances10–20 kb. The expected products were obtained (Figure 3), which indicates that the assembling is correct. The sequences of these 266 oligonucleotides are presented at <u>http://spock.jouy.inra.fr</u>.

The average redundancy of the L. lactis genome sequence is two. Such low redundancy does not allow to eliminate all errors by comparing multiple sequences corresponding to the same genome region. The error rate of this sequence is therefore determined by individual gel reading quality. We counted the number of ambiguities in the raw sequence data used for the as sembling and found 46,954 ambiguities for a total of 4,687,630 bases. From this estimation the accuracy of the L. lactis diagnostic sequence is about 1% (one ambiguity/100 bases). However, assembling usually decreases the number of errors in

145 the final consensus sequence and the real error rate may be lower. We therefore carried out a different 146 quality test, aiming to detect the level of frame-shift errors in the open reading rames present in the 147 genome sequence. For this purpose we used the GENMARK programme (Borodovsky & Mc Ininch 148 1993), which predicts the genome regions statistically fit to encode proteins. Some 3544protein coding 149 regions were thus detected. If the real density of genes in L. lactis were similar to that observed in other 150 bacterial genomes, we would expect only about 2300 such regions. There should therefore be over 1200 151 frame-shift errors in our sequence (the difference between 3544 regions detected and 2300expected), 152 corresponding to about 1 error for two genes, or 2 kb. We suggest therefore that the overall error rate of 153 the diagnostic quality sequence after assembling, at a redundance of 2, may be close to 1 in1000.

154

#### 155 Genome analysis

156 GC skew, replication origin and terminus. L. lactis IL1403 chromosome has the size of 2345 5 kb. 157 The average GC-content is 35.4%, its variation over the chromosome is shown on Figure 4. By analogy 158 with the analysis performed on the B. subtilis genome (Kunst et al. 1997), the deviation from the mean 159 GC content may indicate the presence of foreign insertion elements, such as transposons or prophages. 160 We did not detect, however, in the L. lactis genome, a correlation of GC-content with location of these 161 elements, determined by other approaches (see below). Several regions of highly elevated GC-content 162 were revealed (Figure 4). Six such peaks with GC-content higher than 46%, at positions 540, 1970, 163 2210, 2250, 2325 and 2340 (Figure 4, bottom) correspond to rRNA operons. Another GC rich region, 164 near position 2150 kb (Fig 4, bottom), corresponds to the cluster of ribosomal protein genes. We 165 conclude that the regions encoding ribosomes have a higher GC content than the other regions in L. 166 lactis. In two other AT-rich bacteria, B. subtilis and Rickettsia prowazekii, the regions encoding 167 ribosomal genes are not particularly GC-rich (Kunst et al. 1997; Andersson et al. 1998).

GC skew, replication origin and terminus. GC or AT skews are useful to predict positions of replication origin and terminus (Lobry 1996a, b). The distributions of the values (C-G)/(C+G) and (A-T)/(A+T) over the chromosomal region in the vicinity of dnaA gene is shown in Figure 5, top. A sharp transition between positive and negative values is observed, and indicates the presence of the replication origin (Figure 5A). This region contains four DnaA boxes (Figure 6), which also indicates the presence of the replication origin. We choose the start point for the presentation of the circular L. lactis genome map at the middle of HindIII site near the replication origin and the map is oriented to be colinear with thetranscription direction of the dnaA and dnaN genes (see below, Figure 9).

GC and AT skews may also indicate location of the replication terminus. This is seen for L. lactis genome from Figure 5, bottom. The transition between positive and negative values occurs near the position 1260 kb. These data correlate with the replication terminus location based on orientation of transcription of potential genes and distribution of chi-sites over the genome (see below).

180 IS-elements and prophages in L.lactis IL1403. Three different IS elements in the genome of L. lactis 181 IL1403 were known previously, designated IS981, IS982 and IS1076. Their number of copies (ten, one 182 and seven, respectively) and approximate locations were reported previously (Le Bourgeois et al. 1992, 183 1995; Polzin et al. 1993; Schouler et al. 1998). The element IS1076 was initially identified in the strain 184 L. lactis subsp. lactis CNRZ270 on the plasmid pUCL22 (Huang et al. 1991). Nucleotide sequence of 185 this element (Genbank accession X53013) shows complete identity to IS904, known from nisin-186 producing lactococcus (Engelke et al. 1992). Our sequencing data confirmed that in all chromosome 187 locations where IS1076 was mapped, the nucleotide sequence identical to IS904 is present, and we 188 therefore keep the latter name on the map. We found, however, that another element, which we designate 189 IS1077, was also present in each of these seven sites. At two sites the IS1077 element is flanked by two 190 sequences identical to IS904. The orientation of IS904 relative to IS1077 is different in five cases out of 191 seven. A possible explanation for the fact that the two elements always occur together in this genome 192 would be that one of these elements carry a sequence essential for the transposition of the other. Since 193 IS904 can be found without IS1077 in other genomes, the essential sequence must be in IS904. By 194 searching Genbank we identified another copy of IS1077 in the plasmid pK214, (sequence accession 195 number is X92946). IS904 is also present on this plasmid.

Fifteen copies of an element, which was not described earlier for lactococcus species and is designated
here IS983, were detected in the IL1403 genome. The closest relative from other species is IS1239 from
Streptococcus pyogenes (Ashbauch et al. 1998), and, from other lactic acid bacteria, it is IS1070,
discovered in the plasmid pNZ63 in Leuconostoc lactis NZ6009 (Vaughan & de Vos 1995).

Chopin et al. (1989) detected in the chromosome of IL1403 two different prophages, bIL285 and
bIL286, which can be induced for lysogenic development by UV irradiation. Two more prophages,
bIL309 and bIL310, can also probably be induced if supplied in trans by some functions of the first two

203 phages (Chopin & Perreira, pers. comm.). We tried to identify potential prophages in the chromosome 204 by using homology search against a database containing known phage protein sequences. The database 205 consisted of 1219 protein sequences, including the complete set of 50 putative proteins derived from the 206 sequence of the r1t temperate phage of L. lactis (van Sinderen et al. 1996). A distribution of 207 nonredundant homology hits over L. lactis genome is shown on Figure 7. This distribution indicates the 208 presence of three regions, around 460, 1060 and 1410 kb, which may contain the pro-phages identified 209 by Chopin et al. (1989). Two areas, around 40 and 2005 kb, may indicate a fourth and a fifth prophage. 210 More detailed analysis of these areas will help to elucidate the correspondence between the prophages 211 detected by sequencing and by induction of the lysogenic development.

212

213 Distribution of chi-sites over the chromosome. Recent analyses suggested that so-called chi-sites, which 214 in L. lactis have sequence 5'-GCGCGTG-3', protect DNA from exonuclease degradation (Biswas et al. 215 1995). The same sequence was reported to modulate the activities of RexAB exonuclease corresponding 216 to RecBCD of E. coli and is thus involved in the regulation of homologous recombination (el Karoui et 217 al. 1998). In E. coli and B. subtilis such sequences are over-represented and most of them are found to 218 be co oriented with DNA replication (Burland et al. 1993; Chédin et al. 1998). The latter property was 219 correlated either with the involvement of RecBCD in recombination, and therefore preferring the same 220 DNA structures as the RecA protein (Tracy et al. 1998), or with a statistical bias of base distribution, 221 due to codon usage (Biaudet et al. 1998). The chi sequence is presented in L. lactis on average once per 222 13.2 kb (178/2350 kb) and tends to be co-oriented with replication (Figure 8). Interestingly, the density 223 of chi sequences increases up to one site per 9 kb (34/300 kb) in the region close to the replication origin. 224 Also, chi-site density decreases in the regions near 460, 1060, 1410 and 2000 kb, where the putative 225 prophages were detected (see above).

226

*RNA genes.* Six rRNA operons were mapped on the L. lactis chromosome (Tulloch et al. 1991; Le
Bourgeois et al. 1992) and one was sequenced (Beresford& Condon 1991; Chiaruttini & Milet 1993).
We did not resequence all other operons since the diagnostic sequencing would not reveal reliably any
difference. However, we confirmed map positions of these operons by PCR amplification of the
corresponding genome regions.

tRNA genes were identified with the computer programme tRNA scan-SE (Lowe & Eddy 1997). We
detected 62 tRNA genes, corresponding to the 20 amino acids. Most of the tRNA genes were found to
be organised in four large operons, three of them transcribed as parts of rrnB, rrnE and rrnF rRNA
operons. The trnA operon, encoding seven tRNAs, was described earlier (Nilsson & Johansen 1994).
Twenty genes encoding tRNA were found to be isolated from other tRNA genes. RNA component of
RNAse P (rnpB gene) and 10S RNA (ssrA) were detected by homology at 1703 and 1458 kb,
respectively.

239

240 Protein-coding genes. Prediction of protein-coding regions by methods based on statistical properties 241 of DNA is limited for the sequences of diagnostic quality, since potential frameshifts will hamper the 242 prediction of true stop codons. It is, however, possible to predict genes encoding proteins homologous 243 to proteins from other organisms. We used for the comparison 30757protein sequences, corresponding 244 to prokaryotic and phage genes, available from SwissProt (release of 17.02.98). Several home-made Perl 245 5.0 or UNIX shell scripts had been used for automatic extraction of L.lactis protein sequences and other 246 parameters from the standard BLASTx or FASTx output files and organising them into clickable tables 247 or genome map drawings. The extracted protein set of L. lactis genome was then again used for 248 homology searches, to find all paralogous proteins encoded in the genome. The largest protein from the 249 FASTx comparison, or the one, having BLASTx homology hits to the same Swissprot entry, was 250 considered as really encoded by a particular area of the L. lactis genome. The final protein set consists 251 of 1495 proteins. If the true number of genes in the L. lactis genome were close to 2300 (a density of 252 one gene per kb), our analysis would have identified about two thirds of them. A version of the 253 automatically generated ORF map of L. lactis IL1403genome is shown on Figure 9. There is a strong 254 bias of gene orientations to be colinear with the direction of replication. The same phenomenon was 255 seen for another AT-rich Gram positive bacterium B. subtilis (Kunst et al. 1997), but not for the GC-256 rich M. tuberculosis (Cole et al. 1998). It may be a characteristic of AT-rich gram positive 257 microorganisms.

Another automatic tool, based on the proposed functional classifications of genes in prokaryotic genomes (Riley 1993; Fleischmann et al. 1995) and commentaries from SwissProt, has been used to classify the genes. The programme uses list of functional categories and the relevant keywords with 261 assigned weights corresponding to each category for a given keyword. The advantages of such a 262 classification method are: it is completely automatic, it can be applied to genes with hypothetical 263 functions and needs the interaction with an expert only at the stage of construction of the keyword list. 264 After a keyword list was constructed and the programme had been educated y using several functionally 265 annotated genomes, it provided satisfactory results, which can be used by experts as a draft for more 266 precise functional annotation of the genome and classification of the genes. Any protein database can 267 be automatically classified by using this approach and then used in turn to classify a set of new proteins. 268 Presumably, such method of automatic functional classification of protein databases can be further 269 developed to give tools, which are completely independent from human expert and use different sources 270 for functional description of proteins. Parameters of homology with several proteins, rather than with 271 the best one, can be used to increase the performance of the approach for classification of hypothetical 272 proteins. The functional classification of predicted genes is colour-encoded on Figure 9 and summarised 273 in Figure 10 and in Table 3. A more detailed and systematically updated version of Table 3can be found 274 at http://spock.jouy.inra.fr.

275

## 276 Metabolic potential of L. lactis IL1403.

The automatic procedure for protein finding, function assignment and classification, described above,
allows to estimate the potential of L. lactis as a free-living microorganism. Several of the detected
systems were characterised experimentally earlier, by biochemical, genetic or gene cloning means.

- 280
- 281 Amino acid, vitamin and nucleotide biosynthesis

282 Lactic acid bacteria are nutritionally fastidious. The presence of a gene for synthesis of a metabolite 283 does not mean that a strain of L. lactis where the gene was found will not require this metabolite in the 284 growth medium. The studies performed long ago (Anderson & Elliker 1953) and recently (Jensen & 285 Hammer 1993; Cocaign-Bousquet et al. 1995) showed that synthetic medium for L. lactis should contain 286 at least six amino acids (isoleucine, valine, leucine, histidine, methionine and glutamic acid) and seven 287 vitamins (biotin, pyridoxal, folic acid, riboflavin, niacinamide, thiamine and pantothenic acid). Our 288 analysis showed that L.lactis has a genetic potential to synthesise 20 standard amino acids and at least 289 four cofactors (folic acid, menaquinone, riboflavin and thioredoxin). The genes for biosynthesis of 290 aromatic amino acids, threonine, branched chain amino acids and histidine were cloned and 291 characterised earlier (Bardowski et al. 1992; Delorme et al. 1992; Godon et al. 1992; Griffin & 292 Gasson1995; Madsen et al. 1996). The regulation of transcription of the tryptophane operon was studied 293 in detail (Raya et al. 1998; van de Guchte et al. 1998). The problem of fastidious nutritional requirements 294 of L. lactis strains has recently been addressed by application of the single-omission technique (Cocaign-295 Bousquet et al. 1995; Novak et al. 1997) and genetic approaches (Lapujade et al. 1998). It was shown 296 also that auxotrophy of IL1403, used as a dairy strain, for histidine and branched-chain amino acids is 297 due to the recently acquired mutations (Delorme et al. 1993; Godon et al. 1993).

298 Biosynthesis and salvage of nucleotides and nucleosides in L. lactis were explored earlier and several 299 pyrimidine and purine biosynthetic genes were cloned and sequenced (Martinussen et al. 1994; 300 Andersen et al. 1996; Nilsson & Kilstrup 1998). It was demonstrated that milk does not contain sufficient 301 purine compounds to support growth and therefore de novo biosynthesis is necessary (Dickely et al. 302 1995). Nucleoside compounds are not needed in the minimal synthetic medium to maintain exponential 303 growth of L. lactis (Jensen & Hammer 1993). We detected 47genes implicated in this metabolism. Most 304 of the genes for biosynthesis of purines are clustered near the purDEK operon, which was recently 305 characterised (Nilsson & Kilstrup 1998). A copy of IS983 is detected between the purDEK operon and 306 other genes of purine biosynthesis.

307

308 *Energy metabolism and transporters.* 

309 The main feature of the energy metabolism in L. lactisis that fermented carbon sources are used mostly 310 to maintain the energetic potential of the cells (Poolman1993; Cocaign-Bousque et al. 1996). About 311 5% of the fermented sugar is used as the source of substrates for synthetic reactions (Novak et al. 1998). 312 L.lactis does not have a functional citric acid cycle and gluconeogenesis enzymes and is unable to carry 313 out many anaplerotic reactions. The exponential growth of this bacterium appears to be 'programmed' 314 to happen only in sugar rich complex media, like milk. As mentioned above, many metabolites have to 315 be added into the synthetic medium (Jensen & Hammer 1993), although the corresponding biosynthetic 316 genes seem to be present.

317 It is interesting to compare the genetic potential of L. lactis to grow on different carbon sources with the318 available experimental data. The genetic potential can be estimated from the presence of the

319 biodegradation genes and the relevant transporters. IL1403 has genes which can be used to grow on 320 different carbon sources: glucose (glycolysis genes), fructose (positions 1519and 2230 kb), N-acetyl 321 glucosamine (1032 kb), xylose(1550 kb), ribose (1685 kb), mannose (777 kb), gluconate(606 and 2253 322 kb), maltose (692, 700 and 1526kb), lactose (2040 kb), galactose (2045 kb), mannitol(33 kb), different 323 -glucosides (186, 419, 830, 1490and 1520 kb). Glucuronate or galacturonate catabolic operon (1670 324 kb) can be used for utilisation of pectin degradation products as a supplementary source of energy and 325 carbon. Components of sugar-specific enzyme II of phosphoenol-pyruvate dependent transport systems 326 were found for mannitol (30 kb), sucrose or trehalose (435 kb), fructose (984 and 1747kb), mannose 327 (1748 kb) and -glucosides (175, 416, 830,1144 and 1489 kb). These findings are summarised in Table 328 4, along with references to experimental data on the growth of L. lactis on different carbon sources. The 329 ability to grow more efficiently in particular conditions can be acquired by L. lactis by means of plasmid 330 transfer. This is well illustrated by experimental studies of the system needed for efficient growth of L. 331 lactis in milk. To overgrow other bacteria in this niche L. lactis needs efficient systems for utilisation of 332 lactose and peptides. Such genes, which include PEP-dependent transporter for lactose and proteinase 333 for peptides, were found in the plasmidpLP712 isolated from Streptococcus lactis NCDO 712 (Gasson 334 1983; Maeda & Gasson 1986). The systemin coded by pLP712 contains a PEP-dependent transporter 335 for lactose. This allows efficient entry of lactose into glycolytic pathways through glucose, which is 336 phosphorylated by glucokinase, and galactose-6P, which is metabolised through the tagatose-6P 337 pathway, also encoded by pLP712. Sequence analysis of the IL1403 chromosome revealed that the genes 338 encoding the PTS-dependent pathway of lactose utilisation are absent in this strain. The chromosome 339 contains, however, another system for lactose utilisation, dependent on the transport by the product of 340 the lacS gene, encoding an HC symporter or galactose-lactose antiporter. This system was characterised 341 earlier for Streptococcus thermophilus. Special selection is needed for S. thermophilus strains to be able 342 to ferment galactose (Thomas & Craw, 1984; Hutkins et al. 1985). Strain IL1403 was isolated from 343 cheese starter culture and cured from plasmids for the purpose to be used as a general genetic engineering 344 host (Chopin et al. 1984; Simon et al. 1985). Probably one of the eliminated plasmids contained genes 345 for efficient utilisation of lactose, similar to the ones encoded by pLP712.

346 Chromosomal genes for galactose and lactose utilisation were cloned and characterised recently from347 different L. lactis strains (Grossiord et al. 1998; Vaughan et al. 1998). It appeared that the strains can be

divided in two groups by their possession or lack of the inducible -galactosidase gene. Since we found
the gene in IL1403, this strain belongs to the former group. It is different in this respect from another
model strain cured of plasmids, MG1363 (Gasson 1983), which does not have -galactosidase.

Automatic analysis detected 14 genes involved in glycolysis, completing the description of this system and revealed a second glyceraldehyde-phosphate dehydrogenase gene. It also confirmed the absence of a complete citric acid cycle, revealing only the genes working around pyruvate, like citrate lyase (5 genes), malate oxidoreductase and pyruvate dehydrogenase (4 genes). Close analysis of the genes automatically classified as relevant to glyconeogenesis confirmed that this process is not present in L.lactis. No genes for fructose 1,6 bisphosphatase, phos71phoenolpyruvate carboxy kinase or phosphoenolpyruvate synthetase were found.

It is interesting to mention that all genes of the pentose-phosphate pathway were detected, but not a putative trans-aldolase. It is not yet clear which gene is encoding this function in B. subtilis. It seems that the structure of the corresponding enzyme in AT-rich gram positive bacteria is different from that in gram negative and GC-rich gram positive bacteria. The corresponding gene in AT-rich gram positive bacteria still has to be identified.

363

364 *Cell envelope* 

365 The cell surface structure has a large impact on the properties of lactic acid bacteria relevant for their 366 application in milk industry, such as resistance to stress, cell lysis, sensitivity to phages antimicrobial 367 agents and influence on the product texture. However, very few studies, mostly related to the potential 368 application of lactic acid bacteria as a live vehicle for vaccine delivery, were reported (Pouwels et al. 369 1998). Our analysis revealed 73 genes implicated in cell envelope function, including 29 membrane 370 proteins, 23 murein succulus and peptidoglycan biosynthesis genes and 21 surface polysaccharide 371 biosynthesis genes. Operons for the biosynthesis of extracellular polysaccharides were identified 372 recently in the chromosome of Streptococcus thermophilus (Stingele et al. 1996) and on a plasmid in L. 373 lactis (van Kranenburg et al. 1997). We did not find similar genes in the chromosome ofIL1403. This 374 may be another property of industrial interest which is encoded and propagated predominantly by 375 plasmids in L. lactis.

#### **377** *Cellular processes*

378 L. lactis is not known as a good secretor of proteins compared to, for example, Bacillus species. 379 Optimised gene constructions allow L. lactis to produce up to 20 mg of foreign protein per litre (Wells 380 et al. 1993;Le Loir et al. 1998), compared to 800 mg produced by B. subtilis (Hemila et al. 1992). The 381 reasons maybe the lack of some components of the secretion machinery or the inefficiency of energy 382 metabolism. We did not detect components such as secDF genes, which are known to improve the 383 secretion efficiency in gram negative and gram positive bacteria (Pogliano& Beckwith1994; Duong & 384 Wickner 1997; Bolhuis et al. 1998). Also, only one signal peptidase gene was foundin IL1403, compared 385 to five detected in the B. subtilis genome (Kunst et al. 1997). Probably, the useful genes Figure 10. 386 Distribution of the detected genes by functional categories. Colours designating different categories are 387 defined in the legend of Figure 9. The number and the percentage of homology hits to SwissProt are 388 indicated for each category. Classification method is presented in the text. for protein secretion can be 389 acquired by lactococci from closely related species through plasmid transfer, if selective conditions for 390 this are created by industrial applications.

391 Natural competence for DNA-mediated transformation was not described for L. lactis species. However, 392 we found that the L. lactis genome contains four operons, comE, comF, comC and comG, which encode 393 nine genes that share strong similarity with the late competence genes from B. subtilis and S. 394 pneumoniae. Since L. lactis seems to possess a complete set of these genes and since no function other 395 than the involvement in DNA-mediated transformation is known for them, it is possible that L. lactis 396 can acquire natural competence. Sequence studies of late competence genes showed that they are quite 397 similar in different AT-richgram positive bacteria, like B. subtilis or Streptococci (Dubnau 1997; 398 Campbell et al. 1998). It is apparental so that a big difference exists in the molecular mechanisms which 399 regulate the development of this process in Streptococci and Bacilli. In B. subtilis the regulator ComK 400 assembles the signals from earlier stages of competence development (van Sinderen et al. 1995; Hahn 401 et al. 1996). A functional counterpart of such a regulator was not yet discovered for Streptococci. A way 402 to discover the conditions for acquiring the competence may be the study of regulation of the late genes. 403 We analysed the regions preceding the first ORF in the four late competence operons. The corresponding 404 alignment is shown in Figure 11. It is apparent that a common feature exists for these regions, which 405 suggests that they may be recognised by a common transcription regulator. An interesting feature, which 406 seems to be unique for these genes, is the presence of a strictly conserved sequence AGTATG, in which 407 ATG always corresponds to the start codon of the first gene in each operon. This is different from the 408 usual ribosome binding site in AT-rich gram positive bacteria, which has a sequence (SD) homologous 409 to the 30-end of 16S rRNA (Vollenoweth & Rabinowitz1992). Several recent reports show that the 410 efficiency of translation may be not much lower for mRNAs that start directly from ATG codon than 411 for mRNAs withlong leaders and strong SD-sequences (Resch et al. 1996; Moll et al. 1998; Van Etten 412 & Janssen 1998), and that the ribosomal protein S1 is not needed for the translation of unleadered mRNA 413 (Tedin et al. 1997). It appears that the absence of the leader region is a common feature of mRNAs of 414 late competence genes in L. lactis.

415 Studies of the regulation of competence in Streptococci revealed the presence of a gene, encoding a 416 small peptide, that stimulates the induction of expression of the whole competence regulon (Havarstein 417 et al. 1995, 1997). In Streptococci the gene encoding competence-stimulating peptide (CSP) precursor 418 was always found to be the first gene of an operon encoding a two-component regulatory system, which 419 is involved in the induction of competence (Havarstein et al. 1996). Homology search over the L. lactis 420 genome sequence did not reveal any two-component system which resembles the one regulating 421 competence in Streptococci. However, we found an operon encoding proteins homologous to DprA or 422 Smf protein, supposed to be required for chromosomal transformation in H. influenzae, and DNA 423 topoisomerase I from B. subtilis. Interestingly, upstream of the dprA gene there is a sequence resembling 424 that found in the putative com-promoters, described above (Figure 11B). A small ORF between this 425 putative promoter and initiation codon of the dprA gene, may be a candidate for the gene of CSP 426 precursor, since the C-terminal part of the encoded peptide resembles that of CSP from Streptococci. 427 This potential CSP precursor does not have, however, a Gly-Gly pattern that is always found in the 428 Streptococcal CSP precursors (Havarstein et al. 1997).

429

#### 430 *Regulatory functions*

Regulation of gene expression in L. lactis was not yet thoroughly explored. A few examples of
experimental study of chromosomal gene regulation are known (Bardowski et al. 1994; Kilstrup &
Martinussen 1998;Luesink et al. 1998; Raya et al. 1998; van de Guchte et al. 1998; Vaughan et al. 1998;
Wouters et al. 1998).Automatic analysis revealed 83 genes potentially involved in regulation, which is

about 6% of the total number of the identified ORFs. This figure is about two times higher than that for
M. genitalium (Fraser et al. 1995), coincides with that found in H. influenzae (Fleischmann et al. 1995)
and is about two-fold lower than that found in B. subtilis using the same classification criteria (Lapidus
et al. 1997). These ratios support the hypothesis that the increase of genome size in bacteria results in
the proportional increase of the number of different regulatory systems.

Seven two-component systems were detected. They are all organised in operons, consisting of a cognate
sensor kinase and a response regulator. The genes of five two-component systems were cloned recently
from the strain MG1363 by complementation of E.coli mutants (O'Connell-Motherway et al. 1997). All
of them were identified in our sequence.

444 An interesting class of regulatory genes are the RAS-like GTP-binding proteins. Several such regulators 445 were found in other bacteria, including the most intensively studied Era protein of E. coli, Obg of 446 B.subtilis and several others, usually revealed by genome sequencing. Exact biological functions of most 447 of these proteins are unknown, although they are sometimes essential and have pleiotropic functions. 448 Interestingly, although all these proteins are homologous and can be considered as a family of paralogs. 449 Each of the nine L. lactis proteins has its clear counterpart in B. subtilis or other bacteria. This suggests 450 that each of these proteins may have a unique biological function in the cell and that revealing it in one 451 microorganism will be directly applicable to the others. It would be interesting to test whether the 452 counterparts of the B. subtilis genes from L. lactis can complement the corresponding mutations in B. 453 subtilis and vice versa. A gene encoding the extra cytoplasmic function (ECF) -factor was detected in 454 L. lactis. This finding can be interesting for studies of regulation of stress response in L. lactis. It is not 455 clear if any of the 11ECF -factors from B. subtilis has the same biological function as the one detected 456 in L. lactis. The most similar proteins are SigV, SigX and YlaC, butthe biological function of none of 457 them has yet been established in B. subtilis.

458

#### 459 *Replication, transcription and translation*

460 Seventy-seven, 30 and 134 genes were assigned to replication, transcription and translation functional 461 categories, respectively. It is apparent that the replication system of L. lactis is very similar to that of 462 B.subtilis. Counterparts of dnaB and dnaD genes, essential for DNA replication in B. subtilis and not 463 presen tin gram negative bacteria were detected. Two DNA polymerase III -chain genes, one 464 corresponding to polC and another to dnaE of B. subtilis, were also detected in L. lactis. E. coli has only
465 the latter gene. The transcription and translation machinery does not seem to have any remarkable
466 difference compared to B. subtilis. Presumably B. subtilis with its well-developed genetic tools can be
467 a convenient host organism to study gene regulation of L. lactis systems.

468

## 469 **Conclusions and perspectives**

We present here the data on a diagnostic sequencing study of the L. lactis IL1403 genome. The sequencing data with a low average redundancy (about 2) allowed to reveal 1495 proteins, encoded by the L. lactis genome, and to classify them by functions predicted on the basis of homology to known proteins. Some statistical properties of the L. lactis genome sequence were also calculated.

474 The data presented here allow to evaluate L. lactisas a model organism for studies of bacterial 475 metabolism, physiology and regulation. Compared to the well established models, like E. coli or B. 476 subtilis, L.lactis represents a simplified system and is, therefore, potentially more amenable for detailed 477 understanding. The absence of numerous genes, relative to E. coli orB. subtilis, should facilitate, in the 478 case of L. lactis, detecting of phenotypes associated with genes of unknownfunction. With regard to 479 even more simple microorganisms, such as Mycoplasma, the advantage of L. lactis is the ease of 480 manipulation and the absence of any pathogenicity for humans. These properties, with the complete 481 genome information available, place L.lactis among the best model bacteria, to be used for fundamental 482 biological research.

483

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  transcriptional analysis of a family of five csp genes of Lactococcus lactis MG1363.Microbiology 144
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- 707



*Figure 1*. Probability of successful amplification in MLA PCR as a function of the number of oligonucleotides used in the same mixture. The calculation was done by generating the results of 10,000 independent random experiments and averaging these results. The longest distance between primers still allowing the amplification was supposed to be 20 kb. The genome sizes used for calculation are: 1 Mb (dashed line); 2.35 Mb (bold line); 4.2 Mb (thin line); 8 Mb (dotted line).

A



contains 8 (N) primers. The numbers at the top designate reaction mixtures, the numbers on the left designate individual primers, the '+' sign indicates presence of a given primer in a reaction mixture. The three last rows indicate the reaction mixtures in which amplification does (y) or does not (n) take place, if the primer couples 1 and 8, 3 and 4 or 12 and 15, respectively, give a product. To identify the primers which give a product from the analysis of the reactions the following rule is used: If N<sub>1</sub> and N<sub>2</sub> are the first and the last positive reaction, respectively, the primers giving the product will be:  $P_1 = N_1$ ;  $P_2 = N_2 - N+1$ , if  $N_2 > N_1$  (the cases  $1 \times 8$  and  $3 \times 4$ ), or  $P_2 = M + N_2 - N+1$ , if  $N_2 < N_1$  (the case  $12 \times 15$ ). (B) Part of a real experiment with 96 primers, where each reaction contained 32 primers and *L. lactis* IL1403 chromosome as template. Sizes and positions of identified fragments are shown on the left. Numbers on the top designate the reaction mix. Arrows on the top indicate the reactions that are used to identify the primers which gave the 10 kb fragment. These primers are  $P_1 = N_1 = 7$ , and  $P_2 = N_2 - N+1 = 34 - 32 + 1 = 3$ .

Figure 2. MLA PCR procedure. (A) The table illustrates a theoretical experiment with a total of 16 (M) primers, where each reaction mixture





Figure 3. Whole-genome PCR amplification of the L. lactis IL1403 chromosome. 266 oligonucleotides were used in 133 LR PCR reactions to amplify the entire genome. Correspondence of the sizes of amplified fragments and the physical map predicted from the sequence (Figure 9) indicates the correctness of sequence assembling. Left slot on each panel shows size marker (DNA of phage  $\lambda$  cut by HindIII). The PCR product designations correspond to the ones shown on Figure 9. The first panel from the top, left to the right: BA7, BA8, BB1, BB2, CC1, CC3, BB3, BB4, CC5, CC6, BB5, BB6, BB7, BA1, CB8, BB8, BC1, BC2, CL1, CL2, BC4, BA2, BC5, BC6, BC7, CB3, BC8, BD1, BD2; second panel: BD3, CB4, CC7, CC8, CD1, CD2, CD3, CG4, BD4, CD4, cg7, BD5, BD6, BD7, BD8, BE1, CH4, CE1, BE2, BE3, BE4, BE5, BE6, BE7, BE8, BF1, BF2, BF3, BF4; third panel: BF5, BA3, BF6, BF7, BF8, BG1, BG2, BG3, BG4, BG5, BG6, BG7, BG8, BH1, BH2, BH3, BH4, BA4, BH5, BH6, BH7, BH8, CB5, BI1, BI2, BI3, BI4, DA1, DA2; fourth panel: BI5, BI6, BI7, BI8, BJ1, BJ2, BJ3, BJ4, BJ5, BJ6, BJ7, BJ8, BK1, CB7, BK2, BK3, BK4, BA5, BK5, BK6, BK7, BK8, BL1, BL2, BL3, BL4, BL5, BL6, CE3; fifth panel: CE4, CK5, CK7, BA6, BL8, CE7, CE8, CA1, CA2, CA3, CA4, CA5, CA6, CA7, CA8, CB1, CF3. The sequences of the used oligonucleotides can be found at http://spock.jouy.inra.fr. Chromosome drawing, which is complementary to the one shown on Figure 9, approximately corresponds to the PCR fragments above it.







Figure 4. Distribution of the GC-content over the *L. lactis* chromosome. Zero point corresponds to the position of the origin of replication. Top panel: a sliding window of 20 kb and a step of 5 kb were used. Bottom panel: a sliding window of 5 kb and the step of 2 kb were used. The peaks near coordinates 540, 1970, 2210, 2250, 2325 and 2340 correspond to tRNA operons. A peak near 2150 kb corresponds to the cluster of ribosomal protein genes.





Figure 5. GC and AT skew distribution over the L. lactis genome. Top panel: a sliding window of 10 kb and step of 1 kb were used. Inset: a sliding window of 1 kb and step of 0.1 kb, were used. In both cases a region near the *dnAd* gene was analysed. Change of the skew distribution sign indicates the position of replication origin. Bottom panel: a sliding window 20 kb and a step of 5 kb were used. Lactis genoeme was analysed. Change of the skew distribution sign indicates the position of replication origin.

tattaggcacgccggccagccagtcggtacaagtaccaacttcagcgctcaacttgcatg ataatccgtgcggcggtcggtcagccatgttcatggttggaagtcgcgagttgaacgtac	2344620
cgttcgtcctgagccaggatcaaactctcaaataaagtatttaagtcaccttagtgactg gcaagcaggactcggtcctagtttgagagtttattcaataaattcagtggaatcactgac	2344680
gcttgtctttcattattgattgacagatttttgatgtatttactacatcatgagtca cgaacagaaagtaataactaactgtctaaaaactacatagaatgatgtagtgtactcagt	2344740
ttettetttatteagtttteaatggtetagettategetteaagaeeetegtetettgeg aagaagaaataagteaaaagttaeeagategaatagegaagttetgggageagagaaeege	2344800
acaactattatattetateaaacctaactaacttgtcaagaattaactgtgactttlat tgttgataatataagatagtttggattgatttgaacagttettaattgacactgaaaata	2344860
acctttttttatettacgttegettttteceteteetgtattegetttattteatgecac tggaaaaaatagaatgeaagegaaaaageggaggggeataagegaaataaagtaeggtg	2344920
cactagettiggiaaattaaaaaattägiettittiaaettigettittettittitaa gtgategaaaeeatttaattittitaateagaaaaattgaaegaaaaaagaaaaaatt	2344980
taagataaggtgcttattttagtcttctttaccttatgagaataaaattctttgattitt attctattccacggataaaatcagaagaaatggaatactcttattttaagaaactaaaaa	2345040
acgtagaaatgatgtttttaaacttaactaaatttttattataastagtagaaaattgaa tgcatctttactacaaaaatttgaattgatttaaaaaataatatttatcatcttttaactt	2345100
ttetetttatttattgeaaatagtttgtetetatatteegtetttatatagtaga <b>AAG</b> aagagaaaataaaataaegtttateaaacagagatataaggeagaaatatateatet <b>TTC</b>	0
Hind	III
Hind	111
Hind CTTassatttascaatcattttcaaattcttagattctattacattagagataaaatat GAAttttaaattgttagataasagtttaagataatgtaatcttattttäta	<i>111</i> 60
Hind CTTassatttaacaatctatttcaaattcttagattctattacattagagataaaatat GALttaaattgttagataaagttLaagaatctaagataatgtaactcttatttäta ccccaaagatagaaagactgtctaaaagttgtggaaatttttcttaatttttttt	60 120
Hind CTTmemettLascentcttlttcanettcttegeittcattacattegggtananatte GM-tttanaltgtLagatanangttLaggatctaggtagtdatcttatttaa geggtttctatcttttctggggttctaatttttctttttttt	111 60 120 180
Hind CTTassastttaacaatctatttcaaattcttagattctattacattagogataaaatat GALttaaattgttagataaagttlaagaatctagataatgtaactctatttata ccccaaagatagaaagactgtcaaaagctgtgggtaaattttcttaattttttettt ggggttctattttttgacagatttcgaccacttaaaagaattaaaaaaaa	50 120 180
Hind CTTmemetttascentotttttcaanttottagottaatta GAAtttaanttyttagotamaagttaagaatotagataatgotatottatta eccommigatagaaagactgtotaaaagttggtmaattttottattttöttt ggggttotatottttotgacagattttogacaccattamamagaattaanamagaaaa tocaagtaaatamtotatamattgactttttttgattggtggtaagtotgtotgat ggggtatttagtatttagaatttaaattgaacttggtggtaagtotgtogtat Dinah box ttgatattaatottttttgggtgataagaaagttttagesttt	111 60 120 180 240
Hind CTTmemetitaacaatottitticaaattottagattaatataattagagtaattaa GAAttitaaattgutagtaanagttaagaatctaggatagtaattottatta gaggttotatottittigaagattutogaaccattaamaagaattaanaaagaaaa tocaaagtaaataatotataaattgacttittitgattgiggataagtotgutogat aggtgtattatagatattaaatgagaaaaaataaaaaacaaac	50 120 180 240
Hind CTTaeaaatttaacaatctatttcaaattcttagattctattacattagogataaaatat GALttaaattgttagataaagtttagoattaagataatgtaactctatttata ccccaaagatagaaagactgtcaaaagtgtggtaaattttcttaattttttctt tgggttctatttttgacattttcgacctattaaaagaataaagaaa tccacagtaaataatctataaattggactttttggtggtaagtcggtagaat gggtgtatttattagattttcggacatagt bna box ttgatatacttttttggtggtaaaattttcgacaatttggacat Dna box ttaataagttttctagggtggaaacttttggaaatggtgcaaag taataatggtgaaagatgctggtggaaacttttcgacattgggaa attattggaaagggtgcaaatttcggaaatggtgaaaacttttcgaaatggtgcaaag taataaggtgaaagatgctggtggaaactttttggaaatggtgcaaag taataaggtgaaagataccacttttttgaaatggtggaaagatttcggaa attattggaaaggataccacttttttggaaatggtggaaacttttcaacgatgtggaa	111 60 120 180 240 300
Hind CTTanantttascantctttticaanticttagattagatagatagatagataga GTTanantttascantctttticaantigattagatagatagatagatagataga Coccasagatagatagaaagactgictaaaagutgiggtaaatttticttaattiticittti gygyttictacttttictgagatttticgaacacttttaaamagaata aggtgicatttattagatattagatagagaaaactttitgigggataagitegigtagatag tiggattactattictigigggataagaaacttittagacagatgigtaa aggtgicatttictigigggataagaaacttittagacagatgigtaa tiggatattattgaaaaaggacactttittiggatattgaataggigticaaaag tiggatattattgaaaaaggacacttittiggaaaagigtaataggigtigaaa aattattgaaaaaggatacacttittiggataataaggigtigaaa aattattgaaaaaggatacacttittiggaagaaaacattaaggigtigaaaa	111 60 120 180 240 300
Hind CTTanaatttaacaatctttticaaattcttagattaattaacattagggataacaatta GAAtttaaatgtlagataaaggattaagaactaggataatgtaattottatta GAAtttaaatgtagaaagactgtctaaaagttaggatattgtaatttittatt ggggtttctatcttlttggaggttttcgacaccatttaaaaaggattaaaaaggaaa tccaaggtaaataatctataaattgacttttttggtggtaaggtctgtgtaat ggggtatttatagtatttagatattgaaaaacattacaaagtttg aactataatggtgaaaaggacactttctttggaaatgtgaaaagttg aactataatggtgaaaagattctggaaaacatttaaaagtgtgaaaa auttattgaaaagaataccactttgaaattgaattggaatgacagttggaaa aattattgaaaagaataaccactttgaaatgtgtaattggtggaaagatttggaatgataatgggtataatg ttaataacgtgaatgaataatgaggattaaggagtatatg Maatatgggaatgataaggagttaggttggaaagatagat	III 60 120 180 240 300 dnaA 360
Hind CTTasaatttaacaattattticaaattttagattatacttaggataataatta GAItttaaattyllagataaagttaggatatagataatgtaatttatta coccaaagtagaaagaacgactgtcgtaggtaaattttictatttictitt gggtttctatctttlcigacgattttcgacacatttaaagaata tocacagtaaataatotataaattgacttttigattgggataagtotgjtgtaga agtgtcatttattaggatattaaactgaaaaactaaacootattosgacatacgta tgatattactoattttictgggataagaaaacttataactattosgacatacgta tgatattactaatttictgggataagaaacttttgaaatgtgtcaaaatgtg taataactttttetaggggaaacttotttgaaagaaacattaagtgtcgaaa attattgaaaaggataccacctttgaaagaaaactaagtgtcgaaa attattgaaaaggataccacctttgaaagaaaactaagtgtcgaaa attattgaaaaggataccacctttgaaagaaaactaagtgtcgaaa attattgaaaaggataccacctttgaaagaaaactaagtgtcgaacactgtggaaa attattgaaaaggataccacctttgaaagaaaacataagtgtccacatta	111 60 120 180 240 300 dnaA 360
Hind CTTasaatttaacaatottttcaaattottagattaattaattagatagataaaatt GAAtttaattglagataaaagttaagaattagatatglaattottatttaa Gaattaattagtagaaagatglaaagatttogaactagataglaattottatttaa teccaagtaaataatetaaattgacttttttgglgglaagtteltottattetta ggggttttattattagatttagatttggataagaactaacgaattagaa ttgatattactattttttgggtgataagaacttttttggataggaagttotagtogaa ttgatattactattttttgggtgataagaactttttagaattggagataggtocaagtt gaattatggataagatagcacttttttggataagaatgtgaaag ttgatattactatttttttgggtgaagaacttttttggatatggatgaagtgcagaa ttgatattactatttttttgggtgaagaacttttttgaattggagagtgaagt aattatggaaaagataccactttttagaattaagtgtgaaag attatgaaaagaatggataatgggtaataggagtaatg Maatasctggaaagatgataaggggtaatg A S L N E N O K F W A R V T E L A 0 Q S	111 60 120 180 240 300 dnaA 360 dnaA
Hind CTTasaatttascaattatttictaasttottagattastattasttagatagatasaagtt GNAtttastglagatasaagttlaagaattagatatglaatttittat gggtttctatttittggggttlagaagtttiggtaaattticttatttittittitti ggggtttctattettugacagatttiggacaccatttasaaagaattaasaagaaa tccaagtaaataatctasaattigactttittiggtggtaagtettigatagtotgttgata gggggtatttiggtaagaacattasttiggagaagaatticgggaagtagtgggaa ttgatattastagtagtaaaaggacactattittiggaattiggaagatgggaag ttgatattastagtggaaagaattittigaattiggagaagtgaagt	111 60 120 180 240 300 dnaA 360 dnaA 420
Hind CTEnenetitascantotiticaantotieugaitataacategadeataatata GALtitaaatigtiagataaaagtitaagaatotagatataacategataatigtattotitata GALtitaaatigtiggaaagaatgaatgaaagaatgaaagaatgaaagaagaag	III 60 120 180 240 300 dnaA 420 dnaA

Figure 6. Sequence of the L lactic chromosome near the origin of replication. The HindIII site shown in bold was chosen as a zero point to represent the genetic map of L. lactis IL1403. Putative DnaA boxes are shown in bold. The begining of the dnaA gene and of the rrnA genes are shown. Numbering corresponds to that used in the map shown on Figure 9.

