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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. subtilis, L.lactis represents a simplified system and is, therefore, potentially more amenable for detailed 476 477 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
 (10): 2885–2893
- 707

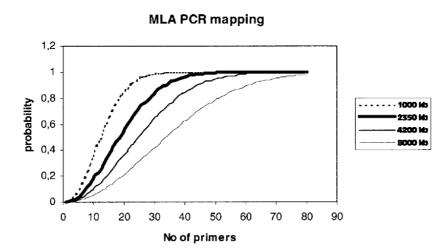


Figure 1. Probability of successful amplification in MLA PCR as a function of the number of oligonucleotides used in the same mixture. The calculation was done by generating the results of 10,000 independent random experiments and averaging these results. The longest distance between primers still allowing 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).

Α

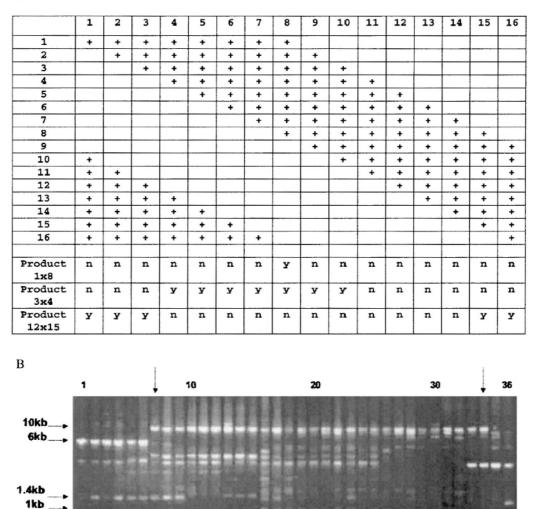


Figure 2. MLA PCR procedure. (A) The table illustrates a theoretical experiment with a total of 16 (M) primers, where each reaction mixture contains 8 (N) primers. The numbers at the top designate reaction mixtures, the numbers on the left designate individual primers, the '+' sign indicates presence 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 N₁ and N₂ are the first and the last positive reaction, respectively, the primers giving the product will be: P₁=N₁, P₂=N₂ - N+1, if N₂>N₁ (the cases 1×8 and 3×4), or P₂=M+N₂-N+1, if N₂<N₁ (the case 12×15). (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 identify the primers which gave the 10 kb fragment. These primers are P₁=N₁=7, and P₂=N₂ - N+1=34-32+1=3.



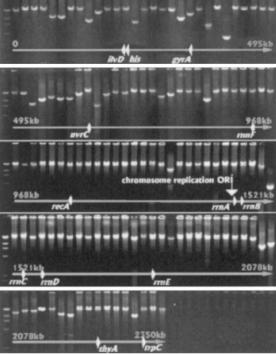
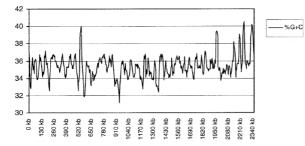


Figure 3. Whole-genome PCR amplification of the L. lactis IL1403 chromosome. 266 oligonucleotides were used in 133 LR PCR reactions to amplify the entire genome. Correspondence of the sizes of amplified fragments and the physical map predicted from the sequence (Figure 9) indicates the correctness of sequence assembling. Left slot on each panel shows size marker (DNA of phage λ 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.





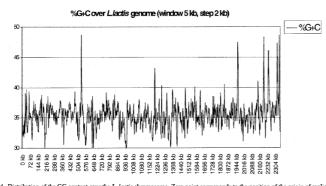
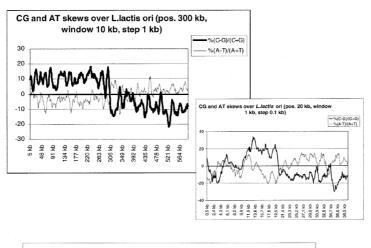


Figure 4. Distribution of the GC-content over the *L. lactis* chromosome. Zero point corresponds to the position of the origin of replication. Top panel: a sliding window of 20 kb and a step of 5 kb were used. Bottom panel: a sliding window of 5 kb and the step of 2 kb were used. The peaks near coordinates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



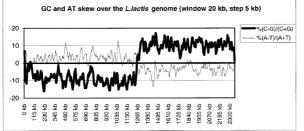
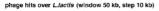


Figure 5. GC and AT skew distribution over the L. lactis genome. Top panel: a sliding window of 10 kb and step of 1 kb were used. Inset: a sliding window of 1 kb and step of 0.1 kb, were used. In both cases a region near the *dnAd* gene was analysed. Change of the skew distribution sign indicates the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

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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.