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Figure 7. Identification of putative prophages in the *L*. lactis IL1403 genome. The distribution shows the number of phage protein hits detected with a sliding window of 50 kb with a step of 10 kb, over the whole genome. Total number of hits on both strands is shown by bold line. Thin line shows difference of the numbers of hits detected separately on each strand and indicates the orientation of most of the phage genes.



Figure 8. Distribution of chi-sites over the *L. lactis* genome. The distribution represents the number of chi sequences detected with a sliding window of 300 kb with a step of 10 kb, over the whole genome. Filled circles show total numbers of chi-sites in the window, open circles show the difference of the numbers of sites detected separately on each strand, refered to as D and R.

Figure 9. Linear representation of the Llactis IL1403 genome.

The map shows predicted protein-encoding genes, IS-elements, RNA genes and the ends of regions amplified by PCR (Fig.3). The genes are shown as arrows, with the best BLASTs hit SwissProt name indicated above. Colours correspond to the functional categories assigned by the automatic gene classification method described in the text: amino acid biosynthesis ( $\rightarrow$ ), biosynthesis of cofactors ( $\rightarrow$ ), cell envelope ( $\rightarrow$ ), cellular processes ( $\rightarrow$ ), central intermediary metabolism ( $\rightarrow$ ), centry metabolism ( $\rightarrow$ ), centry metabolism ( $\rightarrow$ ), centry metabolism ( $\rightarrow$ ), regulatory functions ( $\rightarrow$ ), purines, pyrimidines, nucleosides and nucleotides ( $\rightarrow$ ), transport and binding proteins ( $\rightarrow$ ), other categories ( $\rightarrow$ ), translation ( $\rightarrow$ ), transport and binding proteins ( $\rightarrow$ ), other categories ( $\rightarrow$ ), hypothetical and unknown ( $\neg$ ). The arrows outlined by bold line correspond to the proteins whose size differ less than 20% of their Swissprot homologue. IS-elements and rRNA genes are shown as black arrows with corresponding designation inside. Arrow directions for IS-elements are arbitrary, indicating orientations. tRNA genes are shown as small black triangles. The ends of regions amplified by PCR are indicated by open arrows below the scale line. Identifier and size of the region are indicated near the left end.











Figure 9.





Figure 10. Distribution of the detected genes by functional categories. Colours designating different categories are defined in the legend of Figure 9. The number and the percentage of homology hits to SwissProt are indicated for each category. Classification method is presented in the text.

А

aaattttcggctttt	tt <b>GTTACATT</b> aactg <b>A</b> tta <b>TT</b>	<b>T</b> g <b>CGTATA</b> gtc1	AGTATO	(	comGA	
tgattttaacaaatt	tt <b>GTTACATT</b> ttaac <b>A</b> gca <b>TT</b>	<b>TCGTATA</b> gaat	AGTATG.	c	omFA	
ttataattcaactct	tg <b>G</b> aa <b>AC</b> t <b>TT</b> ccaag <b>A</b> gtt <b>TT</b>	<b>TCGTATA</b> taaa	AGTATG.	c	OMEA	
tttcgctatattta	aa <b>GTTACA</b> aTtetteAtttaT	<b>TCGTATA</b> gtat	t <b>AGTATG</b> .	c	omC	
consensus	GTTACATTnnnnAnnnTTT	<b>FTCGTATA</b> nnnn	AGT			
в						
tgtcagtaattttt	tg <b>GTTACA</b> agtcagtcttt <b>TT</b>	<b>PaCGTATA</b> gaaa	<b>A</b> t <b>T</b> ataa	gccaat	tttaaaa	ittg
	м	ITNF	DLY	RW	КК	А
ctgacaaagctgtca	gtaaaaatGGAGGaattATGa	ataacaaatttt	gatttata	togttg	gaaaaaa	gct

G M T N L G V N K L L K F F H R Y D K K stop ggcatgaccasttaggagtaaataaacttttaaaatttttcatagatatgataaaaaaTAAgtttaagac

Figure 11. Regulatory regions of the L. lactis competence genes. (A) Sequences of the regions upstream of the first gene in the four putative competence operons. Sequences corresponding to the recognition site of a hypothetical regulator are shown in bold capital letters. Start codons of the competence genes are italicised. Consensus sequence of the recognition site is shown at the bottom. (B) Sequence of the upstream region of the dprA gene. Putative recognition is of the hypothetical competence regulator is shown in bold capital letters. Conceptual translation of a small ORF upstream of the dprA gene is shown.

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Table 1. Low-redundancy whole-genome sequencing strategy

Stage	Description
Random small insert and large insert library construction	Shearing DNA randomly to 1–2 kb and 15–20 kb, respectively. Cloning in multicopy plasmids and $\lambda$ -based FIXII vector.
Random sequencing of a limited number of plasmid inserts	Sequencing of plasmid inserts up to coverage of about one. Using forward (M13-21), reverse (M13RP1) and middle primers. The latter are chosen to sequence the middle of plasmid inserts, when necessary. Assembling is done in parallel with sequencing.
Random sequencing of a number of large inserts by primer walking.	Sequencing of large inserts by using synthetic oligonucleotides. Assembling is done in parallel with sequencing to avoid too high redundancy.
Synthesis of new sequencing substrates by MLA PCR approach.	Application of Multiplex Long Accurate PCR protocol for random generation of new sequencing substrates.
Sequencing of MLA PCR products.	Sequencing of MLA PCR products by primer walking. Assembling is done in parallel with sequencing.
Iteration	Iteration of the last two stages until the whole contigous genome sequence is obtained.
Annotation	On-line annotation is done in parallel with the sequencing progress by using automatic computer tools based on BLASTx and FASTx algorithms.



Table 2. Summary of low-redundancy sequencing of the L. lactis IL1403 genome\*

Small insert plasmids	2854
Average insert length (bp)	1520
Forward sequence reactions (M13-21 primer)	2625
Average useful sequence length (bp)	462
Reverse sequence reactions (M13RP1 primer)	2168
Average useful sequence length (bp)	422
Sequencing reactions in the middle of insert	2357
Average read length (bp)	494
Total characters from plasmid insert sequencing (bp)	3292004
Number of selected $\lambda$ -clones	122
Average insert length (kb)	15.6
Number of gel readings from $\lambda$ -inserts	622
Average read length (bp)	409
Total characters from $\lambda$ -insert reads (bp)	254398
Number of gel readings from LR PCR products	1641
Average read length (bp)	470
Total characters read from LR PCR products (bp)	771270
Total oligonucleotides used	4620
Total gel readings	10235
Average read length (bp)	458
Total characters read (bp)	4687630
Size of final contig (bp)	2345160
Undefined letters in the final contig (bp)	3563

\*The figures were estimated by analysis of the assembling database and are therefore approximate ( $\pm 5\%$ ).

Table 3. Functional classification of the L. lactis genes. Genes are ordered by functional categories and their positions on the chromosome. Position on the chromosome (in kb) and the percentage of identity with the most homologous Swissprot entry is also shown

#### BIO01. AMINO-ACID BIOSYNTHESIS

95 genes

BIO01.01 Gene	ral		2 genes
DHSS_SYNP1	29%	485	SOLUBLE HYDROGENASE, SMALL SUBUNIT (EC 1.12)
PATB_BACSU	57%	1974	PUTATIVE AMINOTRANSFERASE B (EC 2.6.1)
BIO01.02 Aron	matic amin	no-acid	family 19 genes
AROF_ECOLI	41%	117	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYR-SENSITIVE {EC
4.1.2.15)			
TRPE_THEMA	26%	736	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
AROG_HAEIN	40%	1278	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATS ALDOLASE (EC 4.1.2.15)
TRPA_LACLA	100%	1492	TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
TRPB_LACLA	100%	1493	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
TRPF_LACLA	99%	1495	N-(5*-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
TRPC_LACLA	100%	1495	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
TRPD_LACLA	1008	1430	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (BC 2.4.2.10)
TRPG_LACLA	99%	1497	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
TRPE_LACLA	100%	1696	ANTHRANILATE SINTHASE COMPONENT 1 (EC. 4.1.5.27)
AROD_BACSU	378	1585	3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)
PHEA_LACLA	1008	1701	PREPHENATE DENIDRATASE (EC 4.2.1.51)
AROK_LACLA	1008	1701	SHIAIMATE AINASE (D. 2./.1./1) 2. Duogduoguittimate 1. (Abboysuitmui gennerrenter (DC 2.5.1.19)
AROA_LACLA	948	1782	DEPENDER DEVELOCENSE (EC 1 2 1 12)
ADOG DACUA	506	1700	CHORTCHARE CONDUCED (DC 4 6 1 4)
AROC_BACSO	206	1704	CHORESPECTE SERVICE (EC. 4.0.1.4) 2 DEDUCDOOUTNING CONTRACT (EC. 4.6.1.2)
AROB_REDFI	376	1795	S-DEMIDROQUINATE SINTASE (E. 4.6.1.5) Nybomupaton, 21.2 No provern IN LDD-ADOD INVERSENTS DEGION
IDIB_ECOLI	376	2261	DEGEDERAL ST.2 KD FROTEIN IN DEF-AROD INTERGENIC RESIDN
AROG_BACSO	325	3201	PROSPHO-2-DEMIDRO-3-DEDAIREPIONATE ADDOLASE (EC 4.1.2.13)
BIO01.03 Aspa	irtate far	mily	19 genes
AAT2_METJA	36%	57	PUTATIVE ASPARTATE AMINOTRANSFERASE 2 (EC 2.6.1.1)
ASSY_SYNY3	57%	125	ARGININOSUCCINATE SYNTHASE (EC 5.3.4.5)
AAT_BACSP	32%	161	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
ASNB_ECOLI	40%	354	ASPARAGINE SYNTHETASE B (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
AK_METJA	30%	746	PROBABLE ASPARTOKINASE (EC 2.7.2.4)
METB_HELPY	65%	789	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
DHOM_LACLA	93%	1169	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
KHSE_LACLA	228	1170	HOMOSERINE KINASE (EC 2.7.1.39)
METF_HAEIN	328	1279	5, 10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
METE_HAEIN	46%	1281	5-METHYDTETRAHYDROPTEROYDTRIGLOTAMATE-"HOMOCYSTEINE
METHYLTRANSFE	RASE (EC	1.500	DINUDDODIDIONINAR DEDUCTOR (EC 1 2 1 26)
DAPB_BACSU	169	1661	DIHIDRODIPICOLIMATE REDOCTAGE (EC 1.5.1.20)
DAPA_BACSU	205	1662	ACAADER CENTAL DELVDE DEUVDECCENACE (EC 1.2.1.152)
DHAS_STRMU	1010	1077	ASPAKTATE SEMIASDERIDE DENIDROGENASE (BC 1.2.1.11)
METE HELDY	419	1976	CVSTATHIONINE CAMMA-SYNTHASE (EC 4.2.99.9)
META_RCOLT	469	1977	HOMOSERINE O-SUCCINVLERANSEERASE (EC 2 3 1 46)
DADH CANAS	569	2067	HEIDVLATE KINASE (EC 2 7 4 -)
THRC DSEAF	38%	2153	THREONINE SYNTHASE (EC 4 2 99 2)
ASNE MYCTH	378	2292	DEPATIVE ASPARACINE SYNTHETASE (GLUTAMINE_HYDROLYZING) (EC
6.3.5.4)	310	2272	TOTALLES ASTARGIAE STATISTASS (SUCCEDERS) (US
HIG01.04 Bran	52%	1199	ACETOLACTATE SYNTHASE (EC 4.1.3.18)
LEU1 SYNY3	45%	1238	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
LEUS LACLA	99%	1239	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
LEU2 ACTTI	53%	1241	3-ISOPROPYLMALATE DEHYDRATASE (EC 4.2.1.33)
LEUD LACLA	100%	1242	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
TLVD LACLA	988	1244	DIHYDROXY-ACID DEHYDRATASE (EC 4.2.1.9)
TLVB LACLA	82%	1246	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
ILVN LACLA	100%	1247	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)
ILVC LACLA	97%	1247	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
THD1_LACLA	998	1249	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4,2,1,16)

TRAD UMPTIN	67%	1320	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
BIO01.05 Gluta	mate fa	mily	21 genes
ARLY CAMJE	458	126	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
ARGE ECOLI	26%	557	ACETYLORNITHINE DEACETYLASE (EC. 3.5.1.16)
ARCC LACPL	48%	802	N_ACCTVL_CAMMA_CLIPTANVL_DUCCDUATE DEDUCTACE (50.1.2.1.20)
ARGI BACSU	49%	803	CLUTAMATE N_ACETVITEANCEEDACE (EC 2 3 1 25)
ARCD SYNY3	429	804	ACETVLODNITUTNE AMINOTRANSFERENCE (PC 2 C 1 11)
ARCH METTA	428	805	DECEMPTICAL PRINTER VINAGE (EC 2.0.1.11)
ANGE_METUA	270	80.5	PROBABLE ACETILADUTADATE RINASE (EC 2.7.2.5)
MURT DACSU	2/5	1210	ARGININE HIDROXIMATE RESISTANCE PROTEIN
MURI_BACSU	608	1310	GLUTAPATE RACEMASE (EC 5.1.1.3)
VODE ROOLT	406	1312	TABA PRUTEIN
NGFT_ECOLI	345	1313	HYPOTHETICAL 59.7 KD PROTEIN IN KDUI-LYSS INTERGENIC REGION
GLTB_ECOLI	39%	1316	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
DCEB_ECOPI	43%	1322	GLUTAMATE DECARBOXYLASE BETA (EC 4.1.1.15)
CARY_BACSU	51%	1397	CARBAMOYL-PHOSPHATE SYNTHASE, ARGININE-SPECIFIC, LARGE CHAIN
(EC 6.3.5.5)			
PROA_ECOLI	468	1647	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
PROB_SYNY3	40%	1648	GLUTAMATE 5-KINASE (EC 2.7,2,11)
OTC2_BACSU	43%	1736	ORNITHINE CARBAMOYLTRANSFERASE CHAIN F (EC 2.1.3.3)
AHRC_BACSU	36%	2097	ARGININE HYDROXIMATE RESISTANCE PROTEIN
PROA_ECOLI	22%	2210	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
GLNA_STAAU	45%	2262	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
GLNA_HAEIN	41%	2263	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
RACD_STRTR	53%	2289	ASPARTATE RACEMASE (EC 5.1.1.13)
BIO01.06 Histid	dine fa	mily	9 genes
PT1P_ECOLI	27%	118	PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE PTSP (EC
2.7.3.9)			
HIS8_LACLA	96%	1226	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
HIS1_LACLA	998	1228	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
HISX_LACLA	988	1229	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
HIS7_LACLA	98%	1231	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
HIS5_LACLA	99%	1232	AMIDOTRANSFERASE HISH (EC 2.4.2)
HIS4_LACLA	96%	1233	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE
ISOMERASE (EC 5	5.3.1.1	6}	
HIS6_LACLA	988	1234	HISF PROTEIN (CYCLASE)
HIS2_LACLA	998	1235	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19) /
PHOSPHORIBOSYL	-ATP PY	ROPHOSPH	OHYDROLASE (EC 3.6.1.31)
BIO01.07 Pyruva	ate fam	ily	2 genes
DDL_ENTHR	54%	339	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4)
DDL_ENTHR ALR_BACSU	54% 43%	339 860	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1)
DDL_ENTHR ALR_BACSU	54% 43%	339 860	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1)
DDL_ENTHR ALR_BACSU BI001.08 Sering	54% 43% a famil;	339 860 ¥	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes
DDL_ENTHR ALR_BACSU BIO01.08 Sering SERC_ECOLI	54% 43% e famil; 32%	339 860 <b>y</b> 463	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY	54% 43% a famil; 32% 30%	339 860 <b>y</b> 463 471	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
DDL_ENTHR ALR_BACSU BIO01.08 Sering SERC_ECOLI GLYA_HELPY CYSK_BACSU	54% 43% e famil; 32% 30% 56%	339 860 9 463 471 524	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) <b>12 genes</b> PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU	54% 43% a famil; 32% 30% 56% 61%	339 860 463 471 524 589	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_FCOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI	54% 43% 32% 30% 56% 61% 47%	339 860 463 471 524 589 591	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) <b>12 genes</b> PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERA_HAEIN	54% 43% 32% 30% 56% 61% 47% 32%	339 860 463 471 524 589 591 592	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) <b>12 genes</b> PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU SERA_HAEIN SERB_HAEIN	54% 43% 32% 30% 56% 61% 47% 32% 42%	339 860 463 471 524 589 591 592 593	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.2.1) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERC_BACCI SERB_HAEIN CYSK_BACSU	54% 43% 32% 30% 56% 61% 47% 32% 42% 53%	339 860 463 471 524 589 591 592 592 593 790	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) D-3-PHOSPHOCLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOCERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA.HELPY CYSK_BACSU SERC_BACSU SERC_BACSU SERA_HAEIN SERB_HAEIN SERB_HAEIN CYSK_BACSU CBH_CLOPE	54% 43% 32% 30% 56% 61% 47% 32% 42% 53% 34%	339 860 463 471 524 599 591 592 593 790 1147	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERD_HAEIN SERB_HAEIN CSH_CLOPE PFLA_HAEIN	54% 43% 32% 30% 56% 61% 47% 32% 42% 53% 34% 50%	339 860 463 471 524 589 591 592 593 790 1147 1860	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCENE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERC_BACCI SERD_HAEIN CYSK_BACSU CBH_CLOPE PFLA_HAEIN CYSE_BACSU	54% 43% 32% 56% 61% 47% 32% 42% 53% 34% 50% 58%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOGERINE AMINOTRANSPERASE (EC 2.6.1.52) D-3-PHOSPHOCLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVARE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSPERASE (EC 2.1.1.30)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERC_BACCI SERB_HAEIN CYSK_BACSU CBH_CLOPE PFIA_HAEIN CYSE_BACSU PKNS_MYCCE	54% 43% 32% 56% 61% 47% 32% 42% 53% 34% 50% 58% 35%	339 860 463 471 524 599 591 592 593 790 1147 1860 1936	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) D-3-PHOSPHOCLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERA_HAEIN SERB_HAEIN CYSK_BACSU CSH_CLOPE PFLA_HAEIN CYSE_BACSU PKNS_MYCGE	54% 43% 32% 56% 61% 47% 32% 42% 53% 34% 50% 58% 35%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE HOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERC_BACCI SERB_HAEIN CYSK_BACSU PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02. BIOSYNT*	54% 43% a famil; 32% 30% 61% 47% 32% 42% 53% 34% 53% 34% 53% 35% 8ESIS 02	339 860 463 471 524 599 591 592 593 790 1147 1860 1900 1936 F COFACT	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) D-3-PHOSPHOCLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes
DDL_ENTHR ALR_BACSU BIO01.08 Sering SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU SERD_HAEIN CYSK_BACSU CBH_CLOPE PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02. BIOSYNTH	54% 43% 2 famil; 32% 56% 61% 47% 42% 53% 34% 53% 35% 35%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 F COFACT	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE HYDROXPATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU SERC_BACSU CSK_BACSU CSK_BACSU CSK_BACSU CSK_BACSU PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02. BIOSYNTF BIO02.01 Biotin	54% 43% a famil; 32% 30% 56% 61% 47% 32% 42% 53% 34% 53% 35% HESIS 02	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b>	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOGERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOGERINE AMINOTRANSPERASE (EC 2.1.52) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes 3 genes DISK
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_HAELPY CYSK_BACSU SERC_BACCI SERC_BACCI SERB_HAEIN CYSK_BACSU PFLA_HAEIN CYSK_BACSU PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02. BIOSYNTF BIO02.01 Biotir BIOY_BACSH	54% 43% 32% 56% 61% 47% 53% 42% 53% 32% 42% 53% 34% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50	339 860 463 471 524 592 592 593 790 1147 1860 1900 1936 <b>F COFACT</b>	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) D-3-PHOSPHOLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE PORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes BLOY PROTEIN PRECURSOR
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU SERC_BACCI SERD_HAEIN SERB_HAEIN CYSK_BACSU CBH_CLOPE PFIA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02. BIOSYNTH BIO02.01 Biotin BIOY_BACSH BIOY_BACSH	54% 43% a famil; 32% 56% 61% 47% 42% 42% 53% 34% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 F COFACT 313 321 321	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE HYDROXERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes BLOY PROTEIN PRECURSOR BLOY PROTEIN PRECURSOR
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU CSK_BACSU CSK_BACSU CSK_BACSU CYSK_BACSU PKIA_HAEIN CYSK_BACSU PKIAS_MYCGE BIO02.01 Biotir BIO2_BACSH BIOY_BACSH BIOY_BACSH BIOY_BACSH	54% 43% 32% 30% 56% 61% 47% 32% 42% 53% 34% 28% 35% HESIS 0 34% 28% 53%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOGERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.52) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU SERC_BACSU CSK_BACSU CSK_BACSU CSK_BACSU PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02.01 Biotir BIOY_BACSH BIOY_BACSH BIOY_BACSH ACCD_SYNP7 (EC 6.4.1.2)	54% 43% 32% 32% 56% 61% 47% 32% 53% 34% 53% 58% 35% HESIS O 34% 28% 53%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.52) D-3-PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 8 JOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU CBH_CLOPE PFLA_HAEIN CYSK_BACSU CYSK_BACSU PKNS_MYCGE BIO02.01 Biotin BIOY_BACSH BIOY_BACSH BIOY_BACSH ACCD_SYNF7 (EC 6.4.1.2) BIO02.02 Folic	54% 43% 56% 56% 61% 47% 32% 53% 34% 55% ESIS 0 34% 28% 53% acid	339 860 443 524 559 591 592 593 790 1147 1860 1900 1936 F COFACT 313 321 787	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) D-3-PHOSPHOCLYCERIE DEHYDROGENABE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLITRANSPERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 100 PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU SERC_BACCI SERA_HAEIN CYSK_BACSU PFLA_HAEIN CYSK_BACSU PFLA_HAEIN CYSE_BACSU BIO02. BIOSYNTH BIO02.01 Biotin BIOY_BACSH BIOY_BACSH BIOY_BACSH BIO02.02 Folic HPPK BACSU	54% 43% 56% 56% 61% 42% 53% 32% 42% 53% 50% 50% 50% 50% 50% 50% 50% 50% 53% 8 28% 53% 42%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE ENDERHYDROGRASE (EC 2.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETVLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE
DDL_ENTHR ALR_BACSU BIO01.08 Sering SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU SERC_BACSI SERA_HAEIN SERB_HAEIN CYSK_BACSU CBH_CLOPE PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02.01 Biotin BIO02.01 Biotin BIO02_BACSH BIO02_SYNP7 (EC 6.4.1.2) BIO02.02 Folic HPPK_BACSU	54% 43% e famil; 32% 30% 56% 61% 42% 53% 34% 28% 53% 42% 53% 34% 28% 53% 42% 53%	339 860 463 471 524 589 591 592 593 790 1147 1860 1936 F COFACT 313 321 787 1164 2,7,6,3	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.52) D-3-PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECU
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU CBH_CLOPE PFLA_HAEIN CYSK_BACSU PKNS_MYCGE BIO02.01 Biotir BIOY_BACSH BIOY_BACSH BIOY_BACSH BIOY_COFFIC PFX_BACSU PYROPHOSPHOKINA GCHI BACSU	54% 43% a famil; 32% 30% 56% 61% 47% 32% 53% 34% 53% 58% 35% tesis o: 34% 28% 53% 42% 53% 34% 28% 53%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787 1164 2.7.6.3 1164	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.1.2) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.1.2) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSPERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes 3 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE ) CTP CYCLOHYDROLASE I (EC 3.5.4.16)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_HELPY CYSK_BACSU GLYA_HACSU SERC_HACSU SERC_HAEIN SERB_HAEIN CYSK_BACSU PFLA_HAEIN CYSK_BACSU PFLA_HAEIN CYSE_BACSU PFLA_HAEIN CYSE_BACSU BIO02.01 Biotir BIO02_BACSH BIO02_BACSH BIO12_BACSH BIO12_BACSH BIO2_SYNF7 (EC 6.4.1.2) BIO02.02 Folic HPPX_BACSU PYROPHOSPHOKINA GCH1_BACSU DHPS NEIME	54% 43% 32% 56% 61% 47% 53% 42% 53% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787 787 1164 2.7.6.3 1164 1165	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE HYDROLYCENATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE PORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLITRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 3 genes BIOY PROTEIN PRECURSOR BIOY PROTEI
DDL_ENTHR ALR_BACSU BIO01.08 Sering SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU SERC_BACCI SERA_HAEIN SERB_HAEIN CYSK_BACSU CBH_CLOPE PFLA_HAEIN CYSE_BACSU PKNS_MYCCE BIO02.01 Biotin BIO02.01 Biotin BIO02.01 Biotin BIO02.02 Folic HPPK_BACSH ACCD_SYNF7 (EC 6.4.1.2) BIO02.02 Folic HPPK_BACSU PYROPHOSPHOKINA GCH1_BACSU DHPS_NEIME FOLC ECOLI	54% 43% a famil; 32% 30% 56% 61% 47% 32% 42% 53% 33% 32% 42% 53% 34% 28% 53% 42% 53% 42% 53% 34% 28% 53% 34% 28% 53% 34% 34% 34% 32% 32% 32% 32% 32% 32% 32% 32% 33% 33	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 F COFACT 313 321 787 313 321 787 1164 2.7.6.3 1164 1165	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.52) D-3-PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes 3 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE ) GTP CYCLOHYDROLASE I (EC 3.5.4.16) DHYDROPTEROATE SYNTHASE (EC 2.5.1.15) FOLVLEOUNGLATEMATE SYNTHASE (EC 2.5.1.15) FOLVLEOUNGLATE SYNTHASE (EC 2.5.1.15)
DDL_ENTHR ALR_BACSU BIO01.08 Sering SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU CSK_BACSU CSK_BACSU CSK_BACSU CSK_BACSU PFLA_HAEIN CYSE_BACSU PFLA_HAEIN CYSE_BACSU PFLA_HAEIN CYSE_BACSU BIO02.01 Biotin BIO2_BACSH BIO2_SYNF7 (EC 6.4.1.2) BIO02.02 Folic HPPX_BACSU PYROPHOSPHOKINA GCH1_BACSU DHPS_NEIME FOLC_ECOLI PABB SALTY	54% 43% 32% 30% 56% 61% 47% 32% 42% 53% 34% 28% 53% 42% 53% 34% 28% 53% 34% 32% 42% 42% 28% 53%	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 F COFACT 313 321 787 1164 2.7.6.3 1164 1165 1167 1345	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.52) D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes 3 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE ) GTP CYCLOHYDROLASE I (EC 3.5.4.16) DIHYDROPTEROATE SYNTHASE (EC 6.3.2.17) PARA-MINOBENZOATE SYNTHASE (EC 6.3.2.17) PARA-MINOBENZOATE SYNTHASE (EC 6.3.2.17) PARA-MINOBENZOATE SYNTHASE (EC 6.3.2.17) PARA-MINOBENZOATE SYNTHASE (EC 6.3.2.17)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU SERC_BACSU SERC_BACSU CBH_CLOPE PFLA_HAEIN CYSK_BACSU CYSK_BACSU PKNS_MYCGE BIO02.01 Biotir BIOY_BACSH BIOY_BACSH BIOY_BACSH BIOY_BACSH BIOY_BACSH BIOY_CFOIC HPPK_BACSU PYROPHOSPHOKINA GCH1_BACSU DHS_NEIME FOLC_ECOLI PABB_SALTY	54% 43% 32% 30% 56% 61% 47% 32% 53% 34% 53% 35% <b>HESIS O</b> 34% 28% 53% <b>acid</b> 42% C 37% 34% 32% 40% 50%	339 860 463 471 524 589 591 592 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787 <b>F COFACT</b> 1164 2.7.6.3 1164 1465 1165 1167 1345	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOGERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOGERINE MUNOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes 3 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE ) GTP CYCLOHYDROLASE I (EC 3.5.4.16) DHYDROPTEROATE SYNTHASE (EC 2.5.1.15) FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17) PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3) PARA-MINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3) PARA-MINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3)
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU SERC_BACCI SERA_HAEIN CYSK_BACSU PFLA_HAEIN CYSK_BACSU PFLA_HAEIN CYSE_BACSU PFLA_HAEIN CYSE_BACSU BIO02.01 Biotir BIO02_BACSH BIO02_BACSH BIO02_BACSH BIO02_BACSH BIO02_BACSH BIO02_BACSH DIO1_BACSH DIO2_BACSH PFNC_BACSU PYROPHOSPHOKINA CCH_SNEIME FOLC_ECOLI PABB_SALTY PABA_SALTY	54% 43% 32% 32% 56% 61% 42% 53% 32% 42% 53% 34% 28% 53% 42% 28% 53% 42% 28% 53% 42% 53% 34% 28% 53% 32% 42% 53% 32% 32% 32% 32% 32% 32% 32% 53% 53% 50% 32% 53% 50% 50% 50% 50% 50% 50% 50% 50% 50% 50	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787 313 321 787 1164 2.7.6.3 1164 1165 1164 1165 1345 31	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSFERASE (EC 2.1.2.1) PHOSPHOSERINE HYDROXERATE DEHYDROGRASE (EC 2.1.1.95) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETVLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 3 genes BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE ) GTP CYCLOHYDROLASE I (EC 3.5.4.16) DHYDROPTEROATE SYNTHASE (EC 6.3.2.17) PARA-AMINOBENZOATE SYNTHASE (EC 6.3.2.17) PARA-AMINOBENZOATE SYNTHASE GUTAMINE AMIDOTRANSFERASE
DDL_ENTHR ALR_BACSU BIO01.08 Serine SERC_ECOLI GLYA_HELPY CYSK_BACSU GLYA_BACSU GLYA_BACSU SERC_BACCI SERE_HAEIN CYSK_BACSU CBH_CLOPE PFLA_HAEIN CYSE_BACSU PKNS_MYCGE BIO02. BIOSYNTF BIO02.01 Biotin BIOY_BACSH BIOY_BACSH BIOY_BACSH ACCD_SYNP7 (EC 6.4.1.2) BIO02.02 Folic HPPXCPHOSPHOKINA GCH1_BACSU PYROPHOSPHOKINA GCH1_BACSU DHPS_NEIME FOLC_ECOLI PABB_SALTY PABA_SALTY	54% 43% 32% 32% 56% 61% 47% 42% 53% 32% 42% 50% 50% 34% 28% 53% 42% 42% 53% 42% 42% 53% 34% 28% 53% 32% 42% 53% 32% 32% 32% 32% 32% 32% 32% 32% 32% 3	339 860 463 471 524 589 591 592 593 790 1147 1860 1900 1936 <b>F COFACT</b> 313 321 787 313 321 787 1164 2.7.6.3 1164 1165 11345 1346 3)	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4) ALANINE RACEMASE (EC 5.1.1.1) 12 genes PHOSPHOSERINE AMINOTRANSPERASE (EC 2.6.1.52) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) CYSTEINE SYNTHASE (EC 4.2.99.8) SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE AMINOTRANSPERASE (EC 2.1.2.1) PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3) CYSTEINE SYNTHASE (EC 4.2.99.8) CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1) ORS, PROSTHETIC GROUPS, AND CARRIERS 100 PROTEIN PRECURSOR BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA 6 genes 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE ) CTP CYCLOHYDROLASE I (EC 3.5.4.16) DHYDROPTEROATE SYNTHASE (EC 6.3.2.17) PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE

REPARTA RABIN	46%	586	HEMK PROTEIN HOMOLOG
BPA1 STRAU	298	832	NON-HAEM BROMOPEROXIDASE BPO-A1 (EC 1.11.1)
HEMN_BACSU	46%	1151	PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC
1) BCHE BHOCA	268	1170	MACHECTIM-DOMODODDUDIN IN MANAMEMUNI DOMD ANTOMOTO ANT LOD
66 KD SUBUNIT	200	**13	ANGNESION-PROIOFORPHIKIN IN MONOMETHIL ESIER ONIDATIVE CICEASE
HEMZ_YEREN	39%	1605	FERROCHELATASE (EC 4.99.1.1)
BIO02.04 Lipoa	te		0 genes
BIO02.05 Menac	uinone a	and ubic	minone 4 genes
MENB_BACSU	73%	732	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
MEND_BACSU	428	735	2-SUCCINYL-6-HYDROXY-2, 4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE
(SHCHC SYNTHAS	E) / 2-0	XOGLUTZ	RATE DECARBOXYLASE (EC 4.1.1.71)
QUEA_HAEIN	44%	1613	S-ADENOSYLMETHIONINE: TRNA RIBOSYLTRANSFERASE-ISOMERASE (EC 5
) GRC2 LACLA	70%	1714	PROBABLE MENAOUTNONE BLOCKWPHERIC METHINFRANCEPRACE (EC. 2.1.1.
)		1,14	TROBADE HERQUINNE DIGSTRITESIS RETHETRANSPERASE (D. 2.1.1.
BIO02.06 Molyb	dopteri	1	0 genes
BIO02.07 Panto	thenate		1 genes
COAA_HABIN	43%	1464	PANTOTHENATE KINASE (EC 2.7.1.33)
BIO02.08 Pyrid	loxine		0 genes
BIO02.09 Ribof	lavin		5 genes
RIBD ACTPL	519	1020	RIBORLAVIN-SPECIFIC DEAMINASE / PC 2 5 4
RISA ACTDL	549	1021	ETBOFLAVIN CYNTUACE ALDUA CUAIN (DC 3 5 1 0)
SCH2 ACTRI	609	1022	CTD CVCLOUVDDOLASS IT /SC 3 5 / 361 / 3 / DIVDDOVV 3 DUBLYOND
A DUOCDUADE C	NUT CE	1022	GIP CICLAHIDROLASE II (AC 3.5.4.25) / 3,4-DIMIDROXY=Z-BUTANONE
TOD ACTD	INTHASE	1000	
ALSB_ACTPD	0.00	1122	5,7-DIMETHYL-8-RIBITYLLOMAZINE SYNTHASE (EC 2.5.1.9)
RIBF_CORAM	38%	1139	RIBOFLAVIN KINASE (EC 2.7.1.26)
BIO02.10 Thior	edoxin,	glutare	doxin, and glutathione 5 genes
SSHR_HAEIN	30%	861	GLUTATHIONE REDUCTASE (EC 1.6.4.2)
PRXB_CLOLI	478	963	THIOREDOXIN REDUCTASE (EC 1.6.4.5)
BSAA_BACSU	56%	1400	GLUTATHIONE PEROXIDASE HOMOLOG BSAA
PHIO_BACSU	54%	1687	THIOREDOXIN (TRX)
PRXB_MYCGE	36%	1691	THIOREDOXIN REDUCTASE (EC 1.6.4.5)
BIO02.11 Thiam	ine		10 genes
ZGD_BACSU	26%	165	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
THID_HAEIN	38%	483	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
ZGD_BACSU	42%	1092	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
THIE_BACSU	39%	1291	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
THID_HAEIN	48%	1292	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
THIM HAEIN	348	1293	HYDROXYETHYLTHIA20LE KINASE (EC 2.7.1.50)
DCIP ENTCL	418	1337	INDOLE-3-PYRUVATE DECARBOXYLASE (EC 4.1.1.74)
ZGD BACSU	31%	1662	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
POXE LACPL	468	2109	PYRIVATE OXIDASE (RC 1 2 3 3)
ZGD_BACSU	40%	2296	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
BIO02.12 Pyrid	ine nucl	eotidea	1 genes
JADE FCOLT	65%	1107	NH(3)-DEPENDENT NAD
http://www.upublice.org			
BIO03. CELL EN	VELOPE		73 genes
31003. CELL EN 31003.01 Membr	VELOPE anes, li	poprote	73 genes ins, and porins 29 genes
BIO03. CELL EN BIO03.01 Membr /QJG_BACSU PRECURSOR	<b>VELOPE</b> anes, li 32%	<b>poprote</b> 129	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU PRECURSOR GRP_STRSU	VELOPE anes, li 32% 29%	<b>poprote</b> 129 147	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECIPSOR (136 KD SURPACE PROTEIN)
BIO03. CELL EN BIO03.01 Membr QJG_BACSU PRECURSOR (RP_STRSU NAPA STEMU	<b>VELOPE</b> anes, 15 32% 29% 26%	<b>poprote</b> 129 147 149	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)
BIO03. CELL EN BIO03.01 Membr QJG_BACSU PRECURSOR RP_STRSU NAPA_STRMU NAPA_STRMU NAPA STRDV	VELOPE anes, 15 32% 29% 26% 392	<b>poprote</b> 129 147 149 152	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR TRYPSINLERSIGNAT SUBJECT TO PROTEIN PRECURSOR
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU RECURSOR (RP_STRSU NAPA_STRMU FEE6_STRPY PEAL KLEDM	VELOPE anes, li 32% 29% 26% 39%	poprote 129 147 149 152 201	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR TRYPSIN-RESISTANT SURFACE 16 PROTEIN PRECURSOR O-AMPLICAN PROPER SYSTEM DEDMESSED PROTEIN PRES
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU RECURSOR (RP_STRSU NAPA_STRMU TEE6_STRPY RFA1_KLEPN N PG PA SUP	VELOPE anes, 13 32% 29% 26% 39% 29%	poprote 129 147 149 152 201	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REPA ONDER MATCHINGTON LIPOPROFERINA SUPERIOR (1990)
BIO03. CELL EN BIO03.01 Membr QJG_BACSU PRECURSOR RP_STRSU NAPA_STRSU NAPA_STRMU TEE6_STRPY RFA1_KLEPN NLPC_PASHA	VELOPE anes, 15 32% 29% 26% 39% 29% 42%	poprote 129 147 149 152 201 315	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR UNAL-ASSOCIATED PROTEIN PRECURSOR O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN PREA OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3)
SICO3. CELL EN SICO3.01 Membr (QJG_BACSU RECURSOR RP_STRSU NAPA_STRMU NER6_STRPY RFA1_KLEPN VLPC_PASHA 2LPA_PASHA	VELOPE anes, 15 32% 29% 26% 39% 29% 42% 36%	129 147 149 152 201 315 316	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR TRYPSIN-RESISTANT SURFACE T6 PROTEIN PRECURSOR O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REPA OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU RECURSOR (RP_STRSU NAPA_STRMU PEE6_STRPY REAL_KLEPN PLPC_PASHA HLPA_HAEIN	VELOPE anes, 13 32% 29% 26% 39% 42% 36% 38%	poprote 129 147 149 152 201 315 316 317	73 genes         ins, and porins       29 genes         HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION         MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)         WALL-ASSOCIATED PROTEIN PRECURSOR         O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REPA         OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3)         OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)         28 KD OUTER MEMBRANE PROTEIN PRECURSOR
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU PRECURSOR (RP_STRSU NAPA_STRMU PEE6_STRPY RPALFLEPN PLLPC_PASHA HLPA_PASHA HLPA_HAEIN (ABC_ECOLI DECURSOP	VELOPE anes, 15 32% 29% 26% 39% 29% 42% 36% 38% 37%	poprote 129 147 149 152 201 315 316 317 318	73 genes         ins, and porins       29 genes         HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION         MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)         WALL-ASSOCIATED PROTEIN PRECURSOR         O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REPA         OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP3)         OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)         28 KD OUTER MEMBRANE PROTEIN PRECURSOR         HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION
BIO03. CELL EN BIO03.01 Membr YQJG_BACSU PRECURSOR KRP_STRSU WAPA_STRMU TEE6_STRPY RFA1_KLEPN PLPC_PASHA PLPA_PASHA HLPA_HAEIN YAEC_ECOLI PRECURSOR	VELOPE anes, 13 32% 29% 26% 39% 29% 42% 36% 38% 37%	poprote 129 147 149 152 201 315 316 317 318	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR TRYPSIN-RESISTANT SURFACE T6 PROTEIN PRECURSOR O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN PRECURSOR OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1) 28 KD OUTER MEMBRANE PROTEIN TPRECURSOR HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION UNDERMEMBRANE JO 5 ND LIPOPROTEIN IN COMPANY
BIO03. CELL EN BIO03.01 Membr YQJG_BACSU PRECURSOR WAPA_STRSU WAPA_STRMU TEE6_STRPY RFA1_KLEPN RFA1_KLEPN PLPC_PASHA HLPA_PASHA HLPA_PASHA HLPA_PASHA HLPA_CECOLI PRECURSOR YOJL_ECOLI	VELOPE anes, 15 32% 29% 26% 39% 42% 36% 38% 37% 27%	poprote 129 147 149 152 201 315 316 317 318 370	73 genes         ins, and porins       29 genes         HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION         MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)         WALL-ASSOCIATED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)         WALL-ASSOCIATED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)         ONTER MEMBRANE SURFACE T6 PROTEIN PRECURSOR (1000)         OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3)         OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)         28 KD OUTER MEMBRANE PROTEIN PRECURSOR         HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSP-ABC INTERGENIC REGION         HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU PRECURSOR (RP_STRSU NAPA_STRMU PEE6_STRPY RPA1_KLEPN PLPA_PASHA HLPA_HAEIN (ABC_ECOLI PRECURSOR (VJL_ECOLI PRECURSOR	VELOPE anes, 13 32% 29% 26% 39% 29% 42% 36% 36% 36% 36% 37% 27%	<b>poprote</b> 129 147 149 152 201 315 316 317 318 370	73 genes         ins, and porins       29 genes         HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION         MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)         WALL-ASSOCIATED PROTEIN PRECURSOR         O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REBA         OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3)         OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR         128 KD OUTER MEMBRANE PROTEIN PRECURSOR         HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSP-ABC INTERGENIC REGION         HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU PRECURSOR (RP_STRSU WAPA_STRSU WAPA_STRMU TEE6_STRPY RFA1_KLEPN PLPC_PASHA PLPA_PASHA PLPA_PASHA HLPA_HAEIN (ABC_ECOLI PRECURSOR COLL_ECOLI PRECURSOR CSTA_MYCTU	VELOPE anes, 13 32% 29% 26% 39% 42% 36% 38% 37% 27% 51%	129 147 149 152 201 315 316 317 318 370 412	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR 0-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN PRECURSOR 0-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN RPEA OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1) 28 KD OUTER MEMBRANE PROTEIN PRECURSOR HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSP-ABC INTERGENIC REGION HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION CARBON STARVATION PROTEIN A HOMOLOG
BIO03. CELL EN BIO03.01 Membr (QJG_BACSU PRECURSOR (RP_STRSU VAPA_STRMU TEE6_STRPY RFA1_KLEPN VLPC_PASHA HLPA_PASHA HLPA_PASHA HLPA_PASHA HLPA_RAEIN (ABC_ECOLI PRECURSOR (OJL_ECOLI PRECURSOR STA_MYCTU SPR_ECOLI	VELOPE anes, 13 32% 29% 26% 39% 42% 36% 32% 36% 32% 27% 27% 51% 35%	poprote 129 147 149 152 201 315 316 317 318 370 412 480	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR TRYPSIN-RESISTANT SURFACE T6 PROTEIN PRECURSOR 0-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REPA OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) 0UTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1) 28 KD OUTER MEMBRANE PROTEIN PRECURSOR HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION CARBON STARVATION PROTEIN A HOMOLOG LIPOPROTEIN SPR PRECURSOR
BIO03. CELL EN BIO03.01 Membr YQJG_BACSU PRECURSOR WRP_STRSU NAPA_STRMU PEE6_STRPY RFA1_KLEPN PLPC_PASHA PLPA_PASHA PLPA_PASHA HLPA_HAEIN YABCC_ECOLI PRECURSOR COJL_ECOLI PRECURSOR CSTA_MYCTU SPR_ECOLI 501M_PSEPU	VELOPE anes, 13 32% 29% 26% 39% 42% 36% 38% 37% 27% 51% 35% 29%	poprote 129 147 152 201 315 316 317 318 370 412 480 562	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REPA OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1) 28 KD OUTER MEMBRANE PROTEIN PRECURSOR HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSP-ABC INTERGENIC REGION HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION CARBON STARVATION PROTEIN A HOMOLOG LIPOPROTEIN SPR PRECURSOR 60 KD INNER-MEMBRANE PROTEIN
BIO03. CELL EN BIO03.01 Membr YQJG_BACSU PRECURSOR WRP_STRSU WAPA_STRMU TEE6_STRPY RFA1_KLEPN PLDA_PASHA HLPA_HAEIN YAEC_ECOLI PRECURSOR COLL_ECOLI PRECURSOR CSTA_MYCTU SPR_ECOLI SOTM_PSEPU IRTK_RHOCA	VELOPE anes, 13 32% 29% 26% 39% 42% 36% 38% 37% 27% 51% 35% 29% 33%	poprote 129 147 152 201 315 316 317 318 370 412 480 562 571	73 genes ins, and porins 29 genes HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR 0-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN PRECURSOR 0-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REBA OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3) 0UTER MEMBRANE LIPOPROTEIN 1 PRECURSOR HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION CARBON STARVATION PROTEIN A HOMOLOG LIPOPROTEIN SPR PRECURSOR 60 KD INNER-MEMBRANE PROTEIN CRTK PROTEIN

			_
BIO04. CELLUL	AR PROCE	SSES	29 genes
BIO03.04 Surf	ace stru	ctures	0 genes
KDTB_HAEIN	39%	2218	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB
RFAK_SAL/TY 2.4.1.56)	28%	2187	LIFOPOLYSACCHARIDE 1, Z-N-ACETYLGLUCOSAMINETRANSFERASE (EC
RFBU_SALTY	25%	2186	RFBU PROTEIN
FAGE_BACSU 2.4.1.52)	23%	1477	PROBABLE POLY(GLYCEROL-PHOSPHATE) ALPHA-GLUCOSYLTRANSFERASE (E
2.4.1.52)			LICENCE CONTRACTOR CONTRACTOR AND
TAGE_BACSU	25%	1475	PROBABLE POLY (GLYCEROL-PHOSPHATE) ALPHA-GLUCOSYLTRANSFERASE (B)
DLTC_LACCA	438	1288	D-ALANYL CARRIER PROTEIN (DCP)
DLTD_BACSU	348	1287	PROTEIN DLTD PRECURSOR
IAGB_BACSU	3 D %	951	TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR
TAGF_BACSU	38%	950	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
TAGD BACSU	499	948	GLYCEROL-3-PHOSPHATE CVTIDVLVLTRANSFERACE (RC 2 7 7 30)
TAGE_BACSU	29%	941	TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR
PAGG_BACSU	29%	937	TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG
PAGH_BACSU	48%	935	TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGH
TAGD_BACSU	55%	217	GLYCEROL-3-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7.7.39)
LICD HARIN	319	213	DIDFERGENOSIL TRANSFERASE REEG (EC Z,-,-) LICD PROTEIN
RBB2_ECOLI	46%	197	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
RFBC_SHIFL	35%	196	DTDP-4-DEHYDRORHAMNOSE 3,5-EPIMERASE (EC 5.1.3.13)
DLTE_BACSU	33%	142	DLTE PROTEIN
BI003.03 Surf	ace poly	sacchari	des, lipopolysaccharides and antigens 21 genes
UNCA_BACAU	204	0612	D-ALANID-D-ALANINE CARBOATPEPTIDASE PRECURSOR (EC 3.4.16.4)
MREC_BACSU	30%	2295	ROD SHAPE-DETERMINING PROTEIN MREC
MRED_BACSU	22%	2294	ROD SHAPE-DETERMINING PROTEIN MRED
(EC 2.7.1.66)			
BACA_ECOLI	34%	2255	BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE)
PBPF_BACSU	31%	2158	PENICILLIN-BINDING PROTEIN 1A (PBP-1A)
DAC STRSO	25%	2111	D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3 4 16 4)
ALVS ENTHR	⊃416 419-	1956	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) AUTOLYSIN PRECIESOR (EC 3.5.1.28)
LIGASE (EC 6.	3.2.13)	1021	UDD-N-ACREVICI UCCEMENT BUTCHUCCHUCCHUCCHUCCHUCCHUCCHUCCHUCCHUCCH
MURE_BACSU	31%	1851	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE2,6-DIAMINOPIMELATE
MURD_BACSU	55%	1630	UDP-N-ACETYLMURAMOYLALANINED-GLUTAMATE LIGASE (EC 6.3.2.9)
PYROPHOSPHORY	L-UNDECA	PRENOL 1	-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1)
MURG_BACSU	45%	1629	UDP-N-ACETYLGLUCOSAMINEN-ACETYLMURAMYL-(PENTAPEPTIDE)
ALYS_ENTHR	398	1400	AUTOLYSIN PRECURSOR (EC 3.5.1.28)
MURB_BACSU	39%	1172	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1 1 1 158)
RODA ECOLI	44%	889 914	PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.13 ROD SHAPE-DETERMINING PROTEIN RODA
PBPB_BACSU	278	888	PENICILLIN-BINDING PROTEIN 2B (PBP-2B)
RODA_HELPY	32%	661	ROD SHAPE-DETERMINING PROTEIN RODA
MURA_ACICA	49%	532	UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
PBPA_STROR	54%	528	PENICILLIN-BINDING PROTEIN 1A (PBP-1A)
PBPD BACSU	28%	390	PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PRP 4)
MURF_BACSU	398 ANVI: 1:108	340 SE (PO 4	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATED- 5 3 2 15)
PBP2_STRPN	46%	336	PENICILLIN-BINDING PROTEIN 2B
2.5.1.7)	550	511	FRODEDDE ODF-N-NORTIDOLOGOANTWE I-CANDONIVINIDIAMOFERADE (EC
BIO03.02 Mure	in saccu	lus and	peptidoglycan 23 genes
nono_ornon	550	2104	ADDIDIN D PRECORDOR (DRUNA-DIRDING PROTEIN)
MRP_STRSU ADHS_STRSA	3/8	2164	MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)
CZCD_ALCEU	30%	1646	CATION EFFLUX SYSTEM PROTEIN CZCD
REGION PRECUP	SOR (ORF	T)	
YDEK_ECOLI	338	1622	HYPOTHETICAL 136.5 KD LIPOPROTEIN IN HIPB-UXAB INTERGENIC
LPLA_BACSU	278	1526	LIPOPROTEIN LPLA PRECURSOR
TMPC TREPA	36%	1460	MEMBRANE LIPOPROTEIN IN PSAA 5 REGION (ORFI)
ADHS_STRPA	588 769	1347	ADHESIN B PRECURSOR (SALIVA-BINDING PROTEIN)
CD59_HSVSA	328	1299	SURFACE GLYCOPROTEIN CD59 HOMOLOG PRECURSOR
MRP_STRSU	31%	1221	MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN)
YD57_METJA	32%	935	PUTATIVE POTASSIUM CHANNEL PROTEIN MJ1357
to a second second second		2.17.14	ALAMAN V APPANULACION PROTECIA N
SP5E_BACSU	3.9%	906	CRACE V COODULATION DROWERN R

DIVC BACSU	31%	22	CELL DIVISION PROTEIN DIVIC
FTSH LACLA	98%	27	CELL DIVISION PROTEIN FISH HOMOLOG (EC 3.4.24)
SPOJ BACSU	44%	96	STAGE 0 SPORULATION PROTEIN J
FTSY BACSU	58%	823	CELL DIVISION PROTEIN FTSY HOMOLOG
FTSE ECOLI	40%	997	CELL DIVISION ATP-BINDING PROTEIN FISE
SPRE BACSU	499	1701	STACE III SDORULATION DROTEIN F
FTSZ BACSU	618	1918	CELL DIVISION PROTEIN FUSZ
FTCA BACCI	279	1919	CELL DIVISION PROTEIN FISH
FISK_DACSO	57.8	1919	CEED DIVISION PROTEIN FISH
BTOOM 02 Col1 1	111100		2 games
MINA DACOR	440	405	J YENES
HLIS_BACCE	446 200	- 493	HEROLISIN III (HUI-III) INFORMETERS 20.7 VD DROWNTN IN BOLD AUDO INFERCENTO DECION
YQXC_BACSU	006	8/9	HYPOTHETICAL 29.7 KD PROTEIN IN FOSD-ARKC INTERGENIC REGION
FRPA_NEIME	30%	1394	IRON-REGULATED PROTEIN FRPA
BIOD4.03 Chapes	rones		4 genes
SUGE_ECOLI	468	122	SUGE PROTEIN
CH10_LACLA	100%	396	10 KD CHAPERONIN (PROTEIN CPNI0)
CH60_LACLA	978	397	60 KD CHAPERONIN (PROTEIN CPN60)
DNAK_LACLA	998	977	DNAK PROTEIN (HEAT SHOCK PROTEIN 70)
BIO04.04 Detox:	ficatio	n	1 genes
SODM_LACLA	100%	410	SUPEROXIDE DISMUTASE (MN) (EC 1.15.1.1)
BIO04.05 Protes	in and p	peptide s	ecretion 5 genes
SECA_STAAU	51%	115	PREPROTEIN TRANSLOCASE SECA SUBUNIT
TIG_BACSU	52%.	534	TRIGGER FACTOR (TF)
LSPA_STAAU	43%	1023	LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.36)
SECY_LACLA	98%	2138	PREPROTEIN TRANSLOCASE SECY SUBUNIT
LEPC BACCL	41%	2330	SIGNAL PEPTIDASE I (EC 3.4.21.89)
BIO04.06 Transf	formatio	m	8 genes
CMA2 BACSU	46%	729	COMA OPERON PROTEIN 2
CME3 BACSU	378	1004	COMP OPPON DEOTETH 3
CME1 BACCU	379	1095	COME OPERON DROFFIN 1
CMF1_DACSU	200	1911	COMP OPERON PROTEIN 1
CHES_BACSU	200	1011	COME OPERON PROTEIN 5
CMEL_BACSU	398	1812	COME OPERON PROTEIN I
CMG3_BACSU	448	2166	COMG OPERON PROTEIN 3 PRECURSOR
CMG2_BACSU	308	2167	COMG OPERON PROTEIN 2
CMG1 BACSU	368	2168	COMG OPERON PROTEIN 1
	550	2700	conto originali propriori a
	550	2100	•
BIO04.07 Other		2100	0 genes
BIO04.07 Other	тытрыя	DIADY ME	0 genes
BIO04.07 Other BIO05. CENTRAL	INTERM	DIARY ME	0 genes TABOLISM 30 genes
BIO04.07 Other BIO05. CENTRAL	INTERM	DIARY ME	0 genes TABOLISM 30 genes
BI004.07 Other BI005. CENTRAL BI005.01 Genera	INTERM	DIARY ME	0 genes TABOLISM 30 genes 7 genes PROBABLE MEDITADEENVI, DIDHOGDHATE SYNTHASE COMPONENT II (EC
BI004.07 Other BI005. CENTRAL BI005.01 Genera GRC3_BACSU	INTERM 31%	DIARY ME	0 genes TABOLISM 30 genes 7 genes FROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30)	INTERME 31%	184	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC
BI004.07 Other BI005. CENTRAL BI005.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR	INTERM 31% 42%	2100 201ARY ME 184 198	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU	INTERM 31% 42% 47%	2100 EDIARY ME 184 198 878	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU	INTERME 31% 42% 47% 48%	184 198 878 985	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLITANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU	INTERME 31% 42% 47% 48% 44%	184 198 878 985 1185	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU	INTERM 31% 42% 47% 48% 44% 35%	184 198 878 985 1185 1378	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30)	INTERM 31% 42% 47% 48% 44% 35%	184 198 878 985 1185 1378	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSPERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU	INTERM 31% 42% 47% 44% 35% 62%	184 198 878 985 1185 1378 1950	0 genes TABOLISM 30 genes 7 genes FROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU	INTERM 1 31% 42% 47% 48% 44% 35% 62%	184 198 878 985 1185 1378 1950	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino	INTERM 1 31% 42% 47% 48% 44% 35% 62% sugars	184 198 878 985 1185 1378 1950	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8	INTERM 31% 42% 47% 48% 35% 62% 50gars 32%	184 198 878 985 1185 1378 1950	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV	INTERME 31% 42% 47% 48% 44% 35% 62% 50gars 32% 37%	184 198 878 985 1185 1378 1950 167 279	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSESB NODB_RHILV GLMS_MYCLE	INTERME 1 31% 42% 47% 42% 44% 35% 62% sugars 32% 37% 36%	184 198 878 985 1185 1378 1950 167 279 1032	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING)	INTERM 31% 42% 47% 42% 47% 44% 35% 62% 5ugars 32% 36% (EC 2.6.	184 198 878 985 1185 1378 1950 167 279 1032 1.16)	0 genes TABOLISM 30 genes 7 genes FROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI	INTERM 31% 42% 47% 48% 44% 35% 62% Sugars 32% 37% 32% 37% 32% 22% 22% 22% 22% 22% 22% 22	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU	INTERME 11 31% 42% 47% 44% 35% 62% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502% 502%	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLITANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NACA_HAEIN	INTERM 1 31% 42% 47% 42% 47% 44% 35% 62% 500 500 500 500 500 500 500 50	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371	0 genes TABOLISM 30 genes 7 genes FROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 3.5.1.2)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU NAGC_HAEIN HASC_STRPY	INTERM 1 31% 42% 47% 48% 44% 35% 62% Sugars 32% 37% 32% 37% 32% 37% 32% 37% 36% 28% 47% 58%	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371 1376	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.2.7.9)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_RCOLI YVYH_BACSU NAGD_HAEIN HASC_STRPY NAGB_HAEIN	INTERME Al 31% 42% 47% 44% 35% 62% sugars 32% 37% 36% (EC 2.6 28% 37% 36% (EC 2.6 28% 32%	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371 1376 1611	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLITANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 3.5.1.25) UTPGLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.1.1.1)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGA_BAEIN HASC_STRPY NAGB_HAEIN	INTERME 1 31% 42% 47% 44% 35% 62% sugars 37% 36% 28% 36% 28% 32% 30% 58% 32%	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371 1376 1611	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACHTYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 3.5.1.25) UTPGLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.1.10)
BIO04.07 Other BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU NAGA_HAEIN HASC_STRPY NAGB_HAEIN BIO05.03 Degrad	INTERM 1 31% 42% 47% 48% 44% 35% 62% 52% 32% 32% 32% 30% 58% 32% 30% 58% 32% 30% 58% 32% 32% 30% 32% 30% 32% 30% 32% 30% 32% 30% 32% 32% 32% 32% 32% 32% 32% 32	184 184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1376 1611 of polysa	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSPERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN FUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) UTPGLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) CCharides 5 genes
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU QRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSESS NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YYYH_BACSU NAGD_HAEIN BIO05.03 Degrad NEPU_THEVU	INTERME A1 31% 42% 47% 42% 47% 35% 62% Sugars 32% 37% 32% 32% 32% 32% 32% 32% 32% 32	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371 1376 1611 0f polysa 701	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGLUCOSAMINE-6-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) KCCHARIGE 5 genes NEOPULLULANASE (EC 3.2.1.135)
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BIO04.07 Other BIO05. CENTRAL BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_RHILV GLMS_STROI UNAGB_HAEIN BIO05.03 Degrad NEPU_THEVU AMY_BACST O16G_BACTR CHIX_STROI CHI1_BACCI BIO05.04 Phosp) DUT HAEIN	INTERM 1 31% 42% 47% 42% 47% 32% 32% 32% 37% 36% (EC 2.6 28% 47% 30% 44% 60% 31% 34% horus co	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371 1376 1611 of polysa 701 1275 1523 2007 2007 2007	0 genes TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 3.5.1.25) UTPGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.20) Cherrides 5 genes NEOPULULANASE (EC 3.2.1.135) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.10) EXOCHITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NACA_HAEIN HASC_STRPY NACB_HAEIN HASC_STRPY NACB_HAEIN BIO05.03 Degrad NEPU_THEVU AMY_BACST O16G_BACTR CHIX_STROI CHI1_BACCI BIO05.04 Phosp1 DUT_HAEIN DUT HAEIN	INTERM 31% 42% 47% 47% 48% 44% 35% 62% 52% 32% 32% 32% 32% 32% 32% 32% 3	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1371 1376 1611 1376 1611 1275 1523 2007 2007 2007 2007	0 genes TABOLISM 30 genes 7 genes FROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSPERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 3.5.1.25) UTPGLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 3.5.1.25) UTPGLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) GLUCOSAMINE-6-PHOSPHATE LSOMERASE (EC 3.2.1.10) CCharides 5 genes NEOPULLULANASE (EC 3.2.1.135) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.14) CLIGO-1, 6-GLUCOSIDASE (EC 3.2.1.14) EXOCHITINASE 1 PRECURSOR (EC 3.2.1.14) 9 genes DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
BIO04.07 Other BIO05. CENTRAL BIO05.01 Genera GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU STRL_STAAU BIO05.02 Amino NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU NAGA_HAEIN HASC_STRPY NAGB_HAEIN BIO05.03 Degrad NEPU_THEVU AMY_BACST O16C_BACTR CHIX_STROI CHI1_BACCI BIO05.04 Phosp1 DUT_HAEIN DUT_HAEIN SUHB_ECOLI	INTERM 1 31% 42% 47% 48% 48% 48% 62% 32% 32% 32% 32% 32% 32% 32% 3	184 198 878 985 1185 1378 1950 167 279 1032 1.16) 1154 1296 1376 1611 376 1611 376 1611 377 1032 1.16) 1154 1296 1376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 1611 376 175 1523 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 20	0 genes TTABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSPERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) 8 genes 6-AMINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) UTPGLUCOSE-1-PHOSPHATE ISOMERASE (EC 5.3.1.10) CCCharides 5 genes NEOPULLULANASE (EC 3.2.1.135) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) OLIGO-1, 6-GLUCOSIDASE (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) P genes DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)

717 ALKALINE PHOSPHATASE LIKE PROTEIN APL LACLA 96% DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23) DUT\_HAEIN 38% 1046 DUT HAEIN 378 1441 PUTATIVE PROTEIN PHOSPHATASE (EC 3.1.3.16) PHOSPHATIDYLCLYCEROPHOSPHATASE B (EC 3.1.3.27) 278 1937 PPH\_MYCPN PGPB\_HAEIN 36% 2122 PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE (EC 35% 2264 Y328 SYNY3 3.1.3.48) BI005.05 Polyamine biosynthesis 1 genes 41% SPERMIDINE N1-ACETYLTRANSFERASE (EC 2.3.1.57) ATDA\_ECOLI 1653 BIO05.06 Other 0 genes BIO06. ENERGY METABOLISM 148 genes BIO06.01 Aerobic 32 genes MANNITOL-1-PHOSPHATE 5-DEHYDROGENASE (EC 1.1.1.17) 61% 34 MTLD STRMU ODO2\_MYCTU 34% 61 DIHYDROLIPOAMIDE SUCCINVLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61) PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE VDLC (EC 1.-VDLC\_HELPY 338 78 - - - 1 HYPOTHETICAL OXIDOREDUCTASE IN RTP 5'REGION (EC 1.-.-.) YOXD BACSU 36% 141 159 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14 (EC 1.6.5.3) NQOE\_THETH 26% DHNA BACSU 50% 334 NADH DEHYDROGENASE (EC 1.6.99.3) L-LACTATE DEHYDROGENASE (EC 1.1.1.27) LDH\_BACSU 54% 377 NADH OXIDASE (EC 1.6.-.-) L-LACTATE DEHYDROGENASE (EC 1.1.1.27) NAOX\_ENTFA 39% 395 24% LDH LISMO 488 HYPOTHETICAL OXIDOREDUCTASE IN USHA-TESA INTERGENIC REGION (EC YBBO\_ECOLI 29% 617 1.-.-) NAOX\_METJA 792 PUTATIVE NADH OXIDASE (EC 1.6.-.-) 34% HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC REGION (EC YWFD\_BACSU 38% 799 1.-.-} BUDC\_KLETE 53% 916 ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5) 916 ACETOACETYL-COA REDUCTASE (EC 1.1.1.36) FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.99.1) PHBB\_CHRVI 378 1136 FRDA SHEPU 45% LDH\_LACCA 378 1140 L-LACTATE DEHYDROGENASE (EC 1.1.1.27) GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5) LACTATE 2-MONOOXYGENASE (EC 1.13.12.4) GLPD MYCLE 348 1268 LA2M MYCSM 40% 1277 1341 PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE VDLC (EC 1.-VDLC\_HELPY 36% - . - 1 GPDA\_ECOLI 25% 1355 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+) (EC 1.1.1.8) LDH\_LACLA 100% 1367 L-LACTATE DEHYDROGENASE (EC 1.1.1.27) GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD 1375 GPDA BACSU 348 HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-.) HYPOTHETICAL OXIDOREDUCTASE IN GLNQ-ANSR INTERGENIC REGION (EC YINL\_LISMO 36% 1506 YQJQ\_BACSU 38% 1569 1.-.-) HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-.) MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67) PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQIG (EC 1.-.-.) YINL\_LISMO 728 1576 MTLK RHOSH 28% 1675 YQIG\_BACSU 428 1730 YPRA\_CORGL 29% 2048 HYPOTHETICAL 33.0 KD PROTEIN IN PROB-PROA INTERGENIC REGION PROBABLE PYRIDINE NUCLEOTIDE-DISULFIDE OXIDOREDUCTASE IN EAEH-YKGC ECOLI 398 2119 BETA INTERGENIC REGION 2175 NADH OXIDASE (EC 1.6.-.-) HYPOTHETICAL 30.8 KD PROTEIN IN GIP-FDRA INTERGENIC REGION NAOX ENTEA 358 338 2278 YBBQ\_ECOLI OXIR\_STRAT 2318 PROBABLE OXIDOREDUCTASE (EC 1.-.-.) 40% BIO06.02 Amino acids and amines 5 genes L-2-HYDROXYISOCAPROATE DEHYDROGENASE (EC 1.1.1.-) L-ASPARAGINASE (EC 3.5.1.1) DHL2\_LACCO 57% 488 ASPG BACLI 741 34% OTCC\_CLOPE 528 ORNITHINE CARBAMOYLTRANSFERASE, CATABOLIC (EC 2.1.3.3) 806 N5- (CARBOXYETHYL) ORNITHINE SYNTHASE (EC 1.5.1.24) DHCO\_LACLA OTCC\_CLOPE 1262 86% ORNITHINE CARBAMOYLTRANSFERASE, CATABOLIC (EC 2.1.3.3) 2093 54% BIO06.03 Anaerobic 2 genes 52% ANAEROBIC RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE (EC 1.17.4.2) ANAEROBIC RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE ACTIVATING NRDD\_ECOLI 269 NRDG ECOLI 46% 270 PROTEIN (EC 1.97.1.-) BIO06.04 ATP-proton motive force interconversion 6 genes ATP SYNTHASE & CHAIN (EC 3.6.1.34) ATP6\_MYCGE 28% 1087 ATP SYNTHASE A CHAIN (EC 3.6.1.34) ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34) ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34) ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34) ATP SYNTHASE B CHAIN (EC 3.6.1.34) ATP SYNTHASE A CHAIN (EC 3.6.1.34) ATPE\_STRMU 64% 1802 ATPA STRMU 79% 1804 ATPA\_SYNP1 65% 1806 ATPF\_STRMU 47% 1807 1808 ATP6 ENTFA 37% BIO06.05 Electron transport 6 genes

PYRUVATE-PLAVODOXIN OXIDOREDUCTASE (EC 1.-.-.) CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-) CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-) NADH DEHYDROGENASE (EC 1.6.99.3) NIFJ\_ANASP 44% 428 CYDA\_BACSU 498 706 CYDB BACSU 707 438 28% DHNA HAEIN 838 DHNA HAEIN 32% 839 NADH DEHYDROGENASE (EC 1.6.99.3) 1193 FIXC\_ECOLI FIXC PROTEIN 378 BIC06.06 Entner-Doudoroff 1 genes KDGK\_BACSU 1668 2-DEHYDRO-3-DEOXYGLUCONOKINASE (EC 2.7.1.45) 46% BIO06.07 Fermentation 8 genes QOR\_PSEAE 32% 231 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) QUINONE OXIDOREDUCTASE (EC 1.6.5.5) SORBITOL DEHYDROGENASE (EC 1.1.1.14) OOR PSEAE 32% 721 DHSO\_BACSU 328 915 FADH\_METMR 378 1587 GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1) HYPOTHETICAL OXIDOREDUCTASE IN CSTA-AHPC INTERGENIC REGION ALCOHOL DEHYDROGENASE I (EC 1.1.1.1) YBDH ECOLI 31% 1595 ADH1\_ZYMMO 60% 1852 2210 SUCD\_CLOKL 408 SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NAD ADHE ECOLI 448 2211 ALCOHOL DEHYDROGENASE (EC 1.1.1.1) BIO06.08 Gluconeogene sis 3 genes OXALOACETATE DECARBOXYLASE ALPHA CHAIN (EC 4.1.1.3) L-SERINE DEHYDRATASE 2 (EC 4.2.1.13) DCOA\_KLEPN 664 40% SDHM ECOLI 36% 842 G6PB BACST 39% 2224 GLUCOSE-6-PHOSPHATE ISOMERASE B (GPI B) (EC 5.3.1.9) BIO06.09 Glycolysis 14 genes PGK\_THEMA 578 241 PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) ENO\_MYCPN ENOLASE (EC 4.2.1.11) 52% 272PMGY\_ZYMMO PGMB\_LACLA PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1) BETA-PHOSPHOGLUCOMUTASE (EC 5.4.2.6) 62% 332 100% 440 G3P\_LACLA 552 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) 99% ENO BACSU ENOLASE (EC 4.2.1.11) ENOLASE (EC 4.2.1.11) 70% 631 ENO\_HAEIN 55% 649 ENCLASE (EC 4.2.1.11) BETA-PHOSPHOGLUCCMUTASE (EC 5.4.2.6) TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) PYRUVATE KINASE (EC 2.7.1.40) 6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11) PROBABLE PHOSPHOGLYCERATE MUTASE 2 (EC 5.4.2.1) FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13) CLYCPER DEFUNDE 2 DEVERDED DEVERDED (EC 4.1.2.13) PGMB\_LACLA 32% 748TPIS LACLA 998 1146 KPYK\_LACLA 1368 54% K6PF\_LACLA 998 1370 PMG2\_ECOLI 288 1749 ALF\_MYCGE 1959 46% G3P LACLA 81% 2313 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) BIO06.10 Pentose phos phate pathway 5 genea DXS\_RHOCA PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) 38% 1508 TKT\_MYCLE 38% 1666 TRANSKETOLASE (EC 2.2.1.1) DXS BACSU 38% 1720 PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) 2282 GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) G6PD\_BACSU 48% RPIA ECOLI 39% 2297 RIBOSE 5-PHOSPHATE ISOMERASE A (EC 5.3,1.6) BIO06.11 Pyruvate dehydrogenase 4 genes DLD1 BACST 55% 60 LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF PYRUVATE DEHYDROGENASE COMPLEX (EC 1.8.1.4) PYRUVATE DEHYDROGENASE EI COMPONENT, BETA SUBUNIT (EC 1.2.4.1) PYRUVATE DEHYDROGENASE EI COMPONENT, ALPHA SUBUNIT (EC 1.2.4.1) LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF PYRUVATE ODPB\_BACST 62% 63 ODPA BACSU 51% 64 DLDH\_ACHLA 26% 840 DEHYDROGENASE COMPLEX (EC 1.8,1,4) BIO06.12 Sugars 53 genes 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) BETA-GLUCOSIDASE (EC 3.2.1.21) 6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86) GLGB\_SYNY3 BGL1\_BACSU 34% 144 174 24% BGLA\_BACSU 418 178 GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24) RMLA STRMU 88% 195 CAPI\_STAAU 27% 210 CAPI PROTEIN ALKVL HYDROPEROXIDE REDUCTASE C22 PROTEIN (EC 1.6.4.-) ENDOGLUCANASE M (EC 3.2.1.4) PHOSPHO-CELLOBIASE (EC 3.2.1.-) AHPC BACSU 76% 333 GUNM\_CLOTM 31% 392 CASB\_KLEOX 420 518 ENDO-1,4-BETA-XYLANASE B (EC 3.2.1.8) 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44) XYNB BUTFI 29% 440 6PGD\_SALTY 68% 606 GAL7\_LACHE 36% GALACTOSE-1-PHOSPHATE URIDYLYLTRANSPERASE (EC 2.7.7.10) 614 PFL\_STRMU FORMATE ACETYLTRANSFERASE (EC 2.3.1.54) 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) 83% 656 MALQ\_ECOLI 298 692 GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (EC 2.7.7.27) GLYCOGEN BIOSYNTHESIS PROTEIN GLGD GLYCOGEN SYNTHASE (EC 2.4.1.21) GLGC BACST 57% 694 GLGD BACST 31% 695 GLGA\_BACSU 697 46% PHSG BACSU 44% 699 GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1) 6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86) BGLA\_BACSU 54% 831 GAL7 STRLI 24% GALACTOSE-1-PHOSPHATE URIDYLYLTRANSFERASE {EC 2.7.7.10} 849 UDP HAEIN 39% 853 URIDINE PHOSPHORYLASE (EC 2.4.2.3)