715



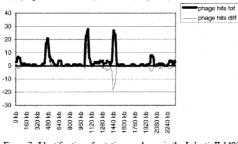


Figure 7. Identification of putative prophages in the *L*. lactis IL1403 genome. The distribution shows the number of phage protein hits detected with a sliding window of 50 kb with a step of 10 kb, over the whole genome. Total number of hits on both strands is shown by bold line. Thin line shows difference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



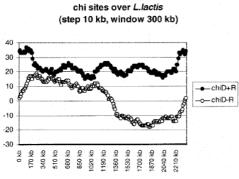
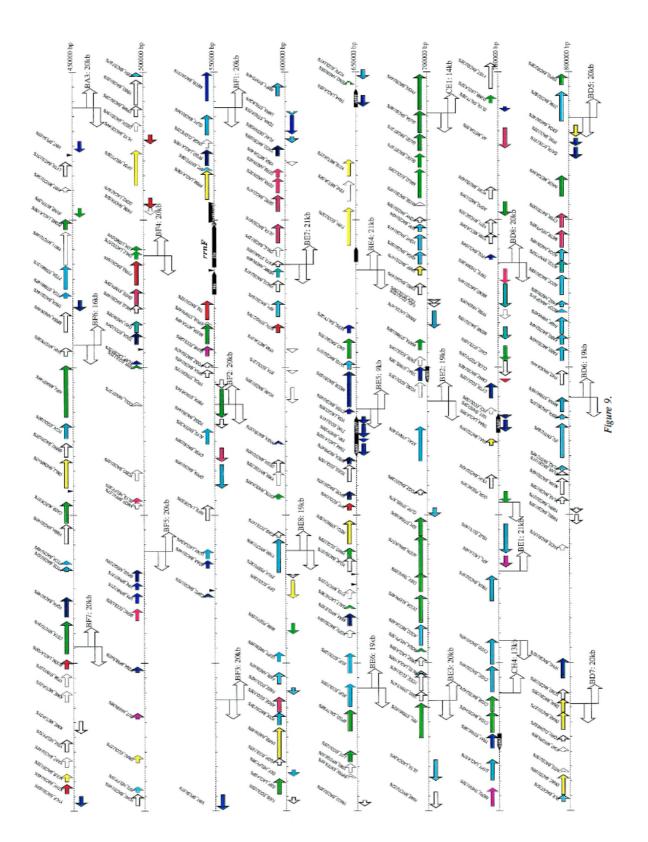
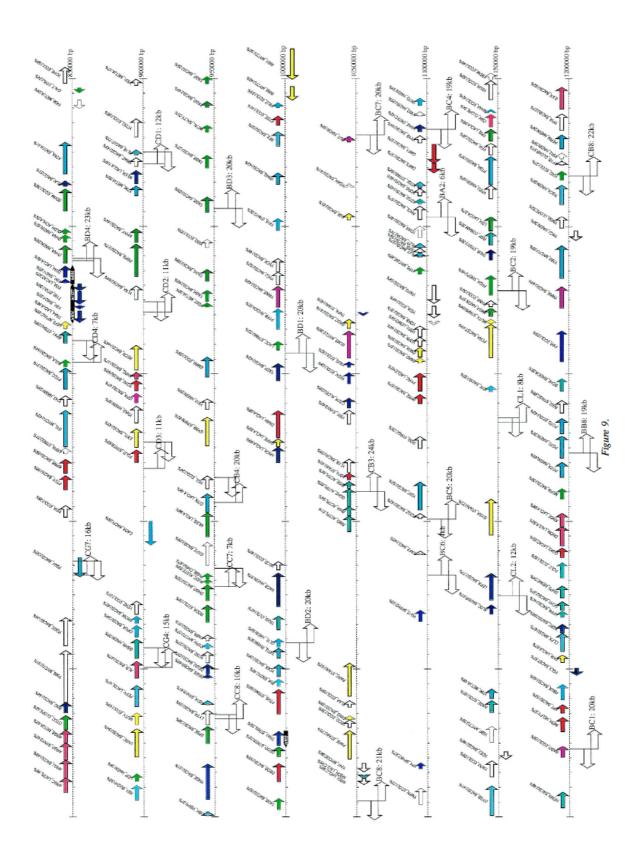