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PHOSPHATIDYLTRA CDSA_PSEAE BIO08. PURINES,	NSFERA 32% PYRIM	2179 2179	NUCLEOSIDES AND NUCLEOTIDES 47 genes
PHOSPHATIDYLTRA CDSA_PSEAE	NSFERA: 32%	SE (EC 2 2179	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41)
PHOSPHATIDYLTRA	INSFERA!	5E (EC 2	. / . 8 . 5 )
			4 A FL
PGSA BACSU	43%	2026	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-
PAC BACSH	45%	1883	PENICILLIN ACYLASE (EC 3.5.1.11)
FABG BACSU	39%	1824	3-OXOACYL- (ACYL-CARRIER PROTEIN) REDUCTASE (EC 1.1.1.1.00)
ATOB HAEIN	44%	1608	ACETYL-COA ACETYL/TRANSFERASE (EC 2 3 1 9)
KDGL STRMU	688	1093	DIACYLGLYCEROL KINASE (FC 2 7 1 107)
AUDHA (EC 6 4 1	21	108	RUDIID-COMMELEE A CARDUAILASE CARBUAIL TRANSFERASE SUBUNIT
ACCC_DACSU ACCA_HARTH	100	700	DIVIIN CARDUAILABE (EU 0.3.4.14) ACETVI COENTVME & CARDOVVIACE CARDOVVI REAMEREDARE CHRVENTE
4.2.1)	Ena	704	DIOMIN CODDONY ACH (EC. 6.3. 6.14)
FABZ_HAEIN	\$UC	184	(3R) - HIDROXYMYRISTOYL- (ACYL CARRIER PROTEIN) DEHYDRATASE (EC
0.4.1.2) Pape (1) CTV	5.00	204	
BCCP_ANASP	519	784	BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC
FABF_VIBHA	428	783	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II (EC 2.3.1.41)
FABG_BACSU	46%	782	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
FABD_BACSU	45%	781	MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39)
ACCC_METJA	48%	662	BIOTIN CARBOXYLASE (EC 6.3.4.14)
DLTA_LACCA	248	653	D-ALANINE-ACTIVATING ENZYME (EC 6.3.2)
FABI_HAEIN	428	559	ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9)
4.2.1>			
FABZ_ECOLI	428	558	(3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC
GLPQ_BACSU	33%	217	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
PLSX_BACSU	478	71	FATTY ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX HOMOLOG
LPLA_MYCPN	368	65	PROBABLE LIPOATE-PROTEIN LIGASE A (EC 6)
BIO07.01 Genera	11		20 genes
BT007 01 0			20
BIO07. FATTY AC	ID AND	PHOSPHO	LIFID METABOLISM 20 genes
BTO07 B3 mmy 54		BUOGBES	
CILA_ECOLI	568	1207	CITRATE LYASE ALPHA CHAIN (EC 4.1.3.6)
CILB_KLEFN	528	1206	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
CILG_HAEIN	528	1205	CITRATE LYASE ACYL CARRIER PROTEIN (CITRATE LYASE GAMMA CHAIN)
CITC_ECOLI	378	1205	CITRATE (PRO-35)-LYASE) LIGASE (EC 6.2.1.22)
MACX_BACST	498	1201	MALATE OXIDOREDUCTASE (NAD) (EC 1.1.1.38)
MLES_LACEA	10°	920	PADOLACTIC ENZYME (EC 1) MALADE OVIDOREDUCTARE (MAD) (EC 1.1.1.20)
IDH_STEMU	00%	009	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
ACON_BRAJA	27.6	660	ACONITATE HYDRATASE (EC. 4, Z, 1, 3)
CISI_THIFE	296	667	ULINALE DINTHAGE (EC 4.1.3.7) $\lambda_{\rm CONTRATE}$ UVDEADAGE (EC 4.2.1.2)
CICY ONTER	200	665	CITERATE CVNTUACE (FC & 1 3 7)
BT006.13 TCA	cle.		9 denes
IVEC_DHCSU	33.6	4400	ASPOINDITCAD 38.6 ND PROIDIN IN NUCH-AROD INTERGENIC REGION
YORC BACSU	538	2250	HYPOTHETICAL 32 8 KD PROTEIN IN NUCR-AROD INTERCENTE PROTON
GNTK BACSU	49%	2249	GLUCONOKINASE (EC 2.7.1.12)
GLK BACSU	478	2081	GLUCOKINASE (EC 2.7.1.2)
GALM HAEIN	36%	2042	ALDOSE 1-EPIMERASE (EC 5.1.3.3)
GAL1 STRMU	58%	2041	GALACTOKINASE (EC 2.7.1.6)
GAL7_STRMU	52%	2039	GALACTOSE-1-PHOSPHATE URIDYLYLTRANSPERASE (EC 2.7.7.10)
THGA_LACLA	100%	2038	GALACTOSIDE 0-ACETYLTRANSFERASE (EC 2.3.1.18)
BGA2_ECOLI	34%	2036	EVOLVED BETA-GALACTOSIDASE ALPHA-SUBUNIT (EC 3.2.1.23)
GALE_STRMU	60%	2034	UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2)
RPE_SYNY3	47%	1983	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
GIDA_BACSU	61%	1895	GLUCOSE INHIBITED DIVISION PROTEIN A
ASCB_ECOLI	53%	1718	6-PHOSPHO-BETA-GLUCOSIDASE ASCB (EC 3.2.1.86)
RBSK_BACSU	47%	1683	RIBOKINASE (EC 2.7.1.15)
UXUA_THENE	57%	1673	MANNONATE DEHYDRATASE (EC 4.2.1.8)
UXAC_ECOLI	44%	1669	URONATE ISOMERASE (EC 5.3.1.12)
ALKH_BACSU	35%	1668	4-HYDROXY-2-OXOGLUTARATE ALDOLASE (EC 4.1.3.16)
XYNX_CLOTM	28%	1618	EXOGLUCANASE XYNX PRECURSOR (EC 3.2.1.91)
XYLA_THETU	50%	1545	XYLOSE ISOMERASE (EC 5.3.1.5)
XYLB_BACSU	49%	1544	XYLULOSE KINASE (EC 2.7.1.17)
GALM_ACICA	29%	1543	ALDOSE 1-EPIMERASE PRECURSOR (EC 5.1.3.3)
XYNB_BACPU	48%	1540	BETA-XYLOSIDASE (EC 3.2.1.37)
STRH_STRPN	29%	1524	BETA-N-ACETYLHEXOSAMINIDASE PRECURSOR (EC 3.2.1.52)
BGLA_THEMA	33%	1518	BETA-GLUCOSIDASE A (EC 3.2.1.21)
GLK_BACSU	34%	1517	GLUCOKINASE (EC 2.7.1.2)
BGL1_BACSU	56%	1488	BETA-GLUCOSIDASE (EC 3.2,1.21)
DEOC_BACSU	60%	1461	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
GIDB_BACSU	60%	1378	GLUCOSE INHIBITED DIVISION PROTEIN B
THGA ECOLI	40%	1319	GALACTOSIDE ACETYLTRANSFERASE (EC 2.3.1.18)
GLPK BACSU	61%	1270	GLYCEROL KINASE (EC 2.7.1.30)
3MGA HAEIN	37%	1134	DNA-3-METHYLADENINE GLYCOSIDASE (FC 3.2.2.20)
LACC STRAT	339	982	TAGATOSE-6-PHOSPHATE KINAGE (EC 2.4.2.1)
DROD 670000	729	947	DURING CODANIC ACTO BIOSININESIS GLICUSIL IRANSFERASE WORL
WORD DATE			AND THE THE THE TABLE TO AND THE ADDRESS OF THE TABLE TO A TAB

	000x00 01	id nucle	oside interconversions 4 genes
DGK2_LACAC	62%	491	DEOXYGUANOSINE KINASE (EC 2.7.1.113) / DEOXYADENOSINE KINASE
(EC 2.7.1.76)	SUBUNIT	2	
KITH_STRGC	79%	583	THYMIDINE KINASE (EC 2.7.1.21)
DGKZ_LACAC	558	.1168	DEOXYGUANOSINE KINASE (EC 2.7.1.113) / DEOXYADENOSINE KINASE
(EC 2.7.1.70)	A09	1740	
RCI_DMC30	426	1/40	PROBADUE CITIDILATE KINADE (EC 2.).4.14)
BIO08.03 Puris	ne ribonu	cleotid	e biosynthesis 22 genes
IMDH_STRPY	82%	219	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
ADD_ECOLI	33%	285	ADENOSINE DEAMINASE (EC 3.5.4.4)
FOLD_STRTR	65%	874	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) /
METHENYLTETRA	HYDROFOL	ALE CACP	OHYDROLASE (EC 3.5.4.9)
FTHS_STRMU	65%	958	FORMATETETRAHYDROFOLATE LIGASE (EC 6.3.4.3)
IMDH_HELPY	. 37%	1156	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
GUAA_BACSU	578	1514	GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.2)
A 1 1 21)	3.5%	1048	PHOSPHORIBOSILAMINOIMIDAZOLE CARBOXILASE ATPASE SUBUNIT (EC
PURS HARIN	598	1549	PHOSPHORTBOSVLAMINOIMIDAZOLE CARROXVLACE CATALVETC SUBINITE (PC
4.1.1.21)	52%	1945	FIOSFIORIDOSIDARINOIRIDAZOBE CARDOXIDASE CAIADITIC SOBORII (BC
PUR2 BACSU	55%	1550	PHOSPHORIBOSYLAMINEGLYCINE LIGASE (EC 6.3.4.13)
PUR9 BACSU	55%	1555	PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYL/TRANSFERASE (EC
2.1.2.3)			
PUR3_BACSU	45%	1561	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2)
PUR5_BACSU	60%	1562	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
PUR1_BACSU	61%	1568	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.14)
PURL_BACSU	58%	1571	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II (EC 6.3.5.3)
PURQ_BACSU	61%	1573	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE I (EC 6.3.5.3)
PUR7_STRPN	999	1574	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC
0.3.2.0) ·	760	1605	ADDING OFFICIENT AND ADD (DO 4 2 2 2)
PURG_DAUSU	2015	1695	ADENYLOSUCCINATE LYACE (EC 4.3.2.2)
KGUA SYNV3	48%	1946	CHANVLATE KINASE (EC 2 7 4 8)
PURA_BACSU	59%	2009	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
PURQ_BACSU	31%	2107	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE I (EC 6.3.5.3)
KAD_LACLA	988	2137	ADENYLATE KINASE (EC 2.7.4.3)
BIO08.04 Pyris	midine ri	bonucle	otide biosynthesis 10 genes
PYRG_BACSU	64%	486	CTP SYNTHASE (EC 6.3.4.2)
PYRE_BACSU	578.	1078	OROTATE PHOSPHORIBOSYL/TRANSFERASE (EC 2.4.2.10)
PIRC_LACLE	426	1200	DIHYDROOROTASE (EC 3.5.2.3)
DCOP_DACLC	978	1381	DEVELOPMENT DEVELOPMENT DECARBOATDASE (EC 4.1.1.23)
CDD BACSU	54%	1461	CVPTDINE DEAMINASE (EC. 3.5.4.5)
TYSY LACLA	98%	1579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
PYDA_LACLC	98%	1589	DIHYDROOROTATE DEHYDROGENASE A (EC 1.3.3.1)
CARA_BACSU	56%	1640	CARBAMOYL-PHOSPHATE SYNTHASE, PYRIMIDINE-SPECIFIC, SMALL CHAIN
(EC 6.3.5.5)			
DVDD CVNV2			
FIRD_SINIS	42%	1641	ASPARTATE CARBAMOYL/TRANSFERASE (EC 2.1.3.2)
PIRE_SINIS	42%	1641	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2)
BIO08.05 Salva	42%	1641	ASPARTATE CARBAMOVILTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes
BIO08.05 Salva	42% age of nu 99%	1641 cleosid 25 401	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDMATE KINSE (EC 2.7.4.9)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT ECOLI	42% age of nu 99% 48% 54%	1641 25 401 621	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS BACSU	42% age of nu 99% 48% 54% 66%	1641 25 401 621 824	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.7.6.1)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU	42% age of nu 99% 48% 54% 66% 55%	1641 25 401 621 824 953	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTOMUTASE (EC 5.4.2.7)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU	42% age of nu 99% 48% 54% 66% 55% 52%	1641 25 401 621 824 953 1157	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYNIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSH-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2)
HRB_SINES BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU HPRT_BACSU	42% 99% 48% 54% 66% 55% 52% 55%	1641 25 401 621 824 953 1157 1557	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) PHOSPHOPENTIOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.6)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU DEOB_BACSU HPRT_BACSU URK_HAEIN	42% age of nu 99% 48% 54% 55% 55% 52% 52% 56% 52%	1641 25 401 621 824 953 1157 1557 1705	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU HPRT_BACSU HPRT_BACSU URK_HAEIN KPRS_BACCL	42% age of nu 99% 48% 54% 55% 52% 52% 52% 52% 26%	1641 25 401 621 824 953 1157 1557 1705 1906	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU HPRT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA	42% age of nu 99% 48% 54% 55% 52% 52% 56% 52% 26% 97%	1641 25 401 621 824 953 1157 1557 1705 1906 1972	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.7.6.1) URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
HAB_SINES BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU UPB_BACSU HPRT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU	42% age of nu 99% 48% 54% 55% 52% 56% 52% 26% 97% 50%	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSH-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU URK_HAEIN KPRS_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO08.06 Suga	42% age of nu 99% 48% 54% 66% 55% 52% 52% 52% 26% 97% 50%	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 ide bio	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1,48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU DEOB_BACSU XPT_BACSU URK_HAEIN KPRS_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO08.06 Sugar	42% age of nu 99% 48% 54% 66% 55% 52% 52% 52% 26% 97% 50% c-nucleot	1641 25 401 621 824 953 1157 1557 1557 1557 1906 1972 2331 <b>ide bio</b>	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) YANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.6) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO08.06 Sugar BIO09. REGULAY	42% age of nu 99% 48% 54% 66% 52% 52% 52% 52% 52% 52% 52% 50% c-nucleot	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 ide bio	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTIOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO08.06 Sugar BIO09. REGULA!	42% age of nu 99% 48% 54% 66% 52% 52% 52% 52% 52% 52% 52% 50% c-nucleot	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 ide bio	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU VPT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO08.06 Sugar BIO09. REGULA: BIO09.01 General	42% age of nu 99% 48% 54% 66% 52% 52% 26% 97% 50% r-nucleot rony FUNC ral	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 ide bio.	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes
BIO08.05 Salva HPRT_LACLA APT_ECOLI KPRS_BACSU DEOB_BACSU DEOB_BACSU XPT_BACSU HPRT_BACSU HPRT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO08.06 Sugar BIO09. REGULA BIO09.01 General YQAE_BACSU	42% age of nu 99% 48% 54% 66% 52% 56% 52% 56% 52% 56% 52% 56% 52% 50% <b>c-nucleot</b> rory FUNC cal 35%	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 <b>ide bio</b> <b>TIONS</b>	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU HPRT_BACSU URK_HAEIN KPRS_BACSU URF_LACLA PURR_BACSU BIO09.06 Sugas BIO09.01 Genes YQAE_BACSU INTERGENIC REX KPR SACSU	42% age of nu 99% 48% 54% 55% 52% 56% 52% 26% 97% 50% r-nucleot rory FUNC ral 35% SION (ORF	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 ide bio TIONS 11 7) 44	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA DURATIVE PROX PEPEFESOR
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU DEOB_BACSU XPT_BACSU URK_HAEIN KPRS_BACSU UPP_LACLA PURR_BACSU BIO08.06 Sugar BIO09.01 Gener YQAE_BACSU INTERGENIC REC XRE_BACSU RELA STREO	42% age of nu 99% 48% 54% 66% 52% 52% 26% 97% 50% c-nucleot rory FUNC ral 35% 3ION (ORF 50% 66%	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 <b>ide bio</b> <b>TIONS</b> 11 7) 44 106	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) PHOSPHOPENTOMUTASE (EC 5.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1) URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA PUTATIVE PBSX REPRESSOR PUTATIVE GCP PYROPHOSPHOKINASE (EC 2.7.6.5)
BIO08.05 Salva HPRT_LACLA KTHY_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU URK_HAEIN KPRS_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO09.01 Genes YQAE_BACSU INTERGENIC REC XRE_BACSU RELA_STREQ TER8_PASPI	42% age of nu 99% 48% 54% 66% 52% 52% 52% 26% 97% 50% c-nucleot rory FUNC cal 35% SION (ORF 50% 66% 29%	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 <b>ide bio</b> <b>TIONS</b> 11 7) 44 106 128	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDVLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA PUTATIVE PBSX REPRESSOR PUTATIVE GTP PYROPHOSPHOKINASE (EC 2.7.6.5) TETRACYCLINE REPRESSOR PROTEIN CLASS H
BIO08.05 Salva HPRT_LACLA HPRT_LACLA APT_ECOLI KPRS_BACSU DEOB_BACSU VPT_BACSU UPAT_BACSU UPAT_BACSU URK_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO09.01 Genes YQAE_BACSU NTERGENIC REC XRE_BACSU RELA_STREQ TER8_PASPI YQAE_BACSU	42% age of nu 99% 48% 54% 66% 52% 56% 52% 26% 97% 50% <b>c-nucleot</b> rory FUNC ral 35% 310N (ORF 50% 66% 29% 34%	1641 cleosid 25 401 621 824 953 1157 1557 1705 1906 1972 2331 ide bio TIONS 11 7) 44 106 128 133	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA PUTATIVE PBSX REPRESSOR PUTATIVE PBSX REPRESSOR PUTATIVE OF PYROPHOSPHOKINASE (EC 2.7.6.5) TETRACYCLINE REPRESSOR PORTEIN CLASS H HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA
BIO08.05 Salva HPRT_LACLA APT_ECOLI KPRS_BACSU APT_ECOLI KPRS_BACSU DEOB_BACSU XPT_BACSU HPRT_BACSU HPRT_BACSU URA_HAEIN KPRS_BACCL UPP_LACLA PURR_BACSU BIO09.01 Genes YQAE_BACSU INTERGENIC REC XRE_BACSU INTERGENIC REC	42% age of nu 99% 48% 54% 66% 52% 52% 52% 52% 50% c-nucleot cal 35% SION (ORF 50% 66% 29% 34% SION (ORF	1641 25 401 621 824 953 1157 1557 1705 1906 1972 2331 <b>ide bio</b> <b>TIONS</b> 11 7) 44 106 128 133. 7)	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) es and nucleotides 11 genes HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.4.2.7) HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) URIDINE KINASE (EC 2.7.1.48) RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR synthesis and interconversions 0 genes 94 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA PUTATIVE PBSX REPRESSOR PUTATIVE PBSX REPRESSOR PUTATIVE GTP PYROPHOSPHOKINASE (EC 2.7.6.5) TETRACYCLIME REPRESSOR PROTEIN CLASS H HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA

CODY_BACSU	49%	162	CODY PROTEIN (VEGETATIVE PROTEIN 286B)
MECB_BACSU	518	549	NEGATIVE REGULATOR OF GENETIC COMPETENCE MECB
CTSR_BACSU	458	627	TRANSCRIPTIONAL REGULATOR CTSR
MECB BACSU	50%	629	NEGATIVE REGULATOR OF GENETIC COMPETENCE MECH
YP20 BACLT	34%	737	HYPOTHETICAL P20 PROTEIN.
CLAS CALEY	268	747	TRANSCRIPTIONAL RECULATOR SLVA (SALMOLVSIN)
VDDA DACTT	226	705	NYDONUWITTAL DO BOOMETN
TP20_DACDI	220	040	DEPENDENT PAO
BEAI_BACLI	318	843	PENICILLINASE REPRESSOR (REGULATORY PROTEIN BLAI)
DEGU_BACSU	398	910	TRANSCRIPTIONAL REGULATORY PROTEIN DEGU (PROTEASE PRODUCTION
ENHANCER PROTE	IN)		
HRCA_LACLA	99%	975	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
SORC_KLEPN	21%	1204	SORBITOL (SOR) OPERON REGULATOR
XRE BACSU	42%	1220	PUTATIVE PBSX REPRESSOR
YOAE BACSU	35%	1300	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA
TWTERGENTC REG	TON (OP	F71	
VIGE VARIA	200 .	1506	HYDOTURTICAL TOANSCOLDTIONAL DECULATOR MIG196
1186_RAEIN	399	1500	THEOLOGICAL THE DECORATE AND A SOLATER AND A
TERZ_ECOLI	298	1551	TETRACYCLINE REPRESSOR PROTEIN CLASS B (TRANSPOSON TNIO)
TFDT_ALCEU	40%	1594	TRANSCRIPTIONAL REGULATORY PROTEIN TFDT
GLNB_FREDI	56%	1631	NITROGEN REGULATORY PROTEIN P-II (PII SIGNAL TRANSDUCING
PROTEIN)			
PYRR BACCL	60%	1644	PYRIMIDINE OPERON REGULATORY PROTEIN PYRR
SMTB SYNY3	348	1645	TRANSCRIPTIONAL REPRESSOR SMTB HOMOLOG
ARR2 FCOLT	318	1730	ARSENICAL RESISTANCE OPERON REPRESSOR
ARR2_BCOBI	110	1730	
GERE_BACSO	418	1/3/	GERMINATION PROTEIN GERE
PHOU_ECOLI	36%	1750	PHOSPHATE TRANSPORT SYSTEM REGULATORY PROTEIN
TENA_BACSU	419	1818	TRANSCRIPTIONAL ACTIVATOR TENA
BIRA_BACSU	348	1820	BIRA BIFUNCTIONAL PROTEIN (BIOTIN OPERON REPRESSOR)
Y186 HAEIN	318	1927	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI0186
BIRA BACSU	338	1953	BIRA BIFUNCTIONAL PROTEIN (BIOTIN OPERON REPRESSOR)
PDC2 BDD22	308	2003	REPRESSOR PROPERN C2
NFCA_DEFEA	249	2002	INFORMETICAL PRANCEDIDITIONAL DECILATION HT0196
1186_HAEIN	3,4 6	2032	APPOTHETICAL TRANSCRIPTIONAL RESOLATOR REGISE
NADR_ECOLI	30%	2047	TRANSCRIPTIONAL REGULATOR NADR
FLP_LACCA	418	2062	PROBABLE TRANSCRIPTIONAL REGULATOR FLP
ACKA_BACSU	54%	2069	ACETATE KINASE (EC 2.7.2.1)
GLNR BACSU	· 50% ·	2264	REGULATORY PROTEIN GLNR
YOAE BACSU	418	. 2276	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOIIIC-CWLA
INTERGENIC REC	TON (OR	F71	
THE THROUGH A C. LOND	2021 JOA		
END DACCH	289	2298	ANAFROBIC PRCHLATORY PROTRIN
FNR_BACSU	28%	2298	ANAEROBIC REGULATORY PROTEIN
FNR_BACSU ACRR_ECOLI	28% 32%	2298 2317	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR
FNR_BACSU ACRR_ECOLI	28% 32%	2298 2317	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c	28% 32%	2298 2317 t system	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR s 13 genes
FNR_BACSU ACRR_ECOLI BIO09.02 Two-C RESE_BACSU	28% 32% cmponen 33%	2298 2317 t system 400	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>s 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3)
FNR_BACSU ACRR_ECOLI BIO09.02 Two-C RESE_BACSU YYCF_BACSU	28% 32% componen 33% 69%	2298 2317 t system 400 401	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG	28% 32% omponen 33% 69% ION	2298 2317 <b>t system</b> 400 401	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS BACBR	28% 32% 33% 69% ION 40%	2298 2317 t system 400 401 909	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>s 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3)
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCP_BICFU	28% 32% 33% 69% ION 40% 39%	2298 2317 <b>t system</b> 400 401 909 1028	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU VERW_ECOLI	28% 32% 33% 69% ION 40% 39% 28%	2298 2317 <b>t system</b> 400 401 909 1028 1030	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROMENE SENSOR PROTEIN VEDV (EC 2.7.3)
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI	28% 32% 33% 69% ION 40% 39% 28%	2298 2317 <b>t system</b> 400 401 909 1028 1030	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>s 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) NEXT ND DEGOCHARDES CONFUENCE TRANSCRIPTIONAL RECULATORY
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU	28% 32% 33% 69% ION 40% 39% 28% 40%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGRNIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP	28% 32% 33% 69% ION 40% 39% 28% 40%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PHOP_BACSU PHOP_BACSU	28% 32% 33% 69% ION 40% 39% 28% 40% 32%	2298 2317 t system 400 401 909 1028 1030 1456 1457	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>s 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3)
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU	28% 32% 33% 69% ION 40% 39% 28% 40% 32% 22%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3)
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOF_BACSU RESE_BACSU C2CR_ALCEU	28% 32% omponen 33% 69% 10N 40% 39% 28% 40% 32% 27% 43%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU	28% 32% 69% ION 40% 39% 28% 40% 32% 22% 40% 32% 32% 33%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>s 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3)
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PHOP_BACSU PHOFEIN PHOP PHOR_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR PESEM	28% 32% 69% 10N 40% 39% 28% 40% 32% 27% 43% 33% 34%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU RESE_BACSU C2CR_ALCEU RESE_BACSU COPR_PEESM YXDK BACSU	288 328 338 698 10N 408 398 288 408 328 278 438 338 338	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1724	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CORR HYPOTHEFICAL SENSOR-LIKE HISTIDINE KIMASE IN IDH 3'REGION (EC
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACSR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PSESM YXDK_BACSU	288 328 000000000 338 698 1001 408 398 288 408 328 278 408 328 278 438 338 348 338	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>S 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CORR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU PHOP_BACSU PROTEIN PHOP PHOP_BACSU PROTEIN PHOP PHOP_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PSESM YZDK_BACSU 2.7.3)	28% 32% 33% 69% 10N 40% 39% 28% 40% 32% 27% 43% 33% 34% 33%	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR FROTEIN TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR FROTEIN TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR FROTEIN TRANSCRIPTIONAL ACTIVATOR PROTEIN TRANSC
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PEESM YXDK_BACSU 2.7.3) YXDJ_BACSU	288 328 338 698 10N 408 398 288 408 328 408 328 338 338 348 338 348	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CORR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU CCOPR_PAESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3.REGION	288 328 338 698 10N 408 398 288 408 328 278 438 338 348 338 428	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU C2CR_ALCEU RESE_BACSU COPR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION	288 328 338 698 408 398 408 328 278 408 328 338 338 338 348 338	2298 2317 <b>t system</b> 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH
FNR_BACSU ACRR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU C0PR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI-	28% 32% omponen 33% 69% 10N 40% 39% 28% 40% 32% 40% 32% 33% 33% 33% 42% family	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CORR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6 genes</b>
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PHOP_BACSU PHOP_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PESSM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI	28% 32% omponen 33% 69% 40% 32% 28% 40% 32% 27% 43% 32% 27% 43% 33% 42% <b>family</b> 28%	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU COPR_PSESM YMDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESE BACSU	28% 32% 33% 69% 20% 40% 32% 27% 40% 32% 33% 33% 32% 42% <b>family</b> 28% 21%	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6</b> genes TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PRESM YXDK_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESE_BACSU	28% 32% omponen 33% 69% 10N 40% 39% 28% 40% 32% 40% 32% 42% 43% 33% 42% family 28% 31% 28% 32%	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CORR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>TS 6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PHOP_BACSU PHOP_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PESSM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU RESR_BACSU	28% 32% omponen 33% 69% 28% 40% 32% 27% 40% 32% 27% 43% 33% 42% <b>family</b> 28% 31% 42%	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1533	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN ALCTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15</b> <b>6</b> genes TRANSCRIPTIONAL REPRESSOR RIBOSE OPERON REPRESSOR RIBOSE OPERON REPRESSOR SIDSON CONTENL PROTEIN A DEDOTABLE CARABOLITE CONTENCIONEDIA DEDOTETN A
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU RESR_BACSU COPA_STAXY	288 328 338 698 10N 408 398 288 408 328 278 438 338 348 338 348 338 348 338 348 338 348 338 348 338 348 28 428	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR FROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR RIBOSE OPERON REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A HUBDRE HUCH DEGULATOR PROTEIN A HUBDRE HUCH DEGULATOR PROTEIN A HUBDRE HUCH DEGULATOR PROTEIN A HUBDRE HUCH DEGULATOR PROTEIN A
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU RESE_BACSU COPR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU RESR_BACSU CCPA_STAXY PURR_HAEIN	288 328 338 698 288 408 328 278 438 328 278 438 348 338 428 <b>family</b> 288 318 428 318 428	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR RIBOSE OPERON REPRESSOR RIBOSE OPERON REPRESSOR PROZABLE CATABOLITE CONTROL PROTEIN À PURINE NUCLEOTIDE SYNTHESIS REPRESSOR
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU PHOP_BACSU PROTEIN PHOP PHOP_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU CCPR_STAXY PURR_HAEIN YYAG_BACSU	288 328 338 698 408 328 288 408 328 278 438 338 338 428 <b>family</b> 288 338 428 <b>family</b> 288 318 428 428 348 348	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>18 6 genes</b> TRANSCRIPTIONAL REPRESSOR RIBOSE OPERON REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RBSR_BACSU CCPA_STAXY PURR_HAEIN YXAG_BACSU REGION	288 328 338 698 10N 408 398 288 408 328 278 438 338 348 338 348 338 428 <b>family</b> 288 318 428 478 348 368	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>S 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>'S 6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOR_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU COPR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3.'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION	288 328 338 698 288 408 328 278 408 328 278 408 328 338 428 <b>family</b> 288 318 428 <b>family</b> 288 318 428 348 348 338 428	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR RIBOSE OPERON REPRESSOR PROMABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PHOP_BACSU PROTEIN PHOP PHOP_BACSU RESE_BACSU C2CR_ALCEU RESE_BACSU COPR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LyER-	28% 32% omponen 33% 69% 40% 32% 28% 40% 32% 27% 43% 33% 32% 27% 43% 33% 32% 22% 42% 42% 42% 42% 42% 42% 42% 42% 4	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>'S 6 genes</b> TRANSCRIPTIONAL REPRESSOR RIBOSE OPERON REPRESSOR RIBOSE OPERON REPRESSOR PRODABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLBOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC <b>15 4 genes</b>
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU C2CR_ALCEU RESE_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RBSR_BACSU RESR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU BIO09.04 LySR- YWEK_BACSU	28% 32% omponen 33% 69% 10N 40% 39% 28% 40% 32% 23% 33% 33% 33% 42% 42% 28% 21% 33% 33% 42% 42% 42% 42% 42% 42% 42% 42% 42% 53% 53% 53% 53% 53% 53% 53% 53% 53% 53	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196 regulato 375	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>'S</b> <b>6 genes</b> TRANSCRIPTIONAL REPRESSOR CYTR RIBOSE OPERON REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC <b>'S</b> <b>4 genes</b> HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU CZCR_ALCEU RESE_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU CCPA_STAXY PURR_HAEIN YVAG_BACSU REGION BIO09.04 LySR- YMFR_BACSU	28% 32% omponen 33% 69% 28% 28% 28% 32% 27% 40% 32% 27% 43% 33% 42% 33% 42% 33% 42% 42% 42% 42% 42% 42% 42% 42% 42% 42	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196 regulato 375 893	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6</b> genes TRANSCRIPTIONAL REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC <b>15 4</b> genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC PERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR
FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU INTERGENIC REG DEGS_BACBR C2CR_ALCEU YEDV_ECOLI PHOP_BACSU PROTEIN PHOP PHOP_BACSU RESE_BACSU C2CR_ALCEU RESE_BACSU COPR_PSESM YXDK_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_ECOLI RESR_BACSU CCPA_STAXY PURR_HAEIN VYAG_BACSU REGION BIO09.04 LySR- YWFK_BACSU	288 328 338 698 200 408 398 208 408 328 278 408 328 278 438 338 348 338 428 428 428 428 478 318 428 478 368 69 258 100 258	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196 regulato 375 893 1253	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>16</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b> <b>17</b>
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FNR_BACSU ACFR_ECOLI BIO09.02 Two-c RESE_BACSU YYCF_BACSU INTERGENIC REG DEGS_BACBR CZCR_ALCEU YEDV_ECOLI PHOP_BACSU PHOP_BACSU PHOP_BACSU RESE_BACSU CZCR_ALCEU RESE_BACSU CZCR_ALCEU RESE_BACSU 2.7.3) YXDJ_BACSU 3'REGION BIO09.03 LacI- CYTR_FCOLI RESR_BACSU RESR_BACSU RESR_BACSU RESR_BACSU RESR_BACSU REGION BIO09.04 LySR- YWFE_BACSU REGION	28% 32% omponen 33% 69% 28% 40% 32% 27% 43% 32% 27% 43% 33% 42% 42% 42% 42% 42% 42% 42% 42% 42% 42	2298 2317 t system 400 401 909 1028 1030 1456 1457 1633 1635 1722 1723 1784 1785 regulato 728 1533 1684 1692 1724 2196 regulato 375 893 1261	ANAEROBIC REGULATORY PROTEIN POTENTIAL ACRAB OPERON REPRESSOR <b>3 13 genes</b> SENSOR PROTEIN RESE (EC 2.7.3) HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCR-PURA SENSOR PROTEIN DEGS (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3) ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3) SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR SENSOR PROTEIN RESE (EC 2.7.3) TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3'REGION (EC HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH <b>15 6 genes</b> TRANSCRIPTIONAL REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC <b>15 4 genes</b> HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC FERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC FERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN EPR-GALK INTERGENIC
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4 genes

BIO09.05 AraC-family regulators

SLAP_LACBR	30%	480	S-LAYER PROTEIN PRECURSOR (SURFACE LAYER PROTEIN)
ADAA_BACSU	448	517	METHYLPHOSPHOTRIESTER-DNA ALKYLTRANSFERASE
LUMQ_PHOLE	32%	1547	PROBABLE TRANSCRIPTIONAL REGULATOR LUMQ
TOXA_CLODI	30%	2284	TOXIN A
BT008 46 CP	t D., familie		
NULLY ECOLT	CR-Tamily	regulator	UNDORUGETON 20 0 KIN DORDEN IN ONDE COM INTERCENTO DECION
INNA_BOODI	440	201	REPOTRETICAL 38.8 KD PROTEIN IN GNIR-GGT INTERGENIC REGION
(F343)	119	121	TRENINGE ODROOM TRANSCOTTREIONAL DEDBECCOD
TRER_BACSU	245	434	TREMADOSE OPERON TRANSCRIPTIONAL REPRESSOR
VINI CODAM	206	1439	PATTY ACTS RESPONSIVE REGULATOR (PSU PROTEIN)
IINI_STRAM	208	10/0	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN INSTABLE DNA LOCUS
(ORF I)	240	2046	
YXAM_BACSU	243	2215	HYPOTHETICAL 44.7 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION
TAMP_BAC50	104	2305	HIPOTRETICAL 44.5 KD PROTEIN IN GNTR-HIPG INTERGENIC REGION
BI009.07 De	oR-family	regulator	rs 8 genes
YXEP_BACSU	33%	278	HYPOTHETICAL 41.6 KD PROTEIN IN IDH-DEOR INTERGENIC REGION
YXEB_BACSU	35%	327	PROBABLE ABC TRANSPORTER BINDING PROTEIN IN IDH-DEOR INTERGENIC
REGION PREC	URSOR		
YXEA_BACSU	37%	575	HYPOTHETICAL 13.0 KD PROTEIN IN IDH-DEOR INTERGENIC REGION
PRECURSOR			
GATR_ECOLI	31%	794	GALACTITOL UTILIZATION OPERON REPRESSOR
YXEP BACSU	43%	980	HYPOTHETICAL 41.6 KD PROTEIN IN IDH-DEOR INTERGENIC REGION
YBJG ECOLI	32%	1031	HYPOTHETICAL 22.4 KD PROTEIN IN DEOR-CMR INTERGENIC REGION
GLPR HAEIN	33%	1330	GLYCERÓL-3 - PHOSPHATE REGULON REPRESSOR
YXEA BACSU	398	1504	NYPOTHETICAL 13 0 KD PROTEIN IN IDH-DEOR INTERCENTS REGION
PRECURSOR	390	1504	ATOTALISADI DIO AD INCIDIA IN IDI DEON INTENDINE REGION
BI009.08 Ma	rR-family	regulator	s 2 genes
YDEA_ECOLI	32%	329	HYPOTHETICAL 42.5 KD PROTEIN IN UXAB-MARR INTERGENIC REGION
PETP_RHOCA	34%	1338	PETP PROTEIN
BTOOD 00 BC	10-familer	nomilator	1
LICT_BACSU	418	1491	TRANSCRIPTION ANTITERMINATOR LICT
BI009.10 GT	P-binding	proteins	9 genes
YYAF_BACSU	68%	12	HYPOTHETICAL 40.1 KD GTP-BINDING PROTEIN IN RPSF-SPO0J
INTERGENIC 1	REGION		
HFLX_ECOLI	44%	222	GTP-BINDING PROTEIN HFLX
			Car manually reconnect the part (
ERA_STRMU	75%	353	GTP-BINDING PROTEIN ERA HOMOLOG
ERA_STRMU YPHC_BACSU	75% 62%	353 760	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC
ERA_STRMU YPHC_BACSU REGION	75% 62%	353 760	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU	75% 62% 77%	353 760 1116	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU	75% 62% 77% 66%	353 760 1116 1163	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX)	758 628 778 668	353 760 1116 1163	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU	758 628 778 668 648	353 760 1116 1163 1626	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3	758 628 778 668 648 518	353 760 1116 1163 1626 1654	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG)
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU	758 628 778 668 648 518 608	353 760 1116 1163 1626 1654 2308	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. BEPT	758 628 778 668 648 518 608	353 760 1116 1163 1626 1654 2308	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 cenes
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL;	75% 62% 66% 64% 51% 60%	353 760 1116 1163 1626 1654 2308	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL: BIO10.01 Deg	75% 62% 77% 66% 64% 51% 60% ICATION gradation	353 760 1116 1163 1626 1654 2308 of DNA	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL; BIO10.01 De; ADDB_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28%	353 760 1116 1163 1626 1654 2308 of DNA 5	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B
ERA_STRMU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL: BIO10.01 Dep ADDB_BACSU ADDA_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32%	353 760 1116 1163 1626 1654 2308 of DNA 5 7	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A
ERA_STEMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL: BIO10.1 Dey ADDB_BACSU ADDA_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPI; BIO10.01 De; ADDB_BACSU ADDA_BACSU UVRB_HAEIN	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B
ERA_STRMU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH	758 628 778 668 648 518 60% ICATION gradation 288 328 328 338 40% 368	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1)
ERA_STRMU YPHC_BACSU YPHC_BACSU LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL: BIO10.1 Dep ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ENWCH EXOA_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40% 32% 33% 40%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-POUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2)
ERA_STRMU YPHC_BACSU YEGION LEPA_BACSU YSXC_BACSU OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPI: BIO10.1 Deg ADDB_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 32% 33% 40% 36% 40% 54%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-POUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C
ERA_STRMU YPHC_BACSU YEGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 De; ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU UVRC_BACSU	758 628 77% 668 648 518 60% ICATION gradetion 28% 32% 32% 33% 40% 36% 40% 54% 54%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODBOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.1.6)
ERA_STRMU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL: BIO10.1 De; ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX7L_BACSU END3_BACSU	758 628 778 668 648 518 60% ICATION gradation 328 328 338 408 368 408 548 438 508	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18)
ERA_STRMU YPHC_BACSU REGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL: BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40% 36% 40% 54% 43% 54% 50% 27%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXCONDUCYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5)
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDF_BACSU BIO10. REPL; BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EX5A_ECOLI EX5A_ECOLI	75% 62% 77% 66% 64% 51% 60% ICATION 28% 32% 33% 40% 36% 40% 54% 43% 54% 43% 52% 27% 32%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (PIPTY-POUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5)
ERA_STRMU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.1 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU EX7L_BACSU EX7L_BACSU EX5A_ECOLI	758 628 77% 668 648 518 60% ICATION gradetion 28% 32% 33% 40% 54% 54% 54% 54% 54% 54% 54% 54% 54% 54	353 760 1116 163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODBOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODBOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5)
ERA_STRMU YPHC_BACSU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU UVRC_BACSU EX7L_BACSU EX7L_BACSU EX5A_ECOLI BIO10.02 DMC	758 628 778 668 648 518 60% ICATION gradation 288 328 328 328 328 328 328 328 328 328	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 stion, rest	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5)
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU (OEFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNS genes NIAA_STRAU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40% 36% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 43% 50% 27% 32%	353 760 1116 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 cion, rest	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.5) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5)
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YEGION LEPA_BACSU VSXC_BACSU OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.1 Deg ADDB_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNX genes DNAA_STAAU DD2B_CZAU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 43% 40% 54% 43% 40% 54% 43% 40% 54% 43% 43% 43% 43% 43% 43% 43% 43% 43% 4	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 cion, rest	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIPTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 7 7 KD POLYPEPTIDE (EC 3.1.11.5)
ERA_STRNU YPHC_BACSU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EXTA_EACSU EX	758 628 778 668 648 518 608 <b>ICATION</b> gradation 288 328 328 408 548 408 548 408 548 438 548 438 548 438 548 438 548 438 548 438 548 458 418	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 cion, rest	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (II (EC 4.2.99.18) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.5) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FRICTION, MODIFICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7)
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU EX7L_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNX genes DNAA_STAAU DP3B_STAAU MFD_BACSU	75% 62% 77% 66% 64% 51% 60% <b>ICATION</b> gradation 28% 32% 33% 40% 36% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 43% 50% 27% 32% <b>A replicat</b>	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 2:ion, rest 1 2 19	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.5) PROBABLE ENDONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICITION, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
ERA_STRMU YPHC_BACSU YPHC_BACSU KEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPI: BIO10.1 Deg ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTA_ECOLI EX5A_ECOLI BIO10.02 DNX genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 NOWN DEGT	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40% 54% 40% 54% 43% 50% 27% 32% A replicat 45% 41% 50% 21%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 tion, rest 1 2 19 38	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICTION, MODIFICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA FMMASE (EC 2.7.7)
ERA_STRMU YPHC_BACSU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPL; BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU UVRC_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNX genes DNAA_STAAU DP3B_STAAU DP3B_STAAU MFD_BACSU MFD_BACSU PRIM_BPP4 YQXL_BACSU	758 628 778 668 648 518 608 <b>ICATION</b> gradation 288 328 328 328 328 328 328 408 368 408 508 278 328 408 548 438 508 278 328 <b>A replicat</b> 458 418 508 218 318	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 2 ion, rest 1 2 19 38 58	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE IARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICTION, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA PRIMASE (EC 2.7.7) HYPOTHETICAL 29.3 KD PROTEIN IN BEX-DNAG/DNAE INTERGENIC REGION
ERA_STRMU YPHC_BACSU YPHC_BACSU YEGION LEPA_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU UVRC_BACSU EX1L_BACSU EX1L_BACSU EX5A_ECOLI BIO10.02 DWI genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BP4 YQXN_BACSU ONEY DACSU VOFU DACSU	75% 62% 77% 66% 64% 51% 60% <b>ICATION</b> gradation 28% 32% 32% 32% 32% 36% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 41% 50% 27% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 stion, rest 1 2 19 38 58	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.5) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) Friction, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA PROTEIN IN BEX-DNAG/DNAE INTERGENIC REGION
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU (OEFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPI; BIO10.01 De; ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTA_ECOLI EXTA_ECOLI BIO10.02 DNX genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXN_BACSU QUAY_SCACSU	75% 62% 77% 66% 64% 51% 60% <b>ICATION</b> gradation 28% 32% 33% 40% 54% 40% 54% 43% 50% 27% 32% A replicat 45% 41% 50% 21% 31%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 2 1081 1777 1778 2 1081 1777 1778 2 1081 122 19 38 58	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICICION, modification, recombination, and repair <b>66</b> CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA FRIMASE (EC 2.7.7) HYPOTHETICAL 29.3 KD PROTEIN IN DRAJ-RDSU INTERGENIC REGION
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU UPHC_BACSU OBG_BACSU OBG_BACSU OBG_BACSU OBG_BACSU OBG_BACSU BIO10.1 Deg ADDA_BACSU ADDA_BACSU UVRD_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNX genes DNAA_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXL_BACSU YAAK_BACSU YAAK_BACSU YAAK_BACSU	75% 62% 77% 66% 64% 51% 60% ICATION gradation 28% 32% 33% 40% 54% 40% 54% 43% 54% 43% 54% 43% 54% 41% 50% 21% 31% 44% 44% 44%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 cion, rest 1 2 19 38 58 103 120 165	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE II (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICTION, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.) TRANSCRIPTION-REPAIR COUPLING FACTOR (TECF) PUTATIVE P4-SPECIFIC DNA PRIMASE (EC 2.7.7) HYPOTHETICAL 29.3 KD PROTEIN IN BEX-DNAG/DNAE INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECH INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECH INTERGENIC REGION
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU (OEFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 De; ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX5A_ECOLI EX5A_ECOLI BIO10.02 DNI genes DNAA_STAAU DP3B_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQEN_BACSU YAAK_BACSU YAAK_BACSU YAAK_BACSU	75% 62% 77% 66% 64% 51% 60% <b>ICATION</b> gradation 28% 32% 32% 33% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 2 ion, rest 1 2 19 38 58 103 120 151	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) Friction, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DUP RING (EC 2.7.7.7) HYPOTHETICAL 28.8 KD PROTEIN IN BEX-DNAG/DNAE INTERGENIC REGION HYPOTHETICAL 28.8 KD PROTEIN IN DNAJ-RPSU INTERGENIC REGION HYPOTHETICAL 28.8 KD PROTEIN IN DNAJ-RPSU INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAZ-RECR INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAZ-RECR INTERGENIC REGION
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EX0A_BACSU EX7L_BACSU UVRC_BACSU EX5A_ECOLI BIO10.02 DNX Genes DNAA_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU DP3B_STAAU MFD_BACSU VAAK_BACSU YAAK_BACSU YAAK_BACSU T3RE_BACCE 3.1.21.5)	75% 62% 77% 66% 64% 51% 60% <b>ICATION</b> gradation 28% 32% 33% 40% 36% 40% 54% 40% 54% 40% 54% 40% 54% 32% 27% 32% 31% 44% 44% 29%	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 2 1081 1777 1778 2 1081 1777 1778 2 109 38 58 103 120 151 230	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ABC SUBUNIT B SINGLE-STRANED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICTION, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA PRIMASE (EC 2.7.7.1) HYPOTHETICAL 29.3 KD PROTEIN IN BEX-DNAG/DNAE INTERGENIC REGION HYPOTHETICAL 1.8 KD PROTEIN IN DNAJ-RPSU INTERGENIC REGION HYPOTHETICAL 1.8 KD PROTEIN IN DNAJ-RESU INTERGENIC REGION
ERA_STRMU YPHC_BACSU YPHC_BACSU YPHC_BACSU YPHC_BACSU (OEFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.1 Deg ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRE_HAEIN RECJ_ERWCH EX0A_BACSU EX7L_BACSU EX7L_BACSU EX5A_ECOLI BIO10.02 DNX genes DNAA_STAAU DP3B_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXN_BACSU YAAK_BACSU YAAK_BACSU YAAK_BACSU T3RE_BACCE 3.1.21.5) UNG_STRPN	758 628 778 668 648 518 608 <b>ICATION</b> gradation 288 328 338 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 408 548 418 508 218 318 318 318 318 318	353 760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 855 876 1081 1777 1778 2 19 38 58 103 120 151 230	GTP-BINDING PROTEIN ERA HOMOLOG HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SPO0B-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF <b>77 genes</b> <b>11 genes</b> ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ARC SUBUNIT B SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ARC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EC 3.1.11.5) PROBABLE ENDOULCLEASE III (EC 4.2.99.18) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) FICITION, modification, recombination, and repair <b>66</b> CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA PRIMASE (EC 2.7.7) HYPOTHETICAL 29.3 KD PROTEIN IN BEX-DNAG/DNAE INTERGENIC REGION HYPOTHETICAL 28.8 KD PROTEIN IN DNAJ-RDSU INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RDSU INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAZ-RECR INTERGENIC REGION

RECR STRTR	76%	338	RECOMBINATION PROTEIN RECR
FPG LACLC	90%	356	FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23)
RECA_LACLA	94%	357	RECA PROTEIN
SSB_BACSU	44%	395	SINGLE-STRAND BINDING PROTEIN (SSB)
HOLB_BACSU	35%	402	DNA POLYMERASE III, DELTA' SUBUNIT (EC 2.7.7.7)
DNLJ_RHOMR	438	423	DNA LIGASE (EC 6.5.1.2)
DNAC_ECOLI	27%	454	DNA REPLICATION PROTEIN DNAC
DP3A_HELPY	26%	494	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
PRIM_LACLA	100%	542	DNA PRIMASE (EC 2.7.7)
DFP_ECOLI	30%	565	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
TIRI_ECOLI	326	640	TYPE I RESTRICTION ENZYME SCORIZGII & PROTEIN (SC 3.1.21.3)
YOIS_METJA	2/15	644	HYPOTHETICAL PROTEIN MUIZIS HYPOTHETICAL 20 7 YO DECOUTE IN MERC-YOCA INTERCONTO DUCTON
VAAT BACSU	519	725	HYPOTHEFICAL 20.7 KD PROTEIN IN SERS-DNAH INTERGENIC REGION
INAC BACSU	56%	752	REPLICATIVE DNA HELICASE (EC 3.6.1.=)
DNAB BACSU	27%	756	REPLICATION INITIATION AND MEMBRANE ATTACHMENT PROTEIN
DNAI BACSU	38%	757	PRIMOSOMAL PROTEIN DNAI
LEF3_NPVAC	26%	833	LATE EXPRESSION FACTOR 3
MUTY_ECOLI	438	857	A/G-SPECIFIC ADENINE GLYCOSYLASE (EC 3.2.2)
RECN_BACSU	448	881	DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N)
GYRB_STRPN	82%	926	DNA GYRASE SUBUNIT B (EC 5.99.1.3)
GRPE_LACLA	998	975	GRPE PROTEIN
RIR2_MYCTU	48%	999	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE BETA CHAIN (EC 1.17.4.1)
RIR1_MYCTU	50%	1001	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
PARE_STAAU	708	1005	TOPOISOMERASE IV SUBUNIT B (EC 5.99.1)
DING_BACSU	205	1007	TOBATION TO SUDDING A (TO 5 00 1 -)
PARC_STARU	419	1033	DNA REPAIR PROFFIN RADC HOMOLOG (ORFR)
SSB BACSU	61%	1041	SINGLE-STRAND BINDING PROTEIN (SSB)
DNAD. BACSU	378	1081	DNA REPLICATION PROTEIN DNAD
GYRA STAAU	23%	1120	DNA GYRASE SUBUNIT A (EC 5.99.1.3)
PCRA_BACST	49%	1132	ATP-DEPENDENT HELICASE PCRA (EC 3.6.1)
MUTX_STRPN	34%	1134	MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE)
DYR_LACLA	878	1161	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
DPRA_HAEIN	43%	1251	DNA PROCESSING CHAIN A
TOP1_BACSU	64%	1253	DNA TOPOISOMERASE I (EC 5.99.1.2)
DNAC_ECOLI	278	1446	DNA REPLICATION PROTEIN DNAC
SSB_BACSU	68%	1447	SINGLE-STRAND BINDING PROTEIN (SSB)
MUTS_AQUPY	34%	1689	DNA MISMATCH REPAIR PROTEIN
RECO_ECOLI	358	1854	ATP-DEPENDENT DNA HELICASE RECO (EC 3.5.1)
DING_BACSU	288	1880	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG
DING_DACSU	58%	1944	PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)
YAAA BACSU	49%	2030	HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION
RECF LACLC	99%	2031	RECF PROTEIN
DINP_ECOLI	42%	2085	DNA-DAMAGE-INDUCIBLE PROTEIN P
RADA_BACSU	60%	2129	DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS
HOMOLOG)			
DP3A_BACSU	428	2171	DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
DP01_STRPN	68%	2192	DNA POLVMERASE I (EC. 2.7.7.7)
SSB_BACSU			in reprinted i the strift,
	60%	2254	SINGLE-STRAND BINDING PROTEIN (SSB)
DP3X_BACSU	60% 43%	2254 2259	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7)
DP3X_BACSU RUVB_PSEAE	60% 43% 59%	2254 2259 2269	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN	60% 43% 59% 40%	2254 2259 2269 2269	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH PEDATE DEDTEIN HERP
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN	60% 43% 59% 40% 57% 79%	2254 2259 2269 2269 2271 2274	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAL LACLA	60% 43% 59% 40% 57% 79% 99%	2254 2259 2269 2269 2271 2274 2287	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG ECOLI	60% 43% 59% 40% 57% 79% 99% 36%	2254 2259 2269 2269 2271 2274 2287 2311	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI	60% 43% 59% 40% 57% 79% 99% 36%	2254 2259 2269 2271 2274 2287 2311	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCI	60% 43% 59% 40% 57% 79% 99% 36% RIPTION	2254 2259 2269 2271 2274 2287 2311	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVB DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCI	60% 43% 59% 40% 57% 99% 36% RIPTION	2254 2259 2269 2271 2274 2287 2311	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVB DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCI BIO11.01 Degra	60% 43% 59% 40% 57% 79% 99% 36% RIPTION adation	2254 2259 2269 2269 2271 2274 2287 2311 of RNA	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXA DNAJ FROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes
DP3X_BACSU RUVB_PSSAE RUVA_HAEIN HEXE_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCI BIO11.01 Degra TRUA_ECOLI	60% 43% 59% 40% 57% 79% 99% 36% RIPTION adation 34% 26%	2254 2259 2269 2271 2274 2287 2311 of RNA 482 595	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYDOMEDICAL BENA MEREVIACE IN CYSE 3/DECION
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE	60% 43% 59% 40% 57% 79% 99% 36% RIPTION adation 34% 26% 32%	2254 2259 2269 2269 2271 2274 2287 2311 of RNA 482 595 613	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) <b>27 genes</b> <b>18 genes</b> PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RRNA METHYLASE IN CYSS 3'REGION DPORABLE TENA DELTA (2) - ISOPENTEMULEYCOMPOSPHATE TRANSFERASE (EC
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1 &	60% 43% 59% 40% 57% 79% 99% 36% 36% <b>RIPTION</b> 34% 26% 32%	2254 2259 2269 2271 2274 2287 2311 of RNA 482 595 613	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) <b>27 genes</b> <b>18 genes</b> PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RRNA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degre TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) ENC BACSU	60% 43% 59% 57% 79% 99% 36% RIPTION adation 34% 26% 32%	2254 2259 2269 2271 2274 2274 2287 2311 of RNA 482 595 613 807	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RENA METHYLASE IN CYSS 3'REGION PROBABLE TENA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONNICLEASE III (EC 3.1.26.3)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXE_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACB HAEIN	60% 43% 59% 40% 57% 79% 99% 36% <b>RIPTION</b> <b>adation</b> 34% 26% 32% 44% 37%	2254 2259 2269 2271 2274 2287 2311 0f RNA 482 595 613 807 965	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RRNA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEEM_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degr: TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACB_HAEIN ALDC_BACBR	60% 43% 59% 40% 57% 79% 99% 36% 36% adation 34% 26% 32% 31%	2254 2259 2269 2271 2274 2311 00f RNA 482 595 613 807 965 1114	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) <b>27 genes</b> <b>18 genes</b> PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RRNA METHYLASE IN CYSS 3 REGION PROBABLE TRNA DELTA (2) -ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACE_HAEIN ALDC_BACSU VACE_HAEIN	60% 43% 59% 40% 57% 79% 99% 36% 36% adation 34% 26% 32% 44% 37% 31% 39%	2254 2259 2269 2271 2274 2287 2311 of RNA 482 595 613 807 965 1114 1138	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RRNA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA (2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TRNA PSEUDOURIDINE 55 SYNTHASE (PSI55 SYNTHASE)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACB_HAEIN ALDC_BACBR TRUB_SYNY3 YGL3_BACST	60% 43% 59% 40% 57% 99% 36% 36% 36% 32% 44% 37% 31% 39% 57%	2254 2259 2269 2271 2274 2287 2311 0 <b>of RNA</b> 482 595 613 807 965 1114 1138 1160	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RRNA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TRNA PSEUDOURIDINE 55 SYNTHASE (PSI55 SYNTHASE) HYPOTHETICAL 18.2 KD PROTEIN IN GLDA 3'REGION (ORF3)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXE_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECCLI BIO11. TRANSCI BIO11.01 Degra TRUA_ECCLI TRUA_ECCLI VACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACE_HAEIN ALDC_BACSR TRUB_SYNY3 YGB3_BACST ALDC_BACSU	60% 43% 59% 57% 79% 36% 36% <b>RIPTION</b> <b>adation</b> 34% 32% 44% 37% 31% 39% 57% 35%	2254 2259 2269 2271 2274 2287 2311 0f RNA 482 595 613 807 965 1114 1138 1160 1250	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RUNA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TRNA PSEUDOURIDINE 55 SYNTHASE (PSI55 SYNTHASE) HYPOTHETICAL R.2 K PROTEIN IN GLDA 3'REGION (ORF3) ALPHA-ACETOLACTATE DECARBOXYLASE (EC 4.1.1.5)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXE_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11.01 Degr: TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACB_HAEIN ALDC_BACSU TRUB_SYNY3 YGL3_BACST RNH2_ECOLI	60% 43% 59% 40% 57% 79% 99% 36% <b>adation</b> 34% 26% 32% 34% 32% 31% 35% 44% 37% 31% 35% 47%	2254 2259 2269 2271 2274 2287 2311 00 RNA 482 595 613 613 807 965 1114 1138 1160 1250 12250 1226	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ PROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RENA METHYLASE IN CYSS 3'REGION PROBABLE TENA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TENA PSEUDOURIDINE 55 SYNTHASE (PSI55 SYNTHASE) HYPOTHETICAL 18.2 KD PROTEIN IN GLDA 3'REGION PHYPOTHETICAL 18.2 KD PROTEIN IN GLDA 3'REGION(OFF3) ALPHA-ACETOLACTATE DECARBOXYLASE (EC 4.1.1.5) RIBONUCLEASE HII (EC 3.1.26.4)
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BI011. TRANSCJ BI011.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACB_HAEIN ALDC_BACSU TRUB_SYNY3 YGG3_BACST ALDC_BACSU RNH2_ECOLI SBCD_BACSU	60% 43% 59% 40% 57% 79% 99% 36% 36% adation 34% 26% 32% 31% 39% 57% 35% 47% 32%	2254 2259 2269 2271 2274 2277 2311 00 RNA 482 595 613 807 965 1114 1138 1160 1250 1326 1354	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXE DNA MISMATCH REPAIR PROTEIN HOUSE IN COMPARIS IN TABLE RIBONUCLEASE HII (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TRNA PSEUDOURIDINE 55 SYNTHASE (PSI55 SYNTHASE) HYPOTHETICAL 18.2 KD PROTEIN IN GLDA 3'REGION (ORF3) ALPHA-ACETOLACTATE DECARBOXYLASE (EC 4.1.1.5) RIBONUCLEASE HII (EC 3.1.26.4) EXONUCLEASE SECD HOMOLOG (FRAGMENT) MISMATCH REPAIR PROTEIN HEAD AND AND AND AND AND AND AND AND AND A
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCJ BIO11.01 Degra TRUA_ECOLI YACO_BACSU MIAA_MYCLE 2.5.1.8) RNC_BACSU VACB_HAEIN ALDC_BACSU VACB_HAEIN ALDC_BACST ALDC_BACSU RNH2_ECOLI SBCD_BACSU PAPS_BACSU	60% 43% 59% 57% 79% 36% 36% <b>RIPTION</b> adation 34% 26% 32% 32% 37% 31% 37% 31% 35% 44% 35% 42% 35% 42% 35% 42% 32%	2254 2259 2269 2269 2271 2274 2287 2311 0 of RNA 482 595 613 807 965 1114 1138 1160 1250 1326 1354 1598	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXE DNA MISMATCH REPAIR PROTEIN STRATE PSEUDOURIDINATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RENA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA (2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TRNA PSEUDOURIDINE 55 SYNTHASE (PSI55 SYNTHASE) HYPOTHETICAL 18.2 KD PROTEIN IN GLDA 3'REGION (ORF3) ALPHA-ACETOLACTATE DECARBOXYLASE (EC 4.1.1.5) RIBONUCLEASE HII (EC 3.1.26.4) EXONUCLEASE SECD HOMOLOG (FRAGMENT) POLY(A) POLYMERASE (EC 2.7.7.19) VACE DROTEIN HOMOLOG
DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA REG_ECCLI BIO11. TRANSCI BIO11.01 Degra TRUA_ECCLI BIO11.01 Degra TRUA_ECCLI WIAA_MYCLE 2.5.1.8) RNC_BACSU WACB_HAEIN ALDC_BACSU RNC_BACSU RNH2_ECCLI SBCD_BACSU RNH2_ECCLI SBCD_BACSU RNH2_ECCLI SBCD_BACSU RNH2_ECCLI SBCSU RNH2_BACSU	60% 43% 59% 40% 57% 79% 36% 36% 36% 32% 44% 37% 31% 39% 35% 47% 35% 47% 35% 47% 35% 47% 39% 26%	2254 2259 2269 2271 2274 2287 2311 2311 2311 2311 2311 2311 2355 595 613 807 965 1114 1138 1160 1250 1326 1354 1598 1603 1954	SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB DNA MISMATCH REPAIR PROTEIN HEXA DNAJ FROTEIN ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1) 27 genes 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70) HYPOTHETICAL RENA METHYLASE IN CYSS 3'REGION PROBABLE TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) TRNA PSEUDOURIDIE 55 SYNTHASE (PSI55 SYNTHASE) HYPOTHETICAL 18.2 KD FROTEIN IN GLDA 3'REGION (ORF3) ALPHA-ACETOLACTATE DECARBOXYLASE (EC 4.1.1.5) RIBONUCLEASE HII (EC 3.1.26.4) EXONUCLEASE HII (EC 3.1.26.4) EXONUCLEASE SPECH MOMOLOG (FRAGMENT) POLY(A) POLYMERASE (EC 2.7.7.19) 165 RENA PROCESSING PROTEIN RIMM DOLVELEMENTED RECHTS PROTEIN RIMM

YACO\_BACSU 478 1921 HYPOTHETICAL RRNA METHYLASE IN CYSS 3'REGION SPLR\_NPVAC 30% 2008 SPHEROIDIN-LIKE PROTEIN PRECURSOR (SPINDOLIN-LIKE PROTEIN) STREPTOCOCCAL ACID GLYCOPROTEIN SAGE STREY 47% 2094 TRANSCRIPTION ANTITERMINATION PROTEIN NUSG NUSG\_STRGR 43% 2154 BIO11.02 RNA synthesis , modification, and DNA transcription 8 genes RNA POLYMERASE SIGMA FACTOR RPOD (SIGMA-70) RPSD\_NEIGO 248 466 RNA POLYMERASE SIGMA FACTOR RPOD DNA-DIRECTED RNA POLYMERASE DELTA SUBUNIT (EC 2.7.7.6) RPSD\_LACLA 100% 544 RPOE BACSU 33% 621 624 TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE GREA\_RICPR 47% FACTOR GREAD DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6) DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (EC 2.7.7.6) RPOC\_MYCGE 46% 1838 RPOB\_SPICI 31% 1842 57% 2132 RPOA BACSU RNA POLYMERASE SIGMA FACTOR SIGV SIGV\_BACSU 23% 2222 BIO11.03 RNA processing 1 genes 414 PROBABLE RNA HELICASE IN CCCA-SODA INTERGENIC REGION YOFR BACSU 48% BIO12. TRANSLATION 138 genes 26 genes BIO12.01 Amino acyl tRNA synthetases SYW\_CLOLO 68 TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2) 63% OUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) TGT HAEIN 54% 153 SYK\_BACSU 374 LYSYL-TRNA SYNTHETASE (EC 6:1.1.6) 58% SYY1\_BACSU 55% 388 TYROSYL-TRNA SYNTHETASE 1 (EC 6.1.1.1) HYPOTHETICAL PROTEIN MG449 HOMOLOG Y449 MYCPN 34% 393 SYM\_BACSU 62% 798 METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) SYL\_MYCTU 43% 826 LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) GLYCYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.14) 1101 SYGE BACSU 41% SYK\_BACSU 32% 1129 LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) HYPOTHETICAL 38.0 KD PROTEIN IN HISC-HISG INTERGENIC REGION YHI3\_LACLA 978 1228 (ORF3) SERYL-TRNA SYNTHETASE (EC 6.1.1.1) ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) ASPARAGINYL-TRNA SYNTHETASE (EC 6.1.1.22) SYS\_BACSU 57% 1747 SYA THETH 41% 1759 59% 1875 SYN\_BACSU CYSTEINYL-TRNA SYNTHETASE (EC 6.1.1.16) ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) SYC\_HELPY 43% 1898 SYI STAAU 28% 1911 ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) SYT\_CAMJE 1912 43% THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) 42% 45% SYT MYCLE 1968 PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) SYFB\_BACSU 1987 PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.20) ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) SYFA\_BACSU 62% 1989 SYD\_SYNY3 51% 2021 SYH\_STREQ 2023 HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) 63% SYR\_SYNY3 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) 36% 2096 SYE HELPY 45% 2120 PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) VALYL-TRNA SYNTHETASE (EC 6.1.1.9) SYP\_HAEIN 458 2177 SYV THETH 43% 2229 PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) SYFB\_MYCGE 29% 2233 22 genes BI012.02 Degradation of proteins, peptides, and glycopeptides PROBABLE 0-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57) GCP\_HAEIN 41% 291 AMPN\_LACLC 98% 301 AMINOPEPTIDASE N (EC 3.4.11.2) PUTATIVE METHIONINE AMINOPEPTIDASE & (EC 3.4.11.18) 599 AMP1 SYNY3 45% CLPP STRSI 878 670 ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (EC 3.4.21.92) PUTATIVE PEPTIDASE IN GCVT-SPOIIIAA INTERGENIC REGION (EC 3.4.-YQHT\_BACSU 41% 688 - } PEPV LACOL 479 858 XAA-HIS DIPEPTIDASE (EC 3.4.13.3) P54 PROTEIN PRECURSOR P54 ENTFC 40% 959 CLPX\_BACSU ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (EC 3.4.21.92) 678 1162 CLPP SYNP7 29% 1433 CLPB\_HAEIN 56% 1564 CLPB PROTEIN XAA-PRO DIPEPTIDASE (EC 3.4.13.9) PROTEASE MATURATION PROTEIN PRECURSOR PEPQ\_LACDL 50% 1693 PRTM LACPA 32% 1761 PEPF\_LACLA 978 1763 OLIGOENDOPEPTIDASE F (EC 3.4.24.-) MINOPEPTIDASE C (EC 3.4.24.-) AMINOPEPTIDASE C (EC 3.4.24.-) PROTEASE III PRECURSOR (EC 3.4.24.55) HYPOTHETICAL PROCESSING PROTEASE (EC 3.4.-.-) PEPO\_LACLC PEPC\_LACLC 999 1847 98% 1927 PTR\_ECOLI 2028 22% YMXG\_BACSU 238 2029 PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION (EC 3.4.-.-) YEGQ\_ECOLI LEP3\_BACSU 378 2049 2084 TYPE 4 PREPILIN-LIKE PROTEIN SPECIFIC LEADER PEPTIDASE (EC 34% 3.4.99.-) XAA-PRO DIPEPTIDYL-PEPTIDASE (EC 3.4.14.11) PEPX\_LACLC 79% 2115 HYPOTHETICAL PROTEASE IN ROCR-PURA INTERGENIC REGION (EC 478 YYXA\_BACSU 2185 3.4.21.-) HTOA HAEIN 338 PROBABLE PERIPLASMIC SERINE PROTEASE DO/HHOA-LIKE PRECURSOR 2218

BIO12.03 Nucleo	protein	s	2 génes
DBH_BACST	67%	500	DNA-BINDING PROTEIN II (HB)
DBH_VIBPR	378	900	DNA-BINDING PROTEIN HU
BTO12.04 Protei	n modif	ication	2 genes
CYPH MYCTH	318	366	PROBABLE PEPTIDYL-PROLVL CIS-TRANS ISOMERASE (EC.5.2.1.8)
CVDU MYCTU	279	912	PROBABLE PEPTIDYL-PROLVL CIS-TRANS ISOMERASE (EC 5.2.1.8)
CIEN_NICIO	210	310	PROBABILS PERIOD PRODUCTS TRANS TOURARDS (SC 3.2.1.0)
BIO12.05 Riboso	mal pro	teins:	synthesis and modification 55 genes
PRMA BACSU	438	102 .	PROBABLE METHYLTRANSFERASE (EC 2.1.1)
RL34 COXBU	70%	131	50S RIBOSOMAL PROTEIN L34
RL28 BACSU	56%	193	50S RIBOSOMAL PROTEIN L28
RS21 BACSU	87%	235	30S RIBOSOMAL PROTEIN S21 (BS-B)
RS4 BACSU	628	281	30S RIBOSOMAL PROTEIN S4 (BS4)
R14H BACSH	359	306	36S RIBOSOMAL PROTEIN S14 HOMOLOG
DEAD VIEDN	159	351	AMP-DEPENDENT PNA HELTCASE DEAD
VUVD PACCU	519	630	HYPOPHEPICAL 22 0 KD DEODETN IN FLIT-SECS INTERCENTC REGION
IVID_BACSU	1006	650	EAG DIDOGOMAL DEOGETA 122
RL33_LACLA	1004	009	SVS RIBUSUNAL PROTEIN LA (DL12)
RL9_BACST	548	751	SUS RIBUSUMAL PROTEIN LA (BELT)
YLXQ_ENTFC	488	113	PROBABLE RIBOSOMAL PROTEIN IN INFE 5 REGION
RS1_BUCAP	328	852	305 RIBOSOMAL PROTEIN 51
RL19_BACST	738	895	50S RIBOSOMAL PROTEIN LIP
RS14_SYNY3	41%	908	30S RIBOSOMAL PROTEIN S14
RL21_BACSU	67%	1088	50S RIBOSOMAL PROTEIN L21 (BL20)
RL27_BACSU	74%	1089	50S RIBOSOMAL PROTEIN L27 (BL30)
RL7_BACSU	61%	1298	50S RIBOSOMAL PROTEIN L7/L12 (BL9)
RL7_STRPN	76%	1299	50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT)
RL10_BACSU	63%	1299	50S RIBOSOMAL PROTEIN L10 (BL5)
RS16_BACSU	59%	1606	30S RIBOSOMAL PROTEIN S16 (BS17)
YKGM ECOLI	45%	1636	HYPOTHETICAL 9.9 KD PROTEIN IN INTF-EACH INTERGENIC REGION
RL20 BACSU	69%	1891	50S RIBOSOMAL PROTEIN L20
RS15 BACSU	62%	1934	30S RIBOSOMAL PROTEIN S15 (BS18)
RL1 BACSU	67%	2058	50.S RIBOSOMAL PROTEIN L1 (BL1)
RL11 STACA	80%	2059	50S RIBOSOMAL PROTEIN L11
RIAH BACSH	30%	2125	30S RIBOSOMAL PROTEIN \$14 HOMOLOG
RL17 BACSU	72%	2131	50S RIBOSOMAL PROFEIN L17 (BL15)
RELT_BACOU	026	2133	30C DIBOGOMAL PROTEIN SIL (BSLL)
RSII_BACSU	706	2122	300 RIBOSOWAL PROTEIN SII (BSII)
RSIS_BACSU	106	2130	SUS RIBUSUMAL PROFEIN 115
RLID_STARU	0/6	21.10	DOG DIDOGONAL PROTEIN DID
RS5_BACSU	778	2140	30S RIBOSOMAL PROTEIN 55 (BS5)
RL6_BACST	638	21,41	50S RIBOSOMAL PROTEIN L6 (BL10)
RS8_BACSU	728	2142	30S RIBOSOMAL PROTEIN S8 (BS8)
RL5_BACST	808	2144	50S RIBOSOMAL PROTEIN L5
RL24_BACST	62%	2144	50S RIBOSOMAL PROTEIN L24
RL14_BACSU	80%	2144	50S RIBOSOMAL PROTEIN L14
RS17_BACSU	778	2145	30S RIBOSOMAL PROTEIN S17 (BS16)
RL16_BACSU	76%	2145	50S RIBOSOMAL PROTEIN L16
RS3_BACSU	738	2146	30S RIBOSOMAL PROTEIN S3 (BS3)
RL22_BACSU	62%	2146	50S RIBOSOMAL PROTEIN L22
RS19_BACST	77%	2147	30S RIBOSOMAL PROTEIN S19 (BS19)
RL2_BACSU	76%	2147	50S RIBOSOMAL PROTEIN L2 (BL2)
RL4 BACSU	60%	2149	50S RIBOSOMAL PROTEIN L4
RL3 BACSU	69%	2149	50S RIBOSOMAL PROTEIN L3 (BL3)
RS10 STRMU	81%	2150	30S RIBOSOMAL PROTEIN S10
RL33 MYCCA	57%	2155	50S RIBOSOMAL PROTEIN L33
RS2 PEDAC	71%	2207	30S RIBOSOMAL PROTEIN S2
RS2 BACSU	100%	2208	30S RIBOSOMAL PROTEIN S2 (BS1)
RS18 BACST	63%	2254	30S RIBOSOMAL PROTEIN S18 (BS21)
RS6 BACSU	58%	2254	30S RIBOSOMAL PROTEIN S6 (BS9)
RS9 BACSU	65%	2326	30S RIBOSOMAL PROTEIN S9 (BS10)
RL13 STACA	638	2327	50S RIBOSOMAL PROTEIN L13
DC7 DC01 T	646	2224	30C REBOSONAL PROPERN C7
DC7 BACCHI	719	2334	305 RIBOSOMAL PROFEIN S7 (BS7)
RS/_DACSU	C 12 B	2334	200 RIBOSONAL PROTEIN S7 (DB7)
RSIA_SINY3	0/6	2335	JUB RIBUBURAL FRUTEIR BIZ
BIO12.06 tRNA m	odifica	tion	8 genes
SP5C BACSU	55%	17	PROBABLE PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29)
RNPA BACSU	47%	129	RIBONUCLEASE P PROTEIN COMPONENT (EC 3.1.26.5)
KSGA BACSU	52%	687	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1)
VCCA HARTN	309	1192	HYPOTHETICAL RNA METHYLTRANSFERASE HI0333 (EC. 2.1.1 -)
TOCH_NABIN	50%	1603	(CUANINE-NI) -METHYLTRANSFERASE (EC 2 1 1 31)
MDMO CREAT	316	1760	A MORENTADAMEDIDACE (DC 2 1 1 -)
MUMC_STRMY	316	1041	V-NEINIJIRANGILRAGE (EL 2.1.1.")
FMT_BACSU	408	. 1341	PETRIONIDTINA PORPLETRANOLERADE $\{L0, 4, 1, 6, 7\}$ UVDORUVETONI DES MERUVIRESSÉE DIGESE ( $L0, 2, 1, 6, 7\}$
IGCA_BASIN	4/5	2233	REPUBLICAL ANA METRIDIANDISKASE H10555 (BC 2.1.1.*)
BIO12.07 Tranel	ation f	actors	23 genes
VDGT BACGH	309	183	PUTATIVE NAD(P)H NITBOREDUCTASE (FC 1)
1001_060.00	300	100	

BI013. 7	RANSPORT	AND BINDI	NG PROTEIN	S 185 genes
EFG_THEN	GA. 55	58 233	3 ELONG	ATION FACTOR G (EF-G)
EFG_BACS	SU 72	28 233	3 ELONGA	ATION FACTOR G (EF-G)
EFTS_BAC	SU 71	7% 220	7 ELONG	ATION FACTOR TS (EF-TS)
EFTS_STF	2PN 71	L% 220	7 ELONG	TION FACTOR TS (EF-TS)
EFTS_HEI	PY 43	3% 220	6 ELONGA	ATION FACTOR TS (EF-TS)
FMNB DES	SVM 39	38 216	1 FMN-BI	NDING PROTEIN
IF1 LACI	A 10	00% 213	4 TRANS	ATION INITIATION FACTOR IF-1
YIHK ECC	LI 55	5% 201	3 65.4 H	CD GTP-BINDING PROTEIN IN GLNA-RBN INTERGENIC REGION
RRF HAEL	N 43	38 206	6 RIBOSO	ME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR)
EFTU_STF	OR 80	0% 190	9 ELÓNGA	ATION FACTOR TU (EF-TU)
IF3 BACS	SU 61	189	2 TRANSI	ATION INITIATION FACTOR IF-3
MVIM ECC	LI 34	18 181	2 VIRULE	ENCE FACTOR MVIM HOMOLOG
YDGI BAC	SU 49	98 150	0 PUTATI	VE NAD(P)H NITROREDUCTASE (EC 1)
RF2 BACS	SU 53	3% 996	PEPTIC	DE CHAIN RELEASE FACTOR 2 (RF-2)
RBFA BAC	SU 31	78 771	RIBOSO	ME-BINDING FACTOR A (P15B PROTEIN)
IF2_ENTF	C 69	98 775	TRANSI	ATION INITIATION FACTOR IF-2
EFP_BACS	3U 48	38 689	ELONG/	TION FACTOR P. (EF-P)
FLAV_DES	SVH. 38	3% 595	PLAVOD	DOXIN
RF1_BACS	SU 54	1% 584	PEPTIC	DE CHAIN RELEASE FACTOR 1 (RF-1)
IF2_ENTF	C - 36	5% 543	TRANSI	ATION INITIATION FACTOR IF-2
RF2_HELF	PY 25	58 451	PEPTIC	DE CHAIN RELEASE FACTOR 2 (RF-2)
RF3_SYNY	3 47	78 349	) PEPTIC	DE CHAIN RELEASE FACTOR 3 (RF-3)

BIO13.01 General 35 genes LACTOCOCCIN & TRANSPORT ATP-BINDING PROTEIN LCNC LCNC LACLA 94% 84 O-ANTIGEN EXPORT SYSTEM ATP-BINDING PROTEIN RFBB RFBB MYXXA 40% 202 CHVA\_AGRTU BETA-(1-->2)GLUCAN EXPORT ATP-BINDING PROTEIN CHVA TRANSPORT SYSTEM PERMEASE PROTEIN P69 35% 260 P69 MYCHR 26% 296 ATP-BINDING PROTEIN ABC ABC\_ECOLI 42% 319 LACTICIN 481/LACTOCOCCIN TRANSPORT ATP-BINDING PROTEIN LCNDR3 ABC TRANSPORTER ATP-BINDING PROTEIN UUP-1 LCN3\_LACLA 34% 517 UUP1 HAEIN 29% 560 LINCOMYCIN RESISTANCE PROTEIN LMRA\_STRLN 34% 597 KUP\_ECOLI KUP\_ECOLI KUP SYSTEM POTASSIUM UPTAKE PROTEIN KUP SYSTEM POTASSIUM UPTAKE PROTEIN 368 608 29% 610 TRANSPORT ATP-BINDING PROTEIN CYDC TRANSPORT ATP-BINDING PROTEIN CYDD CYDC\_BACSU 48% 709 CYDD BACSU 45% 711 GLUTAREDOXIN-LIKE PROTEIN NRDH NRDH\_LACLC 99% 1003 GLOTAREDVAINTINE PERMEASE PERM HOMOLOG MG(2+) TRANSPORT ATPASE, P-TYPE 2 (EC 3.6.1.-) GALACTOSIDE TRANSPORT ATP-BINDING PROTEIN MGLA GALACTOSIDE TRANSPORT ATP-BINDING PROTEIN MGLA HOMOLOG PERM\_HAEIN 26% 1196 ATMB SALTY 518 1284 1352 MGLA\_HAEIN 238 MGLA\_MYCGE 32% 1364 PROBABLE ACTINORHODIN TRANSPORTER AC22 STRCO 26% 1383 LPLC\_BACSU 42% 1527 LPLC PROTEIN LPLB PROTEIN LPLB\_BACSU 278 1528 LACTICIN 481/LACTOCOCCIN TRANSPORT ATP-BINDING PROTEIN LCNDR3 LCN3\_LACLA 418 1559 COMA STRPN 248 1560 TRANSPORT ATP-BINDING PROTEIN COMA PROBABLE ACTINORHODIN TRANSPORTER 28% 1584 AC22 STRCO UUP\_ECOLI ABC TRANSPORTER ATP-BINDING PROTEIN UUP ABC TRANSPORTER ATP-BINDING PROTEIN H11252 31% 1592 YJJK\_HAEIN MVAA\_PSEMV 38% 1593 42% 1607 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.88) YOGI BACSU 548 1753 PROBABLE ABC TRANSPORTER PERMEASE PROTEIN IN SODA-COMGA INTERGENIC REGION (ORF73) 1754 PROBABLE ABC TRANSPORTER PERMEASE PROTEIN IN SODA-COMGA YQGH\_BACSU 32% INTERGENIC REGION (ORF72) 478 1755 PROBABLE ABC TRANSPORTER BINDING PROTEIN IN SOBA-COMGA YOGG BACSU INTERGENIC REGION PRECURSOR (ORF108) NOCQ\_AGRT5 32% 1835 NOPALINE TRANSPORT SYSTEM PERMEASE PROTEIN NOCQ NOCO AGRT5 278 PUTATIVE PERMEASE PERM PERM\_ECOLI 1863 UVRA\_NEIGO 59% 1866 EXCINUCLEASE ABC SUBUNIT A 2054 PROTEIN ECSB ECSB BACSU 28% ECSA BACSU 60% 2055 ABC-TYPE TRANSPORTER ATP-BINDING PROTEIN ECSA FLIP BORBU 27% 2113 FLAGELLAR BIOSYNTHETIC PROTEIN FLIP peptides and amines BIO13.02 Amino acids, 52 genes HYPOTHETICAL TRANSPORT PROTEIN CY39.40 (FRAGMENT) GABA PERMEASE (4-AMINO BUTYRATE TRANSPORT CARRIER) YW40\_MYCTU GABP\_ECOLI 25% 70 23% 70 LYSINE-SPECIFIC PERMEASE PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN) LYSP ECOLT 27% 111 81% 118 PTHP STRSL PT1\_STRSL 119 PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (EC 2.7.3.9) 82% ALYS ENTFA 49% 267 AUTOLYSIN (EC 3.5.1.28) PROBABLE AMINO-ACID ABC TRANSPORTER ATP-BINDING PROTEIN IN YOIZ BACSU 322 34% BMRU-ANSR INTERGENIC REGION OLIGOPEPTIDE-BINDING PROTEIN AMIA PRECURSOR AMIA STRPN 31% 341 343 PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR OPPA\_ECOLI 28% OPPB\_BACSU 46% 345 OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB

DPPC_BACSU	43%	346	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
OPPF_BACSU	61%	348	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPF
CYCA_ECOLI	28%	358	D-SERINE/D-ALANINE/GLYCINE TRANSPORTER
AAPA_BACSU	478	360	AMINO ACID PERMEASE AAPA
LYSP_ECOLI	48%	358	LYSINE-SPECIFIC PERMEASE
OPPA BACSU	30%	523	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR
ALYS ENTER	35%	525	AUTOLYSIN (EC. 3.5.1.28)
DEF HELPY	398	553	POLYPEPTIDE DEFORMYLASE (FC 3.5.1 31)
VOLX BACSU	3.6%	556	PROBABLE AMINO-ACID ABC TRANSPORTER RINDING PROPERTY IN EMPLI-
ANSE INTERO	ENTC REGION	PRECU	ROAD DE MINO METE INC. INNASIONIEN ENDEMENTE INCELLA IN ENRO-
BENO LACOL	479	683	BRANCUED_CHAIN AMINO ACID TRANSDORT SVETEM CARRIER ROOTEIN
(BDANCKED-	CUATN AMINO	ACTD 1	DRANCHED-CHAIN ANIMO ACID INANSPORI SISIEM CARRIER PROTEIN
(BRANCRED-	COAIN APIINO	ACID -	DI (MEIDEDEDE MENNEDORMED
DIFI_DACUA	276	012	DIFTINE TRANSPORTER
IDGF_BACSU	300	817	APPOTRETICAL TRANSPORT PROTEIN IN EAPZ-DING INTERGENIC REGION
OPUA_BACSU	548	863	GLYCINE BETAINE TRANSPORT ATP-BINDING PROTEIN OPUAA
PROW_BACSU	428	863	GLYCINE BETAINE/L-PROLINE TRANSPORT SYSTEM PERMEASE PROTEIN
PROW			
YCKK_BACSU	28%	960	PROBABLE AMINO-ACID ABC TRANSPORTER BINDING PROTEIN PRECURSOR
Y4TG_RHISN	328	961	PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN Y4TG
GLTL_HAEIN	59%	962	GLUTAMATE/ASPARTATE TRANSPORT ATP-BINDING PROTEIN GLTL
POTA_HAEIN	45%	1173	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
POTC_HAEIN	35%	1175	SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC
POTD_ECOLI	438	1176	SPERMIDINE/PUTRESCINE-BINDING PERIPLASMIC PROTEIN PRECURSOR
(SPBP)			
GRSB_BACBR	30%	1290	GRAMICIDIN S SYNTHETASE II (GRAMICIDIN S BIOSYNTHESIS GRSB
PROTEIN) (F	C 6}		
XASA ECOLI	50%	1323	AMINO ACID ANTIPORTER (EXTREME ACID SENSITIVITY PROTEIN)
OPUC BACSU	478	1471	GLYCINE BETAINE-BINDING PROTEIN PRECURSOR
OPUB BACSU	518	1471	GLYCINE BETAINE TRANSPORT SYSTEM PERMEASE PROTEIN OPUAB
OPUA BACSU	58%	1473	GLYCINE BETAINE TRANSPORT ATP-BINDING PROTEIN OPUAA
PMSR BACSU	54%	1590	DEPARTUR DEPARTOR METHIONINE SUBJOYINE REDUCTASE (DEPARTOR MET
GLNW FCOLT	368	1707	CLUTANINE_BINDING DUPID ACMIC DECTEDS REDUCTIONS (CLUED)
VA70 HARIN	365	1700	SUDATERTICAL ANTRO-ACTI ARCHARTER TRACTARD DEPENDENT ELEMENT HIGH TA
VOTZ BACCU	54%	1799	DOODADLE AMINO-ACTO ADC TRANSPORTER PERMEASE PROTEIN HIGT'S DOODADLE AMINO-ACTO ADC TRANSPORTER ATE-DINGING DOOTEIN IN
PMDU_ANCD T	NURRORNIC DI	20102	FRODADDE AFINO-ACID ADC. IRANSFORIER AIF-DINDING FROIEIN IN
CINC POLT	NUBRGENIC RI	1022	(1) THE SALES OF SALESON SOLD THE DESIGNATION OF SALES
GENQ ECOLI	206	1833	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLUQ
HISP_ECOLI	316	1835	HISTIDINE TRANSPORT ATP-BINDING PROTEIN HISP
PEPT_LACLC	958	1821	PEPTIDASE T (EC 3.4.11)
YDGF_BACSU	35%	1870	HYPOTHETICAL TRANSPORT PROTEIN IN EXPZ-DINB INTERGENIC REGION
OPPA_LACLA	908	1885	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR
OPPC_LACLA	100%	1887	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC
OPPB_LACLC	100%	1888	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB
OPPF_LACLA	100%	1889	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPF
OPPD_LACLC	100%	1890	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPD
PMSR_BACSU	53%	2064	PUTATIVE PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET
ARCD_PSEAE	35%	2092	ARGININE/ORNITHINE ANTIPORTER
YXEM_BACSU	338	2118	PROBABLE AMINO-ACID ABC TRANSPORTER BINDING PROTEIN IN IDH-DEOR
INTERGENIC	REGION PRECU	JRSOR	
LYSP_ECOLI	37%	2257	LYSINE-SPECIFIC FERMEASE
BI013.03 An	ions		13 genes
MEGL PSEPU	38%	77	METHIONINE GAMMA-LYASE (EC 4.4.1.11)
ATZN ECOLI	28%	95	ZINC-TRANSPORTING ATPASE (EC. 3.6.1)
5NTD HAEIN	25%	180	PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC. 3.1.3.5)
DHAK CITFR	358	243	DIHYDROXYACETONE KINASE (EC 2.7.1.29)
CN16 YEREN	31%	298	2'.3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC
3.1.4.16)		0,0	a /o create needstrate a institutional institution (se
GLPT BACSU	349	546	GLYCEROL=3=PHOSPHATE TRANSPORTER (C_3_P TRANSPORTER)
MANA STOMI	659	777	MANNORP_6_BUOGRUMPT TOOMPRACE (0-5-1 0)
ADVA PNDRA	419	015	DOMNOSE OF FROSPINALE ISOMERASE (EC. 5.5.1.8)
ATRA_ENTRA	41.6	040	POTASSIDE/COPPER-TRANSPORTING ATPASE A (EC 5.6.1.36)
ENTED LARTH	200	1000	PROBABLE CADMION-TRANSPORTING ATPASE (EC 5.0.1)
SNTD_HAEIN	338	1098	PROBABLE 5'-NUCLEOTIDASE PRECORSOR (EC 3.1.3.5)
SCRK_STRMU	62%	1516	FROCTORINASE (EC 2.7.1.4)
PTA_BACSU	618	1704	PROBABLE PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8)
SPHX_SYNP7	28%	1756	SPHX PROTEIN PRECURSOR
BI013.04 Ca	rbohvdrates,	orga	nic alcohols and acids 13 genes
GLPF ECOLI	35%	245	GLYCEROL UPTAKE FACILITATOR PROTEIN
FECE ECOLT	428	324	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
FECD FCOLT	355	326	IRON(III) DICITRATE TRANSPORT SYSTEM DERMEACE DROTEIN FROD
CITN LACLA	48%	921	CITRATE-SODIUM SYMPORT (CITRATE TRANSDORTED)
CLDF STRDM	5.29	1267	CLYCEDOL UDTAKE FACTLITATION DOOTETN
DDCD UNDIN	200	1670	DEDEROD UPTARE PACIDITATOR PROTEIN DEDEROD UPTARE PACIDITATOR PROTEIN DECOMPAND
RESD_RALIN	902 B	1600	D'AIDUGE-DINUING FERIFLAGRIG FRUTEIN PRECURSUR
RESC_BACSU	008	1601	RIDUSE TRANSPORT SISTEM PERMEASE PROTEIN RESC
RBSA_BACSU	428	1001	RIDUSS TRANSPORT ATP-BINDING PROTEIN RBSA
KBSD_BACSU	56%	1682	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
LACY_STRTR	438	2043	LACTUSE PERMEASE (LACTOSE-PROTON SYMPORT)

VDOW_UWDIN	24.6	2103	REDORE TRANSPORT RIF-DINDING PROTEIN ROOK
EBA2_FLAME	27%	2238	ENDO-BETA-N-ACETYLGLUCOSAMINIDASE F2 PRECURSOR (EC 3.2.1.96)
GNTP_BACLI	59%	2246	GLUCONATE PERMEASE
BI013.05 Cati	ons		18 genes
FEOB_ECOLI	39%	188	FERROUS IRON TRANSPORT PROTEIN B
FEOA_ECOLI	3,8%	190	FERROUS IRON TRANSPORT PROTEIN A
TCR1_ECOLI	41%	303	TETRACYCLINE RESISTANCE PROTEIN, CLASS A (TRANSPOSON TN1721)
FHUB_BACSU	378	325	FERRICHROME TRANSPORT PERMEASE PROTEIN FHUB
Y1B2_MYCTU	36%	567	PUTATIVE CATION-TRANSPORTING ATPASE CY21C12.02 (EC 3.6.1)
ATA1_SYNY3	40%	675	CATION-TRANSPORTING ATPASE PMA1 (EC 3.6.1)
NHAA_ECOLI	428	1148	NA (+) /H
PBUX_BACSU	48%	1158	XANTHINE PERMEASE
YIB2_MYCTU	358	1188	PUTATIVE CATION-TRANSPORTING ATPASE CY21C12.02 (EC 3.6.1)
ATCL_SINP/	378.	1402	CATION-TRANSPORTING ATPASE PACE (EC 3.6.1)
FUR_CARDE	206.	1503	PERRIC UPTAKE REGULATION PROTEIN
V058 METTA	319	1632	DITATUR AMMONITIM TRANSDORTER MIGACONIDE PERMEASE)
IRAA HARIN	36%	1643	PROBABLE HEACTL DEPMEASE (HEACTL TRANSPORTER)
FER CLOTH	38%	1741	FEREDOXIN
NAPA ENTHR	48%	1973	NA (+) /H
ATCS SYNY3	36%	2061	CATTON-TRANSPORTING ATPASE PACE (EC. 3.6.1)
ATA1_SYNY3	36%	2315	CATION-TRANSPORTING ATPASE PMA1 (EC 3.6.1)
BT013.05 Nucl	eosides.	nurines	and nurimidinas 1 games
PDP_BACST	56%	1463	PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.2)
BI013.07 PTG	system		13 genes
PTMA ECOLI	46%	31	PTS SYSTEM, MANNITOL-SPECIFIC TIARC COMPONENT (FILARC_MTL)
PTCC BACSU	34%	175	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIC COMPONENT (RIIC-CEL)
PTCB BACSU	52%	416	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIB COMPONENT (RITE-CEL)
PTCA_BACSU	48%	417	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL)
PTSA STRMU	48%	435	PTS SYSTEM, SUCROSE-SPECIFIC HIABC COMPONENT (EHABC-SCR)
PTSA STRMU	31%	436	PTS SYSTEM, SUCROSE-SPECIFIC IIABC COMPONENT (EIIABC-SCR)
PTCC_BACSU	31%	830	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIC COMPONENT (EIIC-CEL)
PTFB_RHOCA	52%	984	PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU)
PTBA_BACSU	37%	1144	PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-
BGL)			
PTBA_ERWCH	41%	1489	PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC HIABC COMPONENT (EHABC-
BGL)			
DINNE DOWNER	419	1742	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN)
PINW_RCOPT	47.0	1 / 14	
PINC_ECOLI	46%	1743	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN)
PINC_ECOLI PIND_ECOLI	468	1743 1744	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN)
PINA_BCOLI PTNC_ECOLI PTND_BCOLI BI013.08 Mult	46% 57%	1743 1744 sistance	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes
PINA_BCOLI PTNC_ECOLI PTND_BCOLI BIO13.08 Mult BMR2_BACSU	46% 57% idrug re: 46%	1743 1744 sistance 123	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2)
PINA_BCOLI PTNC_ECOLI PTND_BCOLI BI013.08 Mult BMR2_BACSU EMRB_ECOLI	46% 57% 46% 26%	1743 1744 sistance 123 930	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B
PINA_BCOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI	46% 57% 46% 26% 36%	1743 1744 sistance 123 930 1302	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe	46% 57% 46% 26% 36%	1743 1744 sistance 123 930 1302	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL 37 genes
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BI013.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BI013.09 Othe: YBJZ_ECOLI	46% 57% 46% 26% 36% r 34%	1743 1744 sistance 123 930 1302	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ
PINA_ECOLI PIND_ECOLI PIND_ECOLI BI013.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BI013.09 Other YBJZ_ECOLI YCHM_ECOLI	46% 57% 46% 26% 36% r 34% 37%	1743 1744 sistance 123 930 1302 15 53	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL 37 genes HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL 58.4 KD PROTEIN IN PTH-PRSA INTERCENIC REGION
PINC_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult HMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Other YBJZ_ECOLI YCHM_ECOLI YBJT_ECOLI	46% 57% 46% 26% 36% r 34% 37% 32%	1743 1744 sistance 123 930 1302 15 53 74	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult HMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Other YBJZ_ECOLI YCHM_ECOLI YHES_ECOLI YHES_ECOLI	46% 57% 46% 26% 36% r 34% 37% 32% 35%	1743 1744 sistance 123 930 1302 15 53 74 100	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe: YBUZ_ECOLI YCHM_ECOLI YHES_ECOLI YHIH_ECOLI	468 578 468 268 368 r 348 378 328 358 508	1743 1744 sistance 123 930 1302 15 53 74 100 248	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL 58.4 KD PROTEIN IN PTH-PRSA INTERCENIC REGION HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BI013.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI YBJZ_ECOLI YCHM_ECOLI YHES_ECOLI YHIH_ECOLI YHIH_ECOLI YHIH_ECOLI	46% 57% 46% 26% 36% 34% 37% 32% 35% 50% 39%	1743 1744 <b>sistance</b> 123 930 1302 15 53 74 100 248 257	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe: YBJZ_ECOLI YHIT_ECOLI YHIT_ECOLI YHIT_ECOLI YHIT_EACSU 3'REGION	46% 57% 46% 26% 36% 7 34% 37% 32% 35% 50% 39%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN HYPOTEIN HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN HYPOTHEN
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult HMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe YBJZ_ECOLI YCHM_ECOLI YHES_ECOLI YHES_ECOLI YHIB_BACSU 3'REGION Y179_MYCCE ULSO MYCCE	46% 57% 46% 26% 36% 36% 34% 32% 32% 35% 50% 39% 44%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHIH HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC
PINA_ECOLI PTNC_ECOLI PTNC_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe YBJZ_ECOLI YCHM_ECOLI YHES_ECOLI YHES_ECOLI YHES_ECOLI YHIB_BACSU 3'REGION Y179_MYCGE Y180_MYCGE Y180_MYCGE	46% 57% 46% 26% 36% 36% 37% 32% 35% 50% 39% 44% 47%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 275	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHIS HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHIS HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179
PINA_ECOLI PTNC_ECOLI PTNC_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe: YBJ2_ECOLI YCHM_ECOLI YHES_ECOLI YHES_ECOLI YHIH_ECOLI YHIH_ECOLI YFIB_BACSU 3'REGION Y179_MYCGE Y180_MYCGE Y112_METJA	46% 57% 46% 26% 36% 37% 32% 35% 50% 39% 44% 47% 37% 37%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 207	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHIH HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MIL HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG180 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG180 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG19
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe: YBJZ_ECOLI YBJT_ECOLI YHIH_ECOLI YHIH_ECOLI YHIH_ECOLI YFIB_BACSU 3'REGION Y179_MYCGE Y180_MYCGE Y12_METJA YFIB_BACSU 3'REGION	46% 57% 46% 26% 36% 7 34% 37% 32% 35% 50% 39% 44% 47% 37% 33%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 307	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (BIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (BIIC-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHHH HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHHH HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG180 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG142 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0412 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0412
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult HMR2_BACSU RMRB_ECOLI MDL_ECOLI BIO13.09 Othe: YBJZ_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY_ECOLI YHEY YHEY YHEY_ECOLI YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY YHEY	46% 57% 46% 26% 36% 7 34% 32% 35% 50% 39% 44% 44% 47% 37% 33% 41%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 307 309	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG190 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC
PINA_BCOLI PTNC_ECCLI PTND_ECCLI BIO13.08 Mult BMR2_BACSU EMRB_ECCLI MDL_ECCLI BIO13.09 Other YBJZ_ECCLI YHES_ECCLI YHES_ECCLI YHES_ECCLI YHES_ECCLI YHIB_BACSU 3'REGION Y179_MYCGE Y180_MYCGE Y112_METJA YFIB_BACSU 3'REGION YFIC_BACSU 3'REGION	46% 57% 46% 26% 36% 37% 32% 35% 50% 39% 44% 47% 33% 41%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 307 309	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBHS HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHIH HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG180 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG142 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG19 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG100 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC
PINA_BCOLI PTNC_ECCLI PTND_BCOLI BIO13.08 Mult HMR2_BACSU EMRB_ECCLI MDL_ECCLI BIO13.09 Othe YBJZ_ECCLI YCHM_ECCLI YHIH_ECCLI YHIH_ECCLI YHIH_ECCLI YHIB_BACSU 3'REGION YFIC_BACSU 3'REGION YFIC_BACSU 3'REGION YAEE ECCLI	46% 57% 46% 26% 36% 7 34% 37% 32% 35% 50% 39% 44% 47% 37% 33% 41% 41%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 307 309 320	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG180 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC
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PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Othe: YBJZ_ECOLI YBJT_ECOLI YHIH_ECOLI YHIH_ECOLI YFIB_BACSU 3'REGION YFIC_BACSU 3'REGION YFIC_BACSU 3'REGION YFIC_BACSU 3'REGION YAEL_ECOLI YHIH_ECOLI YO81_MYCTU YCFV_ECOLI YCFV_ECOLI S'REGION YBJZ_ECOLI Y796_METUA Y795_MCSU 5'REGION YBJZ_ECOLI Y796_METUA Y415_SYNY3	46% 57% 46% 26% 36% 7 34% 37% 32% 35% 50% 39% 44% 47% 37% 33% 41% 44% 60% 41% 35% 40% 35% 35%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 307 309 320 321 347 426 650 715 718 892 990	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG19 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG19 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG19 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0412 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YAEE HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YAEE HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YCJV HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PRO
PINA_BCOLI PTNC_ECCLI PTND_ECCLI BIO13.08 Mult BMR2_BACSU EMRB_ECCLI MDL_ECCLI BIO13.09 Other YBJZ_ECCLI YHEN_ECCLI YHEN_ECCLI YHIH_ECCLI YHIH_ECCLI YHIH_ECCLI YHIH_ECCLI YHIH_ECCLI YFIE_BACSU 3'REGION YA12_METJA YFIC_BACSU 3'REGION YAEE_ECCLI YHIH_ECCLI YHHH_ECCLI YHHH_ECCLI YCFV_ECCLI YCFV_ECCLI YWJA_BACSU 5'REGION YBJZ_ECCLI Y796_METJA Y415_SYNY3 YRHC_BACSU	46% 57% 46% 26% 36% 34% 32% 35% 39% 44% 47% 37% 33% 41% 44% 60% 41% 35% 40% 35% 40% 35% 43%	1743 1744 <b>sistance</b> 123 930 1302 15 53 74 100 248 257 273 274 295 307 309 320 321 347 426 650 715 718 892 990 993	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG190 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0412 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0412 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0412 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YAEE HYPOTHETICAL ABC TRANSP
PINA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Mult HMR2_BACSU RMRB_ECOLI MDL_ECOLI BIO13.09 Othe YBJZ_ECOLI YHES_ECOLI YHES_ECOLI YHES_ECOLI YHES_ECOLI YHES_ECOLI YHIL_ECOLI YFIB_BACSU 3'REGION YFIC_BACSU 3'REGION YAEE_ECOLI YHIL_ECOLI YHIL_ECOLI YHIL_ECOLI YHIL_ECOLI YO81_MYCTU YCJV_ECOLI YCJV_ECOLI YCJV_ECOLI YUJA_BACSU 5'REGION YBJZ_ECOLI YJ96_METJA YHLS_SYNY3 YRHG_BACSU YBJZ_ECOLI	46% 57% 46% 26% 36% 36% 32% 32% 35% 50% 39% 44% 44% 44% 44% 44% 60% 41% 35% 40% 35% 41% 35% 41% 35% 41% 35% 41% 35%	1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273 274 295 307 309 320 321 347 426 650 715 718 892 990 993 993 998	PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) <b>3 genes</b> MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL <b>37 genes</b> HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHET HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHET HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHET HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG179 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MG180 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 1 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLVBC HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YAEE HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YAEA HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YCJV HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YCJV HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YCJV HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN NACDA HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN NACDA

Y796_METJA YLUD_LACLA	48% 100%	1108 1242	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0796 HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN LEUD
3'REGION YSC1_STRGC 5 (OPP1)	62%	1349	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN SCAA
YXBC BACSU	518	1538	HYPOTHETICAL METABOLITE TRANSPORT PROTEIN IN HTPC-IOLE
INTERGENIC REGI	ON		The other works the theorem and the state of
YJEM_ECOLI (0514)	22%	1736	HYPOTHETICAL 56.3 KD PROTEIN IN GENX-PSD INTERGENIC REGION
YEJF_ECOLI	27%	1751	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJF
YQGJ_BACSU	60%	1751	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN SODA-COMGA
INTERGENIC REGI	CON (ORF)	1760	SUDOFURFICAL ADD TRANSPORTS AND DIVIDING DROFTLY IN CODA COMON
INTÉRCENIÓ RECI	ON (ORF.	74)	RIPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN SQUA-COMGA
YXDL_BACSU 3'REGION	49%	1789	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN IDH
YATR_BACFI	43%	1815	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN
YJEM_ECOLI (0514)	39%	1855	HYPOTHETICAL 56.3 KD PROTEIN IN GENX-PSD INTERGENIC REGION
YXDL_BACSU 3'REGION	35%	2076	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN IDH
YYBJ_BACSU	28%	2265	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN COTF-TETB
Y796_MÉTJA	42%	2329	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0796
BIO14. OTHER CA	TEGORIE	s	94 genes
BIO14.01 Adapta	tions as	nd atypi	ical conditions 13 genes
CSP2_LACPL	828	170	COLD SHOCK PROTEIN 2
TCMA_STRGA	288	233	TETRACENOMYCIN C RESISTANCE AND EXPORT PROTEIN
CSPC BACSU	759	515	COLD SHOCK DROTEIN (SDC
TCMA_STRCA	25%	596	TETRACENCELL CAPC
VANZ ENTFC	42%	1097	VANZ PROTEIN
FSR ECOLI	25%	1182	FOSMIDOMYCIN RESISTANCE PROTEIN
ARSC BACSU	51%	1409	PUTATIVE ARSENATE REDUCTASE
TCMA_STRGA	29%	1553	TETRACENOMYCIN C RESISTANCE AND EXPORT PROTEIN
TCMA_STRGA	278	1678	TETRACENOMYCIN C RESISTANCE AND EXPORT PROTEIN
CMCT NOCLA	348	1925	CEPHAMYCIN EXFORT PROTEIN CMCT
7.110 1 _140/0.114			
FRI_LISIN	448	2082	NON-HEME IRON-CONTAINING FERRITIN
FRI_LISIN MSCL_ECOLI	448	2082 2150	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA	44% 44% ind analo 100%	2082 2150 og sensi 1232	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage	44% 44% nnd analo 100% related	2082 2150 og sensi 1232 functio	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL tivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6	44% 44% 100% related 37%	2082 2150 og sensi 1232 functic 36	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA	44% 44% 100% related 37% 26%	2082 2150 og sensi 1232 functio 36 49	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METDA VINT_BPL54	44% 44% 100% related 37% 26% 25%	2082 2150 og sensi 1232 functic 36 49 445	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) Ons and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GDDD 6 DDDGDDL (DDC4)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VG64_BPML5	44% 44% 100% related 37% 26% 25% 45%	2082 2150 og sensi 1232 functic 36 49 445 460 464	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL tivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) DORTAL DECTEIN (CD2)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 UP4_BPUK7	44% 44% 100% related 37% 26% 25% 45% 21% 31%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROFERAD PROTEACE (GP4)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VC64_BPML5 VP3_BPHK7 VP4_BPHK7 VP4_BPHK7 VINT_BPL54	44% 44% 100% related 37% 26% 25% 45% 21% 31%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VVINT_BPL54 XERC_SALTY	44% 44% 100% related 37% 26% 25% 45% 21% 31% 31% 32%	2082 2150 og sensi 1232 functio 36 49 445 460 464 465 501 633	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE/RECOMBINASE XERC
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB)	44% 44% 100% related 37% 26% 25% 45% 21% 31% 31% 31% 31% 31%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) Ans and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VIA_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU	44% 44% 100% related 37% 26% 25% 45% 21% 31% 32% 31% 32% 31% 45%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VIN	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 31% 32% 31% 32% 31% 45% 27%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE/RECOMBINASE (GP4) INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VINT_BPL54 VF4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 31% 32% 31% 45% 22% 33%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG4_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 31% 31% 31% 31% 32% 33% 27% 33% 32%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) Ans and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE INTEGRASE INTEGRASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHG2_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VINT_BPL54 CODV_BACSU	448 448 100% related 37% 268 258 258 258 258 31% 32% 31% 45% 27% 33% 32% 33% 32% 33% 32% 33% 32% 33%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL <b>itivity</b> 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 XERC_SALTY YHGE_BACSU (OFFB) TNPA_STAAU VP4_BPHK7 VINT_BPL54 CODV_BACSU XERC_HAEIN CODV_BACSU	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 31% 32% 31% 45% 27% 33% 32% 31% 32% 31% 32% 33% 31% 32% 33%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1256 1256	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE/RECOMBINASE (GP4) INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GL/TT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE/RECOMBINASE XERC
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SECC_ECOLI MCP_BEP41	44% 44% 100% <b>related</b> 37% 26% 25% 21% 31% 31% 32% 31% 45% 27% 32% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE/RECOMBINASE (GP4) INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE/RECOMBINASE XERC EXONUCLEASE SECC MAJOR CORET, MENTERNASE XERC EXONUCLEASE SECC
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BEF41 VINT_BP56	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 31% 31% 32% 31% 45% 27% 33% 32% 31% 37% 44% 46%	2082 2150 og sensi 1232 functic 36 49 445 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1350	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) Ms and prophages 21 genes TERMINASE SMALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG4_BPHK7 VP4_BPHK7 VP4_BPHK7 VP4_BPHK7 VP4_BPHK7 VP4_BPHK7 VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BEF41 VINT_BPSF6 PIP LACLA	448 448 100% related 378 268 258 458 218 318 328 318 328 318 328 318 328 318 328 318 328 318 328 318 328 318 279 328 318 328 378 448 448 268	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1257 1350 1358 1454	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL <b>itivity</b> 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) <b>ms and prophages</b> 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SECC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 TERS_BPSF6 TERS_BPSF6 TERS_BPSF6 VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VINT_BPL54 KERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BEF41 VINT_BPSF6 PIP_LACLA VG37_BPML5	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 31% 32% 32% 31% 32% 32% 34% 32% 36% 26% 26% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1256 1257 1350 1258 1454 1716 1257	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL <b>itivity</b> 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) <b>ms and prophages</b> 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (GP37)
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 TERS_BPSF6 TERS_BPSF6 TERS_BPSF6 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 CODV_BACSU VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BFF41 VINT_BPSF6 PIP_LACLA VG37_BPL54 VINT_BPL54	44% 44% 100% <b>related</b> 37% 26% 25% 45% 21% 31% 32% 31% 45% 27% 33% 32% 31% 32% 31% 45% 27% 33% 32% 31% 32% 32% 31% 26% 96% 26% 96% 25%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1256 1257 1350 1256 1257 1350 1258 1454 1716 1257 1350	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL tivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ms and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE
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FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 TERS_BPSF6 TERS_BPSF6 TERS_BPSF6 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 VINT_BPL54 CODV_BACSU VINT_BPL54 CODV_BACSU XERC_HAEIN NG7_BPH12 VINT_BPSF6 PIP_LACLA VINT_BPL54 BIO14.04 Transp YI3A_LACJO TISA_LACJO TISA_LACJO TISA_MCTU	44% 44% 100% related 37% 26% 25% 45% 21% 31% 32% 31% 32% 31% 32% 31% 32% 31% 26% 96% 44% 26% 96% 44% 25% 25% 25% 25% 25% 30%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1257 1350 1256 1257 1350 1256 1257 1350 1256 1257 1350 1256 1257 350 1350 1258 1454 475 455 55 89	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) MA and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150 TRANSPOSASE FOR INSERTION SEQUENCE IS150 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS986
FRI_LISIN MSCL_ECOLI BIO14.02 Drug a KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VINT_BPL54 COV_BACSU XERC_HAEIN SBCC_ECOLI VINT_BPSF6 PIP_LACLA VINT_BPL54 BIO14.04 Transp YI3A_LACJO TI50_ECOLI TRA4_LACLA YI91_SHIDY TRA9_MYCTU (ORFB)	44% 44% 100% related 37% 26% 25% 45% 21% 31% 31% 32% 31% 32% 31% 32% 31% 32% 31% 45% 27% 33% 45% 27% 33% 44% 48% 25% 96% 48% 25% 96% 41% 100%	2082 2150 og sensi 1232 functic 36 49 445 460 464 465 501 633 902 1034 1053 1064 1256 1257 1350 1256 1257 1350 1256 1257 1350 1358 1454 1716 1873 2005 23 53 54 55 89 02	NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL Ativity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) MA and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) INTEGRASE INTEGRASE INTEGRASE INTEGRASE/RECOMBINASE (GP4) INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEASE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHOSENTION ELEMENT IS123 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS926

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1191_00101	258	135	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
TRA4_LACLA	808	135	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YI6A_MYCMY	31%	136	INSERTION ELEMENT IS1296 HYPOTHETICAL 21.4 KD PROTEIN (ORFA)
T150_ECOLI	418	137	PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
TRA4_LACLA	99%	138	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YI91_SHIDY	25%	138	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
TRA4 LACLA	98%	371	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT 15904
VI3A LACIO	30%	372	INSERTION ELEMENT IS1223 HYPOTHETICAL 20 7 KD PROTEIN (ORFA)
T150 ECOLT	41%	373	DUTATIVE TRANSPOSES FOR INSERTION SPOURNCE 19150
TRA4 LACLA	100%	624	TOTALTE TRANSPORTE FOR TRANSPORTER SECOND
NT01_CUTDV	1006	624	TRANSFOSASE FOR INSERTION SEQUENCE ELEMENT 15904
YI91_SHIDY	206	625	INSERTION ELEMENT ISUIT HYDOTHETICAL 12.7 KD PROTEIN
T150_ECOLI	418	626	PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ISISS
YI3A_LACJO	30%	626	INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA)
TRA4_LACLA	398	648	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA1_STRSL	38%	680	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL	38%	705	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA4_LACLA	39%	726	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YIS1_SHISO	28%	727	INSERTION ELEMENT IS600 (ISO-S3) HYPOTHETICAL 11 KD PROTEIN
TRA4 LACLA	98%	834	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT 15904
YI91 SHIDY	25%	834	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
T150 FCOLT	39%	835	PUPATIVE TRANSPOSASE FOR INSERTION SECTIONER 15150
VI3A_LACIO	3.0%	836	INCREMENT DIRECTOR AND TO A ADDRESS OF A DIRECTOR AND A DIRECTOR ADDRESS (ADDRESS)
VIG1 CUIDY	266	036	INDERITOR ELEMENT ISIZZI HIPOTHETICAL 20.7 RD PROTEIN
mand a new a	235	0.30	INSERTION EDEMENT ISTIT REPORTED AT A DEPOSIT.
TRA4_LACLA	998	837	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT 15904
TRAI_STRSL	388	955	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT ISII61
TRA4_LACLA	398	1214	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YIS1_SHISO	28%	1215	INSERTION ELEMENT IS600 (ISO-S3) HYPOTHETICAL 11 KD PROTEIN
YIS1_SHISO	28%	1219	INSERTION ELEMENT IS600 (ISO-S3) HYPOTHETICAL 11 KD PROTEIN
tra4_lacla	39%	1220	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA5_LACLA	97%	1223	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS905
TRA4_LACLA	398	1273	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YIS1_SHISO	28%	1274	INSERTION ELEMENT IS600 (ISO-S3) HYPOTHETICAL 11 KD PROTEIN
TRA1_STRSL	38%	1336	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1 STRSL	38%	1394	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1 STRSL	38%	1552	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE RLEMENT IS1161
TRA4 LACLA	39%	1582	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT 15904
TRAG LACLA	399	1727	TRANSPORTER FOR INSPECTON SPOIPNOR FILMENT ISOA
VISI SHISO	288	1728	INSERTION REPARTMENT ISSUE ISSUED AND REPART ISSUE
mpa1 empet.	309	1734	DEGRADE MEMERI 15000 (150-55) HIPOINEIICAL II AD PROIDIN DEGRADE MEMERICAS POD INCEDITOR_LIVE CEOUDINCE DIEMEND ICIICI
mpai emper	206	1033	PROBABLE TRANSPOSASE FOR INSERTION LIKE SEQUENCE ELEMENT ISTIC
THE MALE OF THE OWNER		1 2 3 3	PRODADLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT ISIIOI
	200	1050	PROPERTY OFFICER OF DESTINATION FOR ADDRESS FOR ADDRESS ADDRESS FOR ADDRESS AD
TRA1_STRSL	38%	1958	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL	38%	1958 1997	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL	38% 38% 42%	1958 1997 2063	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA	38% 38% 42% 39%	1958 1997 2063 2083	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA1_STRSL	38% 38% 42% 39% 38%	1958 1997 2063 2083 2127	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA	38% 38% 42% 39% 38% 98%	1958 1997 2063 2083 2127 2135	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA	388 388 428 398 388 988 418	1958 1997 2063 2083 2127 2135 2136	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1064 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1064 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
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TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TIS0_ECCLI TRA1_STRSL TRA4_LACLA	38% 38% 42% 39% 38% 98% 41% 38% 100%	1958 1997 2063 2083 2127 2135 2136 2183 2195	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE IS150 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE IS150 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE IS150
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY	38% 38% 42% 39% 38% 98% 41% 38% 100% 25%	1958 1997 2063 2083 2127 2135 2136 2183 2195 2196	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE IS150 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE IS150 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE IS150 PROBABLE FOR INSERTION SEQUENCE IS150
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY YH21_HAEIN	38% 42% 38% 38% 98% 41% 38% 100% 25%	1958 1997 2063 2083 2127 2135 2136 2183 2195 2196 2196	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN H11721
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECCLI TRA1_STRSL TRA4_LACLA YI91_SHLDY YH21_HAEIN YI3A_LACJO	38% 42% 39% 38% 98% 41% 38% 100% 25% 41%	1958 1997 2063 2083 2127 2135 2136 2183 2195 2196 2196 2197	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN H11721 INSERTION ELEMENT IS1223 HYPOTHETICAL 22.7 KD PROTEIN (ORFA)
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TIS0_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YH21_HAEIN YH21_STRSL	388 322 328 328 388 388 388 388 388 388	1958 1997 2063 2083 2127 2135 2136 2183 2195 2196 2196 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1064 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN H11721 INSERTION ELEMENT IS123 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PRORABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL	388 322 328 388 388 388 388 388 388 388	1958 1997 2063 2127 2135 2136 2183 2195 2196 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 INSERTION ELEMENT IS11 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION HI1721 INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECCLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YH3A_LACJO TRA1_STRSL BI014.05 Other	38% 38% 42% 39% 98% 41% 38% 41% 30% 47% 31%	1958 1997 2063 2083 2135 2135 2136 2183 2195 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN HI1721 INSERTION ELEMENT IS123 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0</b> genes
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI31_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE	38% 38% 42% 39% 38% 98% 41% 38% 100% 25% 47% 31% 31% 38%	1958 1997 2063 2083 2127 2135 2135 2136 2195 2196 2196 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 O genes 315 genes
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TI50_ECOLI TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIY Y131_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener	38% 38% 39% 39% 38% 98% 41% 38% 100% 25% 47% 38% 31% 38%	1958 1997 2063 2083 2127 2135 2136 2195 2196 2196 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 O genes 315 genes 315 genes
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YH21_HAEIN YH3A_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YABO BACCH	38% 38% 42% 39% 39% 38% 98% 41% 38% 100% 25% 47% 31% 38% 57%	1958 1997 2063 2083 2127 2135 2136 2183 2195 2196 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 O genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MED-DIVIC INTERCENIC RECION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY Y121_HAEIN Y13A_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YACA BACCU	38% 38% 39% 39% 39% 38% 98% 41% 38% 100% 25% 41% 38% 47% 31% 38% **********************************	1958 1997 2063 2127 2135 2136 2183 2195 2196 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERCENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERCENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERCENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TRA5_TRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY YH21_HAEIN Y134_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YAB0_BACSU YACA_BACSU	38% 38% 39% 39% 38% 98% 41% 38% 100% 25% 47% 31% 31% 31% 31% 38% TTICAL 63% 32%	1958 1997 2063 2127 2135 2135 2136 2196 2196 2196 2197 2248 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YH3A_LACJO TRA1_STRSL BIO14.05 Other BIO15.01 Gener YAB0_BACSU YACA_BACSU YE12_HAEIN	38% 38% 39% 39% 39% 39% 38% 25% 41% 38% 20% 47% 31% 38% 57 TICAL 63% 32% 32% 35%	1958 1997 2063 2127 2135 2136 2183 2195 2196 2197 2248 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> <b>315 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 5.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 7.6 KD PROTEIN IN DIND PREM INTERCENIC REGION HYPOTHETICAL 1.6 KN PROTEIN IN DIND PREM INTERCENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY YH21_HAEIN Y13A_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YA60_BACSU YACA_BACSU YE12_HAEIN YAFP_ECOLI	38% 38% 39% 39% 39% 38% 96% 41% 38% 100% 25% 38% 47% 31% 38% 57% 32% 35% 35% 36%	1958 1997 2063 2127 2135 2136 2183 2195 2196 2196 2197 2248 2196 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL PROTEIN HI1412 HYPOTHETICAL 17.6 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL PROTEIN HI1412 HYPOTHETICAL 9.0 A ND PROTEIN IN DINP-PRFH INTERGENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY YH21_HAEIN Y134_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YAB0_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YACA_BACSU	38% 38% 39% 39% 38% 98% 100% 25% 47% 38% 31% 38% 57% 51% 63% 32% 35% 36% 29%	1958 1997 2063 2127 2135 2135 2195 2196 2196 2197 2248 2197 2248 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 Ogenes 315 genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 57.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 17.6 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN SPECI-FIMB INTERGENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TI50_ECOLI TRA4_LACLA TI50_ECOLI TRA4_LACLA YI91_SHIDY YH21_HAEIN BIO14.05 Other BIO15.01 Gener YA80_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YACA_ECOLI YHQ_ECOLI (F181)	38% 38% 39% 39% 39% 39% 38% 25% 41% 38% 25% 47% 31% 38% 57% 31% 38% 57% 31% 38% 57% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	1958 1997 2063 2083 2127 2135 2136 2195 2196 2196 2196 2197 2248 2197 2248 2197 2248	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 INSERTION ELEMENT IS11 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 O genes 315 genes 315 genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 17.6 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 17.6 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN FECI-FIMB INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN FECI-FIMB INTERGENIC REGION
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TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHLDY Y12_HAEIN Y13A_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YABO_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YAFP_ECOLI (F181) Y293_MYCGE YPGQ_BACSU	38% 38% 39% 39% 38% 98% 41% 38% 100% 25% 38% 31% 38% 31% 38% 5% 32% 36% 29% 41% 35%	1958 1997 2063 2127 2135 2135 2195 2196 2196 2197 2248 2197 2248 21 24 43 50 56 66 67	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN H11721 INSERTION ELEMENT IS123 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN FECI-FIMB INTERGENIC REGION HYPOTHETICAL PROTEIN MG293 HYPOTHETICAL PROTEIN MG293 HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI31_LACJO TRA1_STRSL BIO14.05 Other BIO15.01 Gener YAB0_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YACA_COLI (F181) Y293_MYCGE YPC0_BACSU YCSE_BACSU	38% 38% 39% 39% 39% 39% 38% 25% 41% 38% 25% 47% 31% 38% 5% 25% 41% 32% 35% 29%	1958 1997 2063 2127 2135 2136 2183 2195 2196 2197 2248 2197 2248 21 24 43 50 56 66 67 73	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 Ogenes 315 genes 315 genes 315 genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 LKD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 9.7 LKD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN FECI-FIMB INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SPOIL-HTME INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SAA-LLVD INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SIPU 3'REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4 TRA4_TRA4_TRA4_TRA4 TRA4_TRA4_TRA4_TRA4_TRA4_TRA4_TRA4_TRA4_	38% 38% 39% 39% 39% 38% 25% 38% 25% 31% 38% 57% 31% 38% 57% 31% 38% 57% 31% 32% 35% 36% 29% 34%	1958 1997 2063 2127 2135 2195 2196 2196 2196 2197 2248 2197 2248 2195 2196 2196 2197 2248 2195 256 66 67 73 79	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 7.6 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN FECI-FIMB INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN SEA-ILVD INTERGENIC REGION HYPOTHETICAL 21.1 KD PROTEIN IN SEA-ILVD INTERGENIC REGION HYPOTHETICAL 22.1 KD PROTEIN IN SEA-ILVD INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SIPU 3 'REGION HYPOTHETICAL 23.1 KD PROTEIN IN SIPU 3 'REGION HYPOTHETICAL PROTEIN MG293 HYPOTHETICAL 24.1 KD PROTEIN IN SIPU 3 'REGION HYPOTHETICAL 25.1 KD PROTEIN IN SIP
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHLDY Y132_HAEIN Y132_HAEIN Y134_LACJO TRA1_STRSL BIO14.05 Other BIO15. HYPOTHE BIO15.01 Gener YAB0_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YACA_BACSU YAFP_ECOLI (F181) Y293_MYCGE YPG0_BACSU YCSL_METJA Y0A9_MYCTU	38% 38% 39% 39% 38% 98% 100% 25% 31% 38% 31% 38% 31% 38% 32% 35% 35% 35% 35% 35% 35% 34% 42%	1958 1997 2063 2127 2135 2135 2183 2195 2196 2197 2248 2197 2248 21 24 43 50 56 66 67 73 79 97	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 INSERTION ELEMENT IS11 HYPOTHETICAL 12.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 <b>0 genes</b> <b>315 genes</b> <b>315 genes</b> HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL PROTEIN HI1412 HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN FECI-FIMB INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SIPU 3'REGION HYPOTHETICAL 23.1 KD PROTEIN IN SIPU 3'REGION HYPOTHETICAL 270TEIN MQ593 HYPOTHETICAL 270TEIN MJ551 HYPOTHETICAL 270TEIN MJ551 HYPOTHETICAL 270TEIN MJ551 HYPOTHETICAL 47.5 KD PROTEIN CY9C4.09
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YQKD_BACSU YCEE_ECOLI (ORF1)	32% 44%	121 127	HYPOTHETICAL 34.6 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION HYPOTHETICAL 43.9 KD PROTEIN IN MSYB-HTRB INTERGENIC REGION
YCSN BACSU	38%	132	HYPOTHETICAL 34.1 KD PROTEIN IN PBPC 3 REGION
YPH1_MYCCA	29%	133	HYPOTHETICAL 37.9 KD PROTEIN IN PTSH 3'REGION (ORF1)
YQGF_ECOLI	35%	139	HYPOTHETICAL 15.2 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION
(0180)			
YWFA_BACSU	22%	155	HYPOTHETICAL 44.5 KD PROTEIN IN ROCC-PTA INTERGENIC REGION
YXIO_BACSU	27%	156	HYPOTHETICAL 47.3 KD PROTEIN IN WAPA-LICT INTERGENIC REGION
YPNP_BACSU	30%	169	HYPOTHETICAL 48.5 KD PROTEIN IN ILVA 3'REGION
YQGN_BACSU	36%	170	HYPOTHETICAL 21.4 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YQGP_BACSU	33%	171	HYPOTHETICAL 56.4 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YFGB_ECOLI	36%	182	HYPOTHETICAL 43.1 KD PROTEIN IN NDK-GCPE INTERGENIC REGION
YWAB_BACSU	278	185	HYPOTHETICAL 33.8 KD PROTEIN IN DAE-TYRZ INTERGENIC REGION
Y448_MYCPN	578	190	HYPOTHETICAL PROTEIN MG448 HOMOLOG
Y369_MYCGE	318	192	HYPOTHETICAL PROTEIN MG369
Y220 MYCDN	346	193	HIPOTHETICAL 14.7 KD PROTEIN IN ACCC-POLD INTERGENIC REGION
VIED RCOLL	208	204	HIPOTRETICAL FROTEIN MG320 HOMOLOG
VACN DUTCH	288	204	HYPOTRETICAL 45.0 KD PROTEIN IN SECS-TUR INTERGENIC REGION
VC22 METTA	289	209	HIPOTRETICAL DEOTETN M11222
YC11 KLEPN	20%	211	HYPOTHETICAL 55 0 KD PROTEIN IN CPS REGION (OPP11)
YIBD ECOLI	34%	214	HYPOTHETICAL 40.5 KD PROTEIN IN SECS-TDH INTERGENIC REGION
Y060 MYCPN	33%	215	HYPOTHETICAL PROTEIN MG060 HOMOLOG
YOEH BACSU	55%	221	HYPOTHETICAL 41.0 KD PROTEIN IN NUCB-AROD INTERGENIC REGION
YOEI_BACSU	45%	223	HYPOTHETICAL 10.8 KD PROTEIN IN AROD-COMER INTERGENIC REGION
YQEJ_BACSU	35%	224	HYPOTHETICAL 22.2 KD PROTEIN IN AROD-COMER INTERGENIC REGION
YQEK_BACSU	378	225	HYPOTHETICAL 21.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION
YQEL_BACSU	468	226	HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION
YQEM_BACSU	42%	226	HYPOTHETICAL 28.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION
YEBC_ECOLI	40%	229	HYPOTHETICAL 26.4 KD PROTEIN IN RUVC-ASPS INTERGENIC REGION
Y003_HAEIN	33%	239	HYPOTHETICAL PROTEIN HI0003
YBHS_ECOLI	22%	249	HYPOTHETICAL 42.1 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION
YWBD_BACSU	50%	250	HYPOTHETICAL 44.4 KD PROTEIN IN EPR-GALK INTERGENIC REGION
YHIN_ECOLI	32%	254	HYPOTHETICAL 43.8 KD PROTEIN IN RHSB-PIT INTERGENIC REGION
YFOL_STRTR	478	255	HYPOTHETICAL 29.9 KD PROTEIN IN FOLD-PBP2B INTERGENIC REGION
(ORF1091)			
YW05_MYCTU	498	256	HYPOTHETICAL 18.2 KD PROTEIN CY39.05C
YOHE_ECOL1	408	264	HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION
VUCP NETME	308	275	PYPOTHETICAL PROTEIN MG181 HOMOLOG (GT9_ORF434)
VEOC BACSU	619	283	RYPOTHETICAL 83.1 KD PROTEIN IN REGION E HYPOTHETICAL 61 5 KD DROFFIN IN ADRO-DDUA INTERCENTO PROTON
VEAB BACSU	46%	305	HYDOTHETICAL 31 8 KD DROPETN IN CARD-CHAR INTERGENIC REGION
(ORFX)		202	ATTOTALIONS STOCKET AN ONDE CONSTANTS OBJECT ADDITION
YOHE ECOLI	45%	330	HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION
YYBR_BACSU	49%	331	HYPOTHETICAL 14.7 KD PROTEIN IN COTF-TETB INTERGENIC REGION
YWKD_BACSU	50%	331	HYPOTHETICAL 14.8 KD PROTEIN IN TDK-PRFA INTERGENIC REGION
YWAC_BACSU	38%	364	HYPOTHETICAL 24.6 KD PROTEIN IN DAE-TYRZ INTERGENIC REGION
Y128_MYCGE	30%	364	HYPOTHETICAL PROTEIN MG128
YHCT_BACSU	40%	365	HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION
YIEF_ECOLI	33%	369	HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION
YEIH_ECOLI	28%	376	HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION
Y372_MYCGE	32%	381	HYPOTHETICAL PROTEIN MG372
ADCE ECOPI	378	386	HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION
VAAG BACSU	448	403	HYDOWHEPTCAL 31 2 KD DEOWEIN IN YDAG-ABER INTERCENTS REGION
V552 HFLEV	259	403	HYDOTHETICAL SI.Z KD PROTEIN IN APAC-ABRS INTERGENIC REGION
VE56 SYNV3	37%	409	HYPOTHETICAL 37.5 KD PROTEIN SLL1556
YWBA BACSU	40%	419	HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION
Y105 MYCPN	35%	431	HYPOTHETICAL PROTEIN MG105 HOMOLOG
YW11_MYCTU	38%	438	HYPOTHETICAL 145.8 KD PROTEIN CY39.11C
Y097_MYCTU	39%	442	HYPOTHETICAL 18.2 KD PROTEIN CY78.07
LYTR_BACSU	31%	443	MEMBRANE-BOUND PROTEIN LYTR
YQAK_BACSU	46%	451	HYPOTHETICAL 32.2 KD PROTEIN IN SPOIIIC-CWLA INTERGENIC REGION
YMCP_BPF41	27%	471	HYPOTHETICAL PROTEIN IN MCP 3' REGION (FRAGMENT)
YQBO_BACSU	35%	473	HYPOTHETICAL 171.0 KD PROTEIN IN SPOIIIC-CWLA INTERGENIC REGION
YWLG_BACSU	48%	484	HYPOTHETICAL 19.4 KD PROTEIN IN SPOIIR-GLYC INTERGENIC REGION
DEGV_BACSU	34%	496	DEGV PROTEIN
YPMR_BACSU	298	497	HYPOTHETICAL 28.9 KD PROTEIN IN ILVA 3'REGION
YBBD_BACSU	258	499	HYPOTHETICAL 70.6 KD PROTEIN IN FEUA 5'REGION PRECURSOR (ORF1)
YQGX_BACSU	448	526	HYPOTHETICAL 23.2 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
IFOA_STROK	138	525	HIPOTHETICAL 23.1 KU PROTEIN IN PONA 5'REGION
VOGZ BACCU	406	530	HIGHDIICAD 21.1 KU PROTEIN IN COTD-KUUD INTERGENIC REGION
ANCE CLORE	925	545	HYDOPHEFICAL 31 2 KD DROPEIN IN MAR S DIVITAL (OPP)
YJEB_ECOLI	28%	551	HYPOTHETICAL 15.6 KD PROTEIN IN PURA-VACE INTERGENIC REGION
YGDP_ECOLI	33%	553	HYPOTHETICAL 20.8 KD PROTEIN IN PTPH-MUTH INTERGENIC REGION

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YJAB_ECOLI	418	569	HYPOTHETICAL 16.4 KD PROTEIN IN RRFE-META INTERGENIC REGION
(F147)			
Y369_MYCGE	28%	572	HYPOTHETICAL PROTEIN MG369
DEGV BACSU	30%	573	DEGV PROTEIN
YOJW BACSU	35%	578	HYPOTHETICAL 45.9 KD PROTEIN IN GLNO-ANSE INTERGENIC REGION
YF63 METJA	31%	581	HYPOTHETICAL PROTEIN MI1563
YWCG BACSH	41%	585	HYDOPHETICAL 28 3 KD DECENTRY IN COVE-UPP INPERCENTE DECIM
VATE GTANI	200	597	WYDOWNEWICAL 14 6 VD DOCETA IN AN STREAMAN (DED)
VHIC BLOCH	226	200	HYDEREFICAL 10.0 KD PROFEIN IN AND 5 REGION (ORF)
INDBACSU	225	500	HIPOTHEFICAL 37.0 KD PROTEIN IN SPOILE-GLYC INTERGENIC REGION
1553_METUA	40%	594	HYPOTHETICAL PROTEIN MJ0553
YWCD_BACSU	338	601	HYPOTHETICAL 14.3 KD PROTEIN IN EPR-GALK INTERGENIC REGION
Y085_MYCGE	338	603	HYPOTHETICAL PROTEIN MG085
YQFU_BACSU	298	612	HYPOTHETICAL 32.5 KD PROTEIN IN CCCA-SODA INTERGENIC REGION
Y119_MYCTU	25%	615	HYPOTHETICAL 41.2 KD PROTEIN CY277.09
YQJK_BACSU	51%	617	HYPOTHETICAL 34.0 KD PROTEIN IN GLNO-ANSE INTERGENIC REGION
YCEG_ECOLI	30%	623	HYPOTHETICAL 38.2 KD PROTEIN IN PARC-HOLB INTERGENIC REGION
YZ42 METJA	32%	642	HYPOTHETICAL PROTEIN MJECL42
YOA5 MYCTU	228	651	HYPOTHETICAL 40.2 KD PROTEIN CY9C4 05C
V553 SVNV3	47%	658	hypothemical 22 S KD DOODELN CLOSES
YOFE BOOLS	4.76	050	ALFORNETICAL 22.3 KD PROTEIN SLAVESS
ICEE_ECOLI	928	0.59	REPOTHETICAL 43.9 KD PROTEIN IN MSYB-HTRB INTERGENIC REGION
(URFI)			
YRG2_LACLA	95%	660	HYPOTHETICAL PROTEIN IN RPMG 3'REGION (ORF2)
YQGZ_BACSU	38%	672	HYPOTHETICAL 14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YCDQ_ECOLI	35%	678	HYPOTHETICAL 50.8 KD PROTEIN IN PHOH-CSGG INTERGENIC REGION
YADE_ECOLI	28%	680	HYPOTHETICAL 46.3 KD PROTEIN IN HPT-PAND INTERGENIC REGION
PRECURSOR			
YJDJ_ECOLI	35%	684	HYPOTHETICAL 10.5 KD PROTEIN IN DCUB-LYSU INTERGENIC REGION
(O90A)			
VJDI ECOLI	56%	684	NYPOTHETICAL 8 6 KD PROTEIN IN DOUBLINSH INTERCENTS PROTON
(076)			
VARD RACCU	139	695	NYDORUPWICKI 20 3 KD DECRUTH IN NEWS YORK INTERCENTS RECION
TABD_BACBU	306	600	NUPOTHETICAL 29.2 KD PROTEIN IN METS-KSGA INTERGENIC REGION
IQHI_BACSU	396	630	HYPOTHEFICAL 14.7 KD PROTEIN IN ACCC-POLD INTERGENIC REGION
YAJH_BACSU	438	122	HYPOTHETICAL 38.3 KD PROTEIN IN PEPT-RATE INTERGENIC REGION
AICI ECOP1	338	727	HYPOTHETICAL 88.1 KD PROTEIN IN GLTS-SELC INTERGENIC REGION
YFBB_HAEIN	26%	734	HYPOTHETICAL PROTEIN HI0282
Y188_METJA	24%	739	HYPOTHETICAL PROTEIN MJ0188
Y371_MYCGE	28%	740	HYPOTHETICAL PROTEIN MG371
YCSE_BACSU	40%	742	HYPOTHETICAL 28.1 KD PROTEIN IN SIPU 3'REGION
YYBT BACSU	38%	750	HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION
Y347 MYCPN	26%	754	HYPOTHETICAL PROTEIN MG347 HOMOLOG
YCND BACSD	36%	758	HYPOTHETICAL 27 9 KD PROTEIN IN PHRC-GDH INTERGENIC REGION
VHCS_BACSU	319	768	HYDOTHEFTCAL 22 0 KD DEOTETN IN CODE CLEB INTERCENTC REGION
VMBC BACSII	368	770	UVDOTURTICAL 25.8 KD PROTEIN IN COPP-GDFF INTERGENIC REGION
VWBS_DACSU	208	770	WYDORUSDICAL 14 2 NO DECEMBEN IN EPR-GALK INTERCENTC REGION
IWBH_BACSU	2/0	770	HIPOTHETICAL 14.5 KD PROTEIN IN EPR-GALK INTERGENIC REGION
ILAS_BACSU	388	//1	HYPOTHETICAL 17.6 KD PROTEIN IN NOSA 5'REGION (PISA)
YLAR_BACSU	27.6	113	HYPOTHETICAL 10.4 KD PROTEIN IN NUSA-INFB INTERGENIC REGION
(ORF3)			
YHI3_RHOCA	448	779	HYPOTHETICAL 33.7 KD PROTEIN IN HIMA 5'REGION (ORF3)
Y06B_MYCTU	31%	809	HYPOTHETICAL 139.6 KD PROTEIN CY338.11C PRECURSOR
YQGS_BACSU	34%	813	HYPOTHETICAL 73.2 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YIDA_ECOLI	38%	821	HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION
Y143_HAEIN	25%	828	HYPOTHETICAL PROTEIN HI0143
Y456 METJA	24%	848	HYPOTHETICAL PROTEIN MJ0456
YCFB ECOLI	58%	850	HVPOTHETICAL 42.6 KD PROTEIN IN PURB-ICDA INTERGENIC REGION
(ORF-15)			
YEHZ BOOLT	319	864	NYDOWNEWICAL 32 6 VD DOOWEIN IN MOLD-DOLY INVERSENTS SECTOR
PRECURSOR	510	004	ATTOMSTICAL SETURD ROTTIN IN HOLEN INTERGENT, RESTON
VHAD VARIN	509	077	BYDORUPETCAL DOORDIN HIGGOS
VIXA DACCU	549	005	NUCONDERICAL PROTEIN BIODEL IN DEEL SUDDETEN (ODD)
IDAA_BACSU	09.6	885	HIPOTHETICAL 35.3 KD PROTEIN IN PTSL 5 REGION (ORFB)
YWAC_BACSU	45%	894	HYPOTHETICAL 24.6 KD PROTEIN IN DAE-TYRZ INTERGENIC REGION
ACDO ECOP1	28%	897	HYPOTHETICAL 50.8 KD PROTEIN IN PHOH-CSGG INTERGENIC REGION
Y531_METJA	37%	900	HYPOTHETICAL PROTEIN MJ0531
LYTR_BACSU	25%	907	MEMBRANE-BOUND PROTEIN LYTR
YCSE_BACSU	27%	911	HYPOTHETICAL 28.1 KD PROTEIN IN SIPU 3'REGION
YABR_BACSU	31%	912	HYPOTHETICAL 14.2 KD PROTEIN IN DIVIC-SPOILE INTERGENIC REGION
YICL_ECOLI	34%	923	HYPOTHETICAL 33.1 KD PROTEIN IN SELC-NLPA INTERGENIC REGION
Y912_HAEIN	35%	928	HYPOTHETICAL PROTEIN H10912
YIBD ECOLI	33%	939	HYPOTHETICAL 40.5 KD PROTEIN IN SECS-TON INTERGENIC PROTON
YECD ECOLT	400	967	HYPOTHETICAL 21.7 KD PROTEIN IN ASDELBICZ INTERCENTS DESIGN
	44 (2.94)	141	NYDOWNAUTON, 33 0 KD DEOWETN IN COLLEVE INTERCENTO PROTON
WOT BACCU	408	986	THE REPORT OF ALL AND THE REPORT OF THE CHARGE CONTRACTOR AND A DESCRIPTION OF A DESCRIPTIO
YVCJ_BACSU	408 528 469	986	NYDOMUDICAL 34.2 KB DOMENN IN CALL FROM THEREPARE SECTOR
YVCJ_BACSU YVCK_BACSU	408 528 468	986 987	HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRXB INTERGENIC REGION
YVCJ_BACSU YVCK_BACSU Y247_MYCGE	40% 52% 46% 36%	986 987 1003	HYPOTHETICAL 34.7 KD FROTEIN IN CRITICID INTERGENIC REGION HYPOTHETICAL PROTEIN MG247
YVCJ_BACSU YVCK_BACSU Y247_MYCGE YECD_ECOLI	40% 52% 46% 36% 26%	986 987 1003 1006	HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRXB INTERGENIC REGION HYPOTHETICAL PROTEIN MG247 HYPOTHETICAL 21.7 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION
YVCJ_BACSU YVCK_BACSU Y247_MYCGE YECD_ECOLI YLYB_BACSU	40% 52% 46% 36% 26% 59%	986 987 1003 1006 1024	HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRXB INTERGENIC REGION HYPOTHETICAL PROTEIN MG247 HYPOTHETICAL 21.7 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION HYPOTHETICAL 33.7 KD PROTEIN IN LSP-PYRR INTERGENIC REGION
YVCJ_BACSU YVCK_BACSU Y247_MYCGE YECD_ECOLI YLYB_BACSU (ORF-X)	40% 52% 46% 36% 26% 59%	986 987 1003 1006 1024	HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRNB INTERGENIC REGION HYPOTHETICAL PROTEIN MG247 HYPOTHETICAL 21.7 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION HYPOTHETICAL 33.7 KD PROTEIN IN LSP-PYRR INTERGENIC REGION
YVCJ_BACSU YVCK_BACSU Y247_MYCGE YECD_ECOLI YLYB_BACSU (ORF-X) Y501_SYNY3	40% 52% 46% 36% 26% 59%	986 987 1003 1006 1024 1027	HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRXB INTERGENIC REGION HYPOTHETICAL PROTEIN MG247 HYPOTHETICAL 21.7 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION HYPOTHETICAL 33.7 KD PROTEIN IN LSP-PYRR INTERGENIC REGION HYPOTHETICAL 36.7 KD PROTEIN SLL0501
YVCJ_BACSU YVCK_BACSU Y247_MYCGE YECD_ECOLI YLYB_BACSU (ORF-X) YSO1_SYNY3 YQAN_BACSU	40% 52% 46% 36% 26% 59% 42% 41%	986 987 1003 1006 1024 1027 1043	HYPOTHETICAL 34.7 KD PROTEIN IN CRH-TRAB INTERGENIC REGION HYPOTHETICAL PROTEIN MG247 HYPOTHETICAL 21.7 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION HYPOTHETICAL 33.7 KD PROTEIN IN LSP-PYRR INTERGENIC REGION HYPOTHETICAL 36.7 KD PROTEIN SLL0501 HYPOTHETICAL 16.1 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION

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YMFN_ECOLI	23%	1051	HYPOTHETICAL	50.9 KD PROTEIN IN INTE-PIN INTERGENIC REGION
YAF2 BACLI	40%	1068	HYPOTHETICAL	9.7 KD PROTEIN IN CWLL 5'REGION
VOG7 BACSU	479	1070	NYDOWNEETCAL	14 0 VD BEOFFETH IN CODE COMOL INFEREMENTS REGION
1505 24030	440	7010	HIPOINEIICAL	14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YQFN_BACSU	44%	1082	HYPOTHETICAL	23.7 KD PROTEIN IN CCCA-SODA INTERGENIC REGION
YOKB BACSU	35%	1083	HYPOTHETICAL	11.8 KD PROTEIN IN GLNO-ANSE INTERGENIC REGION
VIDA ECOLI	110	1004	UNDORWERST CONT.	20 7 VD DOORTH IN TODA OVDE INTERCONTA SECTOR
IIDA_ECOLI	445	T094	RIPOTRETICAL	29.7 KD PROTEIN IN IBPA-GIRB INTERGENIC REGION
YWFO_BACSU	528	1085	HYPOTHETICAL	51.0 KD PROTEIN IN PTA 3'REGION
YSXB BACSU	38%	1088	HYPOTHETICAL	12.3 KD PROTEIN IN RPLU-RPMA INTERGENIC REGION
(OPE X)		2000	111101110110	abto no incluir in mico mini infiniciate motor
(ORF X)				
YDAR_BACSU	40%	1090	HYPOTHETICAL	45.7 KD PROTEIN IN MUTT-GSIB INTERGENIC REGION
YOFG BACSU	46%	1092	HYPOTHETICAL	17.8 KD PROTEIN IN PHOH-DGKA INTERGENIC REGION
VIVE BACCH	549	1096	HYDOPUPPTONI	BROWEIN IN DECC BACO INTERCENTS DECIMIN (FRACTION)
IVIE_DACSU	246	1030	RIFOTHETICAL	PROTEIN IN DEGS-TAGO INTERGENIC REGION (PRAGMENT)
YXIQ_BACSU	258	1098	HYPOTHETICAL	45.5 KD PROTEIN IN BGLS-KATB INTERGENIC REGION
YADO ECOLI	29%	1103	HYPOTHETICAL	46.0 KD PROTEIN IN HEML-PES INTERGENIC REGION
VORT BACCH	469	1104	LY DOVELLET CAL	22 2 VD DROTETN IN MOOD COMPR INTERPORTATION
1000_04000	406	1104	HIPOTHETICAL	22.2 AD FROTEIN IN AROD-COMER INTERGENIC REGION
Y03F_MYCTU	36%	1106	HYPOTHETICAL	54.3 KD PROTEIN CY130.15C
YFEU HAEIN	52%	1142	HYPOTHETICAL	PROTEIN HI0754
VEIN BACCH	269	1145	UVDOPUPPTCAL	28 3 VE DROTRIN IN CLUC-CLUBC INTERCENTC RECTOR
ITIA_DACOU	200	1440	RIFOIDETICAL	25.5 KD PROTEIN IN GROG-GOVEC INTERGENIC REGION
YBDN_ECOLI	338	1149	HYPOTHETICAL	47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION
YBDM ECOLI	46%	1150	HYPOTHETICAL	23.9 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION
VHOT HARTN	369	1100	HARDOWNERSTON I	PROPERTY HIGHAE
Inco_masin	30%	1105	HIPOTHETICAL	PROTEIN RIGI43
YNGB_CLOPE	338	1190	HYPOTHETICAL	31.2 KD PROTEIN IN NAGH 5 REGION (ORFB)
YPTB_CLOAB	518	1194	HYPOTHETICAL	PROTEIN IN PTB 5'REGION (ORF1)
V912 HARTN	289	1195	HYDOTHETTCAL	DECORPTN HIGGID
UDIA DAGUI	200	1107	INFORMETICAD	LUCIDIN NICOIS
YPIA_BACSU	2/6	1197	HYPOTHETICAL	48.3 KD PROTEIN IN QCRA 5'REGION
YWKB BACSU	26%	1213	HYPOTHETICAL	33.6 KD PROTEIN IN TOK-PRFA INTERGENIC REGION
YHT1 LACLA	929	1225	HYPOTHETICAL	PROTEIN IN HISC 5'REGION (ORE))
THE LONG DR	220	1000	HIPOTHETICAL	PROTEIN IN HISC 5 REGION (ORFI)
YHI6_LACLA	38#	1230	HYPOTHETICAL	30.7 KD PROTEIN IN HISD-HISB INTERGENIC REGION
(ORF6)				
VHIC LACLA	0.7%	1235	HYDOTHETTCAL	31 3 KD DROWRIN IN VICIE 3 (DROIDN (ORDIN)
Inite_Brecha	371	1050	HIPOTHETICAL	SI,S KD FROILIN IN RISIE 5 REGION (ORFIS)
YABJ_BACSU	538	1250	HYPOTHETICAL	13.7 KD PROTEIN IN PURR-SPOVG INTERGENIC REGION
(ORF2)				
VCT1 STRMIT	658	1255	HYDOPHETTONI.	DECTREM 1 IN CORP. DECTON (PRACMEND)
1011_01000	0.00	1000	HIPOTHETICAL	PROTEIN I IN GIPB REGION (PRAGMENT)
YODS_MYCTU	328	1259	HYPOTHETICAL	69.9 KD PROTEIN CYIAII.08
YOHY BACSU	24%	1263	HYPOTHETICAL	14.7 KD PROTEIN IN ACCC-FOLD INTERGENIC REGION
V569 MERIA	359	1283	HYDOPHRETCAL	DDAMPTN MIDSER
1500_REIDA	556	1001	HIPOTHEIICAD	
ACDO ECOLI	20%	1294	HYPOTHETICAL	50.8 KD PROTEIN IN PHOH-CSGG INTERGENIC REGION
YPAA_BACSU	31%	1305	HYPOTHETICAL	20.5 KD PROTEIN IN SERA-FER INTERGENIC REGION
YPUL BACSU	54%	1306	HYPOTHETICAL	26.0 KD PROTEIN IN SPMB-AROC INTERGENIC REGION
(OPEV12)		2000		acto ha thotant at orna faloo infalocitic hastan
(ORFALS)				
YPUH_BACSU	39%	1306	HYPOTHETICAL	22.0 KD PROTEIN IN RIBT-DACB INTERGENIC REGION
(ORFX8)				
VPUG BACSU	37%	1307	HYPOTHETICAL	29.6 KD PROTEIN IN RIBT-DACE INTERCENTE REGION
(00023)	310	2007	min o mini i chin	SYTO RD TROTHIN IN RIDI-DRCD INTERGENTE REGION
(ORFX7)				
YSNB_BACSU	39%	1309	HYPOTHETICAL	19.2 KD PROTEIN IN RPH-ILVE INTERGENIC REGION
YGGV FCOLT	48%	1309	HYPOTHETICAL	21 0 KD PROTEIN IN CSHR-ANSE INTERCENTC RECION
(0107)	400	2000	111101110110110	STIC NO INCIDIN IN COLD MADD INTERCLATC REGION
(0197)				
YBIO_ECOLI	32%	1321	HYPOTHETICAL	86.8 KD PROTEIN IN DING-GLNQ INTERGENIC REGION
Y442 MYCPN	36%	1327	HYPOTHETICAL	PROTEIN MG442 HONOLOG
VOOR DACON	376	1256	In the second second	14 0 KD DDODERN TN CODE CONCE INTERCOMERA DISCION
YQGZ_BACSU	378	1320	HYPOTRETICAL	14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YEBH_ECOLI	348	1362	HYPOTHETICAL	30.4 KD PROTEIN IN MANZ-CSPC INTERGENIC REGION
(ORF30)				
V100 MUCCIN	208	13.05	100000000000000000000000000000000000000	poorate wat 30
1120_MICGE	308	1303	MIPOTHETICAL	PROTEIN MGIZU
Y121_MYCGE	488	1366	HYPOTHETICAL	PROTEIN MG121
YAAN BACSU	50%	1373	HYPOTHETICAL	43.8 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION
VI VD BACCI	160	1202	INDODUDTION	27 6 VD DDODEIN IN DUDAD DUDA INSERGATIO DDOTAN
LOAU_DACCD	406	1362	AIPOIRETICAL	ATTO AD PROTEIN IN FIRAD-FIRD INTERGENIC REGION
(ORF2)				
YMFC_HAEIN	62%	1388	HYPOTHETICAL	PROTEIN HI0694
V882 HAFTM	359	1404	HYPOTHETICAL	PROTEIN HIGHAR
	2.00	1404	HIT OTHER LOAD	
Y531_METJA	348	1409	HYPOTHETICAL	PROTEIN MJ0531
YQBO_BACSU	278	1424	HYPOTHETICAL	171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION
YOBO BACSU	298	1426	HYPOTHETICAL	171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION
VEDO HARTN	205	1451	INDODUDETON	BOORDEN UT1400
IDSS_DAEIN	398	1431	A POTRETICAL	ENGLEIN HI1422
YLXM_BACSU	538	1455	HYPOTHETICAL	13.2 KD PROTEIN IN FFH 5'REGION
YBXB_BACSU	448	1464	HYPOTHETICAL	22.5 KD PROTEIN IN RPLL-RPOB INTERGENIC REGION
(223)				
VDDM DOOLT	174	1467	UNDORUGET OF T	22 0 KD DDORRAN TH OORS DODG SUPPROPRIES DROTOT
IBDM_ECOPI	4/6	1467	REPOTHETICAL	23.3 KD PROTEIN IN CSTA-DSEG INTERGENIC REGION
YBDN_ECOLI	32%	1468	HYPOTHETICAL	47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION
VTRP LACLA	999	1500	HYPOTHETICAL	13 3 KD PROTEIN IN TERE SUPERION
VIOL TROLT	240	1505	INDOMISTICAL	15 I US BROWDIN IN ONLY IN A MARK STREET
ITCT ECOPI	346	1202	REPOTHETICAL	33.1 KD PROTEIN IN SELC-NLPA INTERGENIC REGION
Y709_METJA	26%	1511	HYPOTHETICAL	PROTEIN MJ0709
YBGG ECOLI	29%	1530	HYPOTHETICAL	100.0 KD PROTEIN IN HRSA-CYDA INTERGENIC REGION
VVAL BACCH	220	1520	UVDOTUTTOAT	20 3 VD DEGERINI IN REPRESENTATION DECISION
ITAL_DACSU	228	T23A	REPOTHETICAL	20.2 ND PROTEIN IN TETB-EXUA INTERGENIC REGION
(ORFG)				
YJJG_ECOLI	27%	1554	HYPOTHÉTICAL	25.3 KD PROTEIN IN RIMI-PRFC INTERGENIC REGION
YEXA BACSU	379	1573	HYPOTHERICAL	9 7 KD PROFFIN IN PUR OPERON
VEOD DOOLT	3170	1010	THETTCAL	S. C NE PROTEIN IN FUR VERVIN
X BOOK BOOK T	278	1577	NY REVENERTICAL.	SU Y AD PROPERTY IN ALKA-BAES INPERCENTE PROTON

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	30%	1591	HYPOTHETICAL	36.4 KD	PROTEIN	IN MOCC-MOCA INTERGENIC REGION
(ORF334)	500	* 2 2 2 2	nit vinisi tens	2014 10	110115214	IN NOCE NOCH INTERGENIC REGION
DEGV_BACSU	35%	1601	DEGV PROTEIN			
YQKD_BACSU	25%	1612	HYPOTHETICAL	34.6 KD	PROTEIN	IN GLNQ-ANSE INTERGENIC REGION
YPBG_BACSU	30%	1639	HYPOTHETICAL	28.6 KD	PROTEIN	IN RECQ-CMK INTERGENIC REGION
PRECURSOR						
YH38_HAEIN	30%	1651	HYPOTHETICAL	PROTEIN	HI1738	
YKQC_BACSU	418	1659	HYPOTHETICAL	61.5 KD	PROTEIN	IN ADEC-PDHA INTERGENIC REGION
YHID_ECOLI	428	1660	HYPOTHETICAL	23.2 KD	PROTEIN	IN SLP-HDEB INTERGENIC REGION
(ORF-C)						
YDP1_LACLC	50%	1664	HYPOTHETICAL	30.9 KD	PROTEIN	IN PEPX 5'REGION (ORF1)
YAGG_ECOLI	24%	1672	HYPOTHETICAL	50.6 KD	PROTEIN	IN PERR-ARGF INTERGENIC REGION
YPSC_BACSU	46%	1697	HYPOTHETICAL	43.5 KD	PROTEIN	IN COTD-KDUD INTERGENIC REGION
PRECURSOR						
YQEN_BACSU	32%	1699	HYPOTHETICAL	40.5 KD	PROTEIN	IN COMEC-RPST INTERGENIC REGION
YGJR_ECOLI	36%	1706	HYPOTHETICAL	37.0 KD	PROTEIN	IN EBGC-UXAA INTERGENIC REGION
YADQ_ECOLI	379	1710	HYPOTHETICAL	46.0 KD	PROTEIN	IN HEML-PFS INTERGENIC REGION
YIDD_PROMI	46%	1719	HYPOTHETICAL	9.6 KD 1	PROTEIN	IN RNPA 3'REGION
YVDK_BACSU	60%	1726	HYPOTHETICAL	88.3 KD	PROTEIN	IN CLPP-CRH INTERGENIC REGION
LYTR_BACSU	31%	1739	MEMBRANE-BOUI	ND PROTE	IN LYTR	
YFGA_ECOLI	238	1741	HYPOTHETICAL	36.2 KD	PROTEIN	IN NDK-GCPE INTERGENIC REGION
YQFU_BACSU	28%	1745	HYPOTHETICAL	32.5 KD	PROTEIN	IN CCCA-SODA INTERGENIC REGION
YICO_ECOLI	39%	1768	HYPOTHETICAL	49.9 KD	PROTEIN	IN NLPA-UHPT INTERGENIC REGION
YUPP_MYCHO	328	1770	HYPOTHETICAL	31.6 KD	PROTEIN	IN UPP 3'REGION
YKGE_ECOLI	438	1771	HYPOTHETICAL	26.0 KD	PROTEIN	IN EACH-BETA INTERGENIC REGION
YKGF_ECOLI	32%	1772	HYPOTHETICAL	53.1 KD	PROTEIN	IN EACH-BETA INTERGENIC REGION
YKGG_ECOLI	318	1773	HYPOTHETICAL	31.1 KD	PROTEIN	IN EACH-BETA INTERGENIC REGION
ARHT ECOFT	358	1774	HYPOTHETICAL	25.9 KD	PROTEIN	IN MOAE-RHLE INTERGENIC REGION
YHAP_BACSU	278	1814	HYPOTHETICAL	45.4 KD	PROTEIN	IN SSPB-PRSA INTERGENIC REGION
1455_METUA	2/6	181/	HYPOTHETICAL	PROTEIN	MJ0456	TH LDD LBOD THERDOBILTA DESTAN
YNHE_ECOLI	398	1826	HYPOTHETICAL	56.3 KD	PROTEIN	IN LPP-AROD INTERGENIC REGION
NUDO DACCU	275	1050	HYPOTHETICAL	42.2 KD	PROTEIN	U1496A/B1496_C1_154
V260 SAMAS	369	1962	HIPOTHETICAL	39.0 KD	PROTEIN	IN COTF-TETE INTERGENIC REGION
VAUS SUAID	316	1964	UVDOPUPTICAL	16 6 VD	PROTEIN	IN ADI SIDRCION (ODE)
VUBO FCOLT	359	1869	UVDOTUDTICAL	11 3 KD	PROTEIN	IN SOUN-MEDIUM (ORFS)
(0100)	220	1009	HIFOIRETICAL	11.3 KD	PROTEIN	IN SOMA-MIR INTERGENIC REGION
VEKA BACSH	48%	1882	HYDOTHETICAL	49 0 KD	PROTEIN	IN RUTH-TRYA INTERCENTS DECION
V531 METLIA	26%	1907	HYPOTHETICAL	PROTEIN	MT0531	IN BDID-INNA INTERMINIC RESION
Y556 SYNY3	37%	1917	EXPOTHETICAL	24.0 KD	PROTEIN	SLB0556
DEGV BACSU	28%	1920	DEGV PROTEIN	6410 HD	110010111	01110000
YOUR ROOM		+ 2 6 0	0001 0100020	· · · · · · · · · · · · · · · · · · ·		IN MEDC-SHET INTERGENIC REGION
IONE ECOLI	37%	1924	HYPOTHETICAL	OXIDORE	JUCTASE .	LEA PERCENT LANCE A LANCE DEPENDENT AND A DEPENDENT AND A DEPENDENT
YPEC_LACLC	37% 88%	1924 1928	HYPOTHETICAL HYPOTHETICAL	PROTEIN	IN PEPC	5'REGION (ORF 2)
YPEC_LACLC YQKG_BACSU	37% 88% 54%	1924 1928 1930	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD	IN PEPC PROTEIN	5'REGION (ORF 2) IN GLNO-ANSE INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQHY_BACSU	37% 88% 54% 24%	1924 1928 1930 1939	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD 14.7 KD	IN PEPC PROTEIN PROTEIN	IN ADJC DOR (ORF 2) IN GLNQ-ANSE INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQKY_BACSU YQKY_BACSU YQKG_BACSU	378 888 548 248 348	1924 1928 1930 1939 1942	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD 14.7 KD 21.0 KD	IN PEPC PROTEIN PROTEIN PROTEIN	IN GLOQ-ANSE INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLOQ-ANSE INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQHY_BACSU YQKG_BACSU YIEK_ECOLI	37% 88% 54% 24% 34% 40%	1924 1928 1930 1939 1942 1949	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN	IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TNAB-BGLB INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQHY_BACSU YQKG_BACSU YIEK_ECOLI YLP3_PSEPU	37% 88% 24% 34% 40% 40%	1924 1928 1930 1939 1942 1949 1951	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD 21.0 KD 21.0 KD 23.3 KD 44.7 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	IN GLNG SOLON (ORF 2) IN GLNQ-ANSR INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TNAB-BGLB INTERGENIC REGION IN LPD-3 5'REGION (ORF3)
YPEC_LACLC YOKG_BACSU YOKG_BACSU YOKG_BACSU YIEK_ECOLI YLP3_PSEPU YADS_ECOLI	37% 88% 54% 24% 40% 40% 33%	1924 1928 1930 1939 1942 1949 1951 1966	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	IN GLOG SOLON (ORF 2) IN GLNQ-ANSR INTERGENIC REGION IN ACCC-FOLD INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TNAB-BGLB INTERGENIC REGION IN LED-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YQKG_BACSU YIEX_ECOLI YLP3_PSEPU YADS_ECOLI YDAR_BACSU	37% 88% 54% 24% 40% 40% 33% 30%	1924 1928 1930 1939 1942 1949 1951 1966 1970	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 23.3 KD 24.7 KD 22.1 KD 45.7 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	IN HERE SOLVER AN
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YIEX_ECOLI YLP3_PSEPU YADS_ECOLI YDAR_BACSU Y837_METJA	37% 88% 54% 24% 34% 40% 33% 30% 28%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837	IN HERE SOLVER AN AND A STREAM AND A STREAM AND
YPEC_LACLC YQKC_BACSU YQKG_BACSU YQKS_BACSU YIEK_BCOLI YLP3_PSEPU YADS_ECOLI YB37_METJA YIGN_ECOLI	37% 88% 24% 34% 40% 33% 30% 28% 22%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980 1982	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN 54.7 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN	IN DEPUTION (ORF 2) IN GLNQ-ANSR INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TAB-BGLB INTERGENIC REGION IN LPD-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION
YPEC_LACLC YQKC_BACSU YQKC_BACSU YQKC_BACSU YIEK_BCOLI YLP3_PSEPU YADS_ECOLI YADS_ECOLI YB37_METJA YIGM_ECOLI PRECURSOR	37% 88% 54% 34% 40% 33% 30% 28% 22%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980 1982	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 21.0 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN 54.7 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN	IN GLNG ON (ORF 2) IN GLNQ-ANSR INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TABB-BGLB INTERGENIC REGION IN LPD-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION
YPEC_LACLC YQKC_BACSU YQKC_BACSU YQKC_BACSU YIEX_ECOLI YLP3_PSEPU YADS_ECOLI YDAR_BACSU YBA7_METJA YIGN_ECOLI PRECURSOR YJEQ_HAEIN	37% 88% 54% 24% 34% 40% 33% 30% 28% 22% 29%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980 1982	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD PROTEIN 54.7 KD PROTEIN	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN HI1714	IN HERE SOLVER AN
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YIEX_ECOLI YLP3_PSEPU YADAS_ECOLI YDAR_BACSU Y837_METJA YIGN_ECOLI PRECURSOR YJEQ_HAEIN YABE_BACSU	37% 88% 54% 24% 34% 40% 33% 30% 28% 22% 29%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980 1982 1984 1985	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN 54.7 KD PROTEIN 47.7 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN HI1714 PROTEIN	IN MEDU SOFT IN INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TNAB-BGLB INTERGENIC REGION IN LED-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YIEK_BCOLI YLP3_PSEPU YADS_ECOLI YDAR_BACSU Y837_METJA YIGN_ECOLI PRECURSOR YJEQ_BAEIN YABE_BACSU YE12_HAEIN	37% 88% 54% 24% 40% 30% 30% 28% 22% 29% 39% 31%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980 1982 1984 1985 2002	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 21.0 KD 21.0 KD 21.0 KD 23.3 KD 44.7 KD PROTEIN 54.7 KD PROTEIN 47.7 KD PROTEIN	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN HI1714 PROTEIN HI1714	IN MEDG JOHN (ORF 2) IN GLNQ-ANSR INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TAB-BGLB INTERGENIC REGION IN LPD-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION IN METS-KSGA INTERGENIC REGION
YPEC_LACLC YQKC_BACSU YQKC_BACSU YQKC_BACSU YIEK_ECOLI YLP3_PSEPU YADS_ECOLI YADS_ECOLI YB37_METJA YIGN_ECOLI PRECURSOR YJE0_HAEIN YABE_BACSU YE12_HAEIN	37% 88% 24% 24% 40% 33% 28% 22% 29% 39% 31% 38%	1924 1928 1930 1939 1942 1949 1951 1966 1970 1980 1980 1982 1984 1985 2002 2013	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 14.7 KD 21.0 KD 23.3 KD 23.3 KD 24.7 KD PROTEIN 54.7 KD PROTEIN PROTEIN PROTEIN PROTEIN	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN HI1714 PROTEIN HI1412 MJ1556	IN HERION (ORF 2) IN GLNQ-ANSR INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN CLNQ-ANSR INTERGENIC REGION IN TNAB-BGLB INTERGENIC REGION IN LED-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION IN METS-KSGA INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YLEX_ECOLI YLD3_PSEPU YAD5_ECOLI YDA8_BACSU Y837_METJA YIGN_ECOLI PRECURSOR YJEQ_HAEIN YABE_BACSU YF156_METJA YACC_BACSU	378 888 548 408 338 338 288 298 398 388 298 398 388 388 388 388 388 388 450	1924 1928 1930 1939 1942 1942 1951 1951 1966 1970 1980 1982 1984 1985 2002 2013 2014	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN 47.7 KD PROTEIN PROTEIN 31.8 KD 3.6 KD	IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN MJ0837 PROTEIN HI1714 PROTEIN HI1714 PROTEIN HI1556 PROTEIN	IN HERE SOLVER INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TNAB-BGLB INTERGENIC REGION IN TAB-BGLB INTERGENIC REGION IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION IN METS-KSGA INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YLP3_PSEPU YLP3_PSEPU YDAS_ECOLI YDAS_ECOLI YDAS_MCTJA YIGN_ECOLI PRECURSOR YJEQ_HAEIN YABE_BACSU YE12_HAEIN YACE_BACSU YWDS_BACSU	378 888 548 248 408 338 308 288 288 298 398 318 388 3498 458 408	1924 1928 1930 1939 1949 1951 1966 1970 1980 1982 1984 1985 2002 2013 2014 2015	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN 47.7 KD PROTEIN 47.7 KD PROTEIN 31.8 KD 9.2 4 KD	NOTASE IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN HI1714 PROTEIN HI1412 MJ1556 PROTEIN PROTEIN PROTEIN	IN HERE SOLVER AND A STREAM AND
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YLP3_PSEPU YLP3_PSEPU YDAS_ECOLI YDAR_BACSU YB37_METJA YIGN_ECOLI PRECURSOR YJEQ_HAEIN YABE_BACSU YE12_HAEIN YACE_BACSU YWOE_BACSU YACF_BACSU	378 888 548 408 338 408 338 308 228 298 318 388 408 318 388 408 318 5756	1924 1928 1930 1939 1949 1951 1966 1970 1980 1982 1984 1985 2002 2013 2014 2015 2015	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 21.0 KD 23.3 KD 44.7 KD 22.1 KD 45.7 KD PROTEIN 45.7 KD PROTEIN 47.7 KD PROTEIN 31.8 KD 19.6 KD 37.1 KD	NOTASE IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN HI1714 PROTEIN HI1412 MJ1556 PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	IN HERE SHOE NOT INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN GLNQ-ANSR INTERGENIC REGION IN TAB-BGLB INTERGENIC REGION IN LPD-3 5'REGION (ORF3) IN HEML-PFS INTERGENIC REGION IN MUTT-GSIB INTERGENIC REGION IN UDP-UBIE INTERGENIC REGION IN METS-KSGA INTERGENIC REGION IN FTSH-CYSK INTERGENIC REGION IN ACDA 5 REGION IN FOLK-LYSS INTERGENIC REGION IN FOLK-LYSS INTERGENIC REGION
YPEC_LACLC YQKG_BACSU YQKG_BACSU YQKG_BACSU YIEK_ECOLI YLP3_PSEPU YADS_PSEPU YADS_ECOLI YB37_METJA YIGN_ECOLI PRECURSOR YJEQ_HAEIN YABE_BACSU YE12_HAEIN YF56_METJA YACC_BACSU YACF_BACSU YPAC_BACSU	378 888 548 408 338 408 338 308 222 298 318 458 458 458 458 458 578 578 578 578	1924 1928 1930 1939 1949 1951 1966 1970 1980 1980 1982 2002 2013 2014 2015 2015 2016 2017	HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL HYPOTHETICAL	OXIDORE PROTEIN 21.0 KD 21.0 KD 23.3 KD 24.7 KD 22.1 KD 42.7 KD PROTEIN 54.7 KD PROTEIN 54.7 KD PROTEIN 31.8 KD 31.8 KD 37.1 KD 23.6 KD	NOTASE . IN PEPC PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN HI1714 PROTEIN HI1412 MJ1556 PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	IN HERE ON (ORF 2) IN GLNQ-ANSR INTERCENIC REGION IN ACCC-POLD INTERGENIC REGION IN GLNQ-ANSR INTERCENIC REGION IN TNAB-BGLB INTERGENIC REGION IN TAB-BGLB INTERGENIC REGION IN HEL-PFS INTERGENIC REGION IN WUTT-GSIB INTERGENIC REGION IN WUTT-GSIB INTERGENIC REGION IN METS-KSGA INTERGENIC REGION IN METS-KSGA INTERGENIC REGION IN FTSH-CYSK INTERGENIC REGION IN FOLK-LYSS INTERGENIC REGION IN FOLK-LYSS INTERGENIC REGION IN QCC-DAPB INTERGENIC REGION
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YOBD MYCTU	318	2181	HYPOTHETICAL 13 D KD PROTEIN CY227 13 PRECIDENCE
VERA FOOLT	319	2192	UVDOTUPTICAL 17 2 VD DROTPIN IN MODA DUDD INTERCENTO DECION
TDDA_BCODI	170	2102	informations in a protein in another protection and a second second
TABB_BAUSU	4/6	5130	HYPOTHETICAL 28.3 KD PROTEIN IN XPAC-ABRE INTERGENIC REGION
Y003_HAEIN	288	2194	HYPOTHETICAL PROTEIN HID003
YBHE_ECOLI	28%	2209	HYPOTHETICAL 36.3 KD PROTEIN IN MODC-BIOA INTERGENIC REGION
YOJV BACSU	25%	2221	HYPOTHETICAL 44.7 KD PROTEIN IN GLNO-ANSE INTERGENIC REGION
V661 MERITA	319	2226	EVENTUAL DECENT VIECCI
YNDG DOOLT	459	2220	
TFG_ECOL1	458	4661	APPOTHETICAL 29.7 KD PROTEIN IN RPLI-CPDB INTERGENIC REGION
(F286)			
YYBR_BACSU	42%	2227	HYPOTHETICAL 14.7 KD PROTEIN IN COTF-TETB INTERGENIC REGION
VIER ECOLI	4.0%	2232	HYPOTHETICAL 13 5 KD PROTEIN IN APHA-INDA INTERCENTE PROTON
VIA2 HADTN	209	2252	INTOTIONICAL BOOKEN HALLS
1113_AASIN	308	2222	REPORTED FROM HIGHS
YPBG_BACSU	268	2253	HYPOTHETICAL 28.6 KD PROTEIN IN RECQ-CMK INTERGENIC REGION
PRECURSOR			
YCEE ECOLI	25%	2277	HYPOTHETICAL 43.9 KD PROTEIN IN MSYB-HTRB INTERGENIC REGION
(ORF1)			
VAA1 MEDITA	203	2200	UVDORUERTON, DEORUTH MT0441
1441_METUA	388	2280	HIPOTHETICAL PROTEIN MJ0441
YQEG_BACSU	42%	2283	HYPOTHETICAL 20.1 KD PROTEIN IN NUCB-AROD INTERGENIC REGION
YWFA_BACSU	28%	2299	HYPOTHETICAL 44.5 KD PROTEIN IN ROCC-PTA INTERGENIC REGION
Y531 METJA	32%	2300	HYPOTHETICAL PROTEIN MJ0531
V800 MET-TA	28%	2304	HYPOTHETICAL PROTEIN MIG800
VIDO DOUT	205	3305	INCOMPETION 22 C VD DODDEN IN DDDD IVOG ENERDODING DODDAN
10BC_ECOLI	308	2306	APPOTRETICAL 32.5 KD PROTEIN IN PEPE-LYSC INTERGENIC REGION
YUA5_MYCTÜ	24%	2328	HYPOTHETICAL 40.2 KD PROTEIN CY9C4.05C
YHA2_EIKCO	29%	2333	HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5'REGION
YCXE BACME	41%	2337	HYPOTHETICAL 30.5 KD PROTEIN IN GDHI 5'REGION (ORF 2)
VHCC ECOLT	378	2339	HYDOTHETICAL 34 6 2D DECEMENT IN ADCR-CITE INTERCENTC DECIM
Ince_bcobi	575	2337	INFOLIETICAL SALO AD PROTEIN IN ARCH-GLIS INTERGENIC REGION
BIO16. UNKNOWN			83 genes
	-		-
BIOI6.01 Genera	1		5 genes
NIFS_LACDE	53%	520	NIFS PROTEIN HOMOLOG (FRAGMENT)
NIFS_ANASP	29%	1829	NIFS PROTEIN
NIFS_ANASP	398	1908	NIFS PROTEIN
US45 LACLA	39%	1956	SECRETED 45 KD PROTEIN PRECURSOR
US45 LACLA	99%	2293	SUCREMED 45 KD PROTEIN PRECIRSOR
ob io_bilobili	,,,,		SAMETER AS AN INVISIA PARCASAN
BIO16.02 Unclas	sified		78 genes
BI016.02 Unclas	sified	4.5	78 genes
BIO16.02 Unclas	sified 33%	48	78 genes LACTOCOCCIN A IMMUNITY PROTEIN
BI016.02 Unclas LCIA_LACLA OSMC_ECOLI	33% 48%	48 69	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA	33% 33% 48% 97%	48 69 85	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU	aified 33% 48% 97% 45%	48 69 95 107	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI	33% 48% 97% 45% 33%	48 69 85 107 113	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG BACSU	33% 48% 97% 45% 33% 31%	48 69 85 107 113 131	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILLI ASSOCIATED PROTEIN)
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA	33% 48% 97% 45% 33% 31% 48%	48 69 95 107 113 131 164	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOIIIJ ASSOCIATED PROTEIN) PUTTATIVE ANUDACE (FC 3 5 1 4)
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBD_BACSU ACPD_BCOLI JAG_BACSU AMID_MORCA	sified 33% 48% 97% 45% 33% 31% 48%	48 69 95 107 113 131 164	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4)
BIO16.02 Unclass LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU	33% 48% 97% 45% 33% 31% 48% 62%	48 69 85 107 113 131 164 166	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PTT112-LIKE PROTEIN
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI	33% 48% 97% 45% 33% 31% 48% 62% 42%	48 69 85 107 113 131 164 166 168	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOIIIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1)
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI	sified 33% 48% 97% 45% 33% 31% 48% 62% 42% 40%	48 69 85 107 113 131 164 166 168 225	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN
BIO16.02 Unclass LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU	33% 48% 97% 45% 33% 31% 48% 62% 42% 42% 35%	48 69 85 107 113 131 164 166 168 225 299	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11,1,-)
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI	33% 48% 97% 45% 33% 45% 31% 48% 62% 42% 42% 42% 35%	48 69 85 107 113 131 164 166 168 225 299 384	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARLIER PROTEIN PHOSPHODIESTERASE) (ACP PHOSPHODIESTERASE)
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACCP_ECOLI JAG_BACSU AMID_MORCA Y2DD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACCP_ECOLI SIME_METLA	33% 48% 97% 45% 33% 31% 48% 62% 42% 42% 35% 39%	48 69 95 107 131 164 166 225 299 384 406	<pre>78 genes LACTOCOCCIN &amp; IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN &amp; SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (POILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MUNIAUMETE XINASE, (EC 2.1.1.3)</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI KIME_METJA	33% 33% 48% 97% 45% 33% 31% 48% 62% 42% 35% 32% 31% 31% 31% 32% 31% 31% 31% 31% 31% 31% 31% 31	48 69 85 107 113 131 164 166 168 225 299 384 400	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHON PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11,1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36)
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI XIME_METJA XIME_METJA	<b>sified</b> 33% 48% 97% 33% 31% 48% 42% 42% 42% 39% 31% 39% 31% 39%	48 69 85 107 113 131 164 166 168 225 299 384 406 408	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOIIIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36)</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACCP_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACCP_ECOLI XIME_METJA EMRU_BACSU BMRU_BACSU	<b>sified</b> 33% 48% 97% 45% 33% 31% 48% 62% 40% 35% 39% 31% 29% 27%	48 69 85 107 113 131 164 166 225 299 384 406 408 424	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIM INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIM_AGRVI PHN0_ECOLI TPX_MYCTU ACPD_ECOLI XIME_METJA XIME_METJA XIME_METJA MRU_BACSU MRSA_HAEIN	<b>sified</b> 33% 48% 97% 45% 33% 31% 62% 40% 52% 40% 39% 39% 29% 27% 46%	48 69 85 107 113 131 164 166 168 225 299 384 406 408 424 433	<pre>78 genes LACTOCOCCIN &amp; IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN &amp; SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11,1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36)</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI KIME_METJA XIME_METJA MRSA_HAEIN COLL_HSVS7	<b>sified</b> 33% 48% 97% 45% 33% 42% 40% 35% 39% 29% 27% 40% 35% 39% 29% 27% 46% 37%	48 69 85 107 113 164 166 225 299 384 406 408 424 433 478	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOIIIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PUTATIVE AMIDASE (EC 3.5.1.4) PHOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN HOMOLOG COLLAGEN-LIKE PROTEIN</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACCPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACCPD_ECOLI XIME_METJA KIME_METJA BMRU_BACSU MRSA_HAEIN COLL_HSVS7 FASG_RHOPA	zified 33% 48% 97% 45% 33% 31% 42% 42% 42% 42% 35% 39% 31% 29% 27% 46% 37% 30%	48 69 85 107 113 131 164 166 229 384 406 408 424 433 478 491	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 3.5.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN MRSA PROTEIN HOMOLOG COLLAGEN-LIKE PROTEIN IN AZU 5'REGION (ORF1)</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI KIME_METJA KIME_METJA KIME_METJA KIME_METJA KIME_METJA KIME_METJA KIME_METJA COLL_HSVS7 FAS6_RHOFA EPUA_STRPN	<b>sified</b> 33% 48% 97% 45% 33% 31% 62% 40% 39% 39% 39% 27% 46% 39% 30% 40%	48 69 85 107 113 131 164 166 168 225 299 384 406 408 424 433 478 491 533	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11,1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36)
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI KIME_METJA BMRU_BACSU MRSA_HAEIN COLL_HSVS7 FAS6_RHOFA EPUA_STRPN XYLH PSEPU	zified 33% 48% 97% 45% 33% 62% 42% 40% 35% 39% 29% 27% 46% 35% 39% 29% 27% 46% 35% 30% 40% 35% 39% 40% 42% 40% 42% 42% 42% 42% 42% 42% 42% 42	48 69 85 107 113 164 166 168 225 299 384 406 408 424 433 478 491 533 5566	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOIIIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PUTATIVE AMIDASE (EC 3.5.1.4) PHONO PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN MRSA PROTEIN HOMOLOG COLLAGEN-LIKE PROTEIN HYPOTHETICAL PROTEIN IN AZU 5'REGION (ORF1) EPUA PROTEIN 4-OXALOROTONATE TAUTOMERASE (EC 5.3.2)</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_ECOLI LCND_LACLA CCBB_ECOLI JAG_BACSU ACPD_ECOLI JAG_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI XIME_METJA BMRU_BACSU MRSA_HAEIN COLL_HSVS7 FAS6_RHOFA EPUA_STRPN XYLH_PSEPU STA FCOLI	sified 33% 48% 45% 33% 31% 62% 42% 42% 43% 62% 43% 52% 39% 31% 40% 33% 40% 37% 40% 37% 40% 37% 42% 43% 43% 43% 43% 43% 43% 43% 43	48 69 85 107 113 164 166 168 225 299 384 406 408 424 433 478 491 533 560	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN MEVALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN HYDOTHETICAL PROTEIN IN AZU 5'REGION (ORF1) EPUA PROTEIN 4-OXALOCROTORNATE TAUTOMERASE (EC 5.3.2) STREPEOTHELICUN ACCTVLITAMISEPEACE (FC 3.3)</pre>
BIO16.02 Unclas LCIA_LACLA OSMC_BCOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI TPX_MYCTU ACPD_ECOLI XIME_METJA MRU_BACSU MRSA_HAEIN COLL_HSVS7 FASG_RHOFA EPUA_STREN XYLH_PSEPU STA_ECOLI UNUE ASTREN	sified 33% 48% 97% 45% 33% 48% 62% 42% 40% 35% 29% 27% 30% 31% 30% 30% 31% 30% 31% 31% 29% 31% 31% 31% 31% 31% 31% 31% 31	48 69 85 107 113 164 166 225 299 384 406 408 424 433 478 433 478 533 566 580	<pre>78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) JAG PROTEIN (SPOIIIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PETIL2-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN PROBABLE THIOL PEROXIDASE (EC 1.11.1) ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36) MEVALONATE KINASE (EC 2.7.1.36) MEXALONATE KINASE (EC 2.7.1.36) BMRU PROTEIN MESA PROTEIN HOMOLOG COLLAGEN-LIKE PROTEIN IN AZU 5'REGION (ORF1) EPUA PROTEIN 4-OXALOCROTONATE TAUTOMERASE (EC 5.3.2) STREPTOTHRICIN ACETYLITRANSPERASE (EC 2.3)</pre>
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PHNA_ECOLI	47%	2312	PHNA PROTEIN
TOXB_CLODI	27%	2285	TOXIN B
RGG_STRGC	19%	2268	RGG PROTEIN
GSPA_ECOLI	28%	2239	PUTATIVE GENERAL SECRETION PATHWAY PROTEIN B
YHHF_ECOLI	30%	2219	21.7 KD PROTEIN IN FTSY-NIKA INTERGENIC REGION
RGG_STRGC	31%	2217	RGG PROTEIN
PROTEIN III)			
PQQE_ACICA	308	2216	COENZYME PQQ SYNTHESIS PROTEIN E (COENZYME PQQ SYNTHESIS
NARA_BACSU	278	2213	NARA PROTEIN
STA_ECOLI	31%	2123	STREFTOTHRICIN ACETYLTRANSFERASE (EC 2.3)
ARCL_ECOLI	45%	2090	CARBAMATE KINASE-LIKE PROTEIN 1
HIT_BACSU	418 418	2057	HIT FRUTEIN
DC4C_ACICA	35%	2032	4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44)
FIBI_ADE41	508	2027	FIBER PROTEIN I
RGG_STRGC	198	2024	RUG PROTEIN
BLTD_BACSU	538	7330	TRANSACETILASE BETD (EC 2.3.1)
LAXC_LACLA	50%	1979	LACX PROTEIN, CHROMOSOMAL
YFF1_MYCMY	448	1947	HYPOTHETICAL PROTEIN MGI30
SUN_BACSU	338	1938	SUN PROTEIN (FRAGMENT)
PROC_ECOLI	308	1933	PIRKULINE-5-CARBOATLATE REDUCTASE (EC 1.5.1.2)
PFS_DALIN	. 4.29	1022	PPS PROTEIN HONOLOG
PHPB_ECOLI	348	1000	PRPB PROTEIN
PHDD RCOLT	338	1045	DUDD DDODETN
AYNC_CAUSA	329	1002	ACETTE ESTERASE (EC 3.1;-)
DEDA_BCOLL	229	1900	ACTIVITY TOTTAGE (DC 2 1)
BMRU_BACSU	201	1706	DEDA DECRETA (DSC 1 DECRETA)
SMPB_ENTFA	202	1226	SMALL PROTEIN B HOMODOG
MDD DWDD1	638-	1757	CARDADAID RINADDIJIND FRUIDIN I SMALL DROTFIN B HOMOLOG
NGG_STRGC	40%	1723	CODDAMAGE NIMACE LIVE DECORIN 1
DAAL THELA	270	1712	DACA PROTEIN, CHRONOSOMAD
LANC LACLA	- 208	1671	LACY DECEMPTIN CURCINGE WADE REDUCTEDE (EC 1)
PROG_DACOU	379	1652	POINTAR NAUVELINE DIOSIMINESIS LULIEN LV90
DVCC DACCH	278	1610	DURATIVE SALERASE/DIFRSE 2 (DC 5.1.+)
DC4C_ACICA	348	15/5	DEPARTUR REPRESENTATION DECARDONILASE (EC. 4.1.1.44)
DPRA_SINTS	248	1530	$A_{\rm CARRONNEL}$ A DIFFERENCE DECARRON A CONTRACT (EC. 1.1.1.217)
ARLD_DACSU	403	1650	RUEADIVE DIVENDENT AVONOL-4-REDUCENCE (EC. 1. 1. 1. 218)
POU_LISSE	214	1414	PROTEIN POU PRECORSOR (INVASION-ASSOCIATED PROTEIN)
FMCH_BACNO	315	1408	POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FINC (SEROGROUP HI)
FIBP_ADEB3	29%	1393	FIBER PROTEIN
2DKG_CORSP	40%	1200	2,5-DIKETO-D-GLOCONIC ACID REDUCTASE (EC 1.1.1)
GID_BACSU	69%	1255	GID PROTEIN (FRAGMENT)
GTD DAGGU	600	1055	CID DROBETH (BD3 CMENT)

Table 4. Ability of of L. lactis for growth on different carbon sources

Carbon source	Catabolic genes (position on genome map)	Transport genes (position on genome map)	Experimental growth (reference)
glucose	glycolysis genes		+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
fructose	fructokinase (1519 kb), glucoso-6P isomerase (2230 kb)	PTS (984 kb and 1747 kb)	+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
N-acetyl glucosamine	glucosamine-fructoso-6P aminotransferase (1032 kb)		+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
sucrose		PTS (435 kb)*	- (de Vos 1996)#
mannose	mannose-6P isomerase (777 kb)	PTS (1748 kb)	+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
maltose	maltodextrin glucosidase (700 kb and 1526 kb), $4-\alpha$ -glucanotransferase (692 kb)		+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
trehalose		PTS (435 kb)*	+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
lactose	$\beta$ -galactosidase (2040 kb)	lactose permease (2048 kb)	+ (de Vos 1996) <sup>#</sup>
galactose	gal operon (2045 kb)		+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
ribose	rbs operon (1685 kb)	ribose transport protein (1686 kb)	+ (Bardowski et al. 1994) - (de Vos 1996) <sup>#</sup>
xylose	xyl operon (1550 kb)		
cellobiose	glucosidase (186 kb and 1521 kb), 6-Ρ β-glucosidase (419 kb, 830 kb and 1490 kb)	PTS (175 kb, 416 kb and 830 kb)	+ (Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
salicin	6-P $\beta$ -glucosidase (1722 kb)		+(Bardowski et al. 1994) + (de Vos 1996) <sup>#</sup>
arbutin	See cellobiose	See cellobiose	+ (Bardowski et al. 1994)
esculin	See cellobiose	See cellobiose	+ (Bardowski et al. 1994)
gluconate	6-P-gluconate gehydrogenase (606 kb), gluconate kinase (2253 kb)	gluconate permease (2246 kb)	
mannitol	mannitol-1P 5-dehydrogenase (33 kb)	PTS (29 kb and 32 kb)	

<sup>#</sup>For the strain mg1363 with the plasmid pMG820. \*Presumably a trehalose specific system.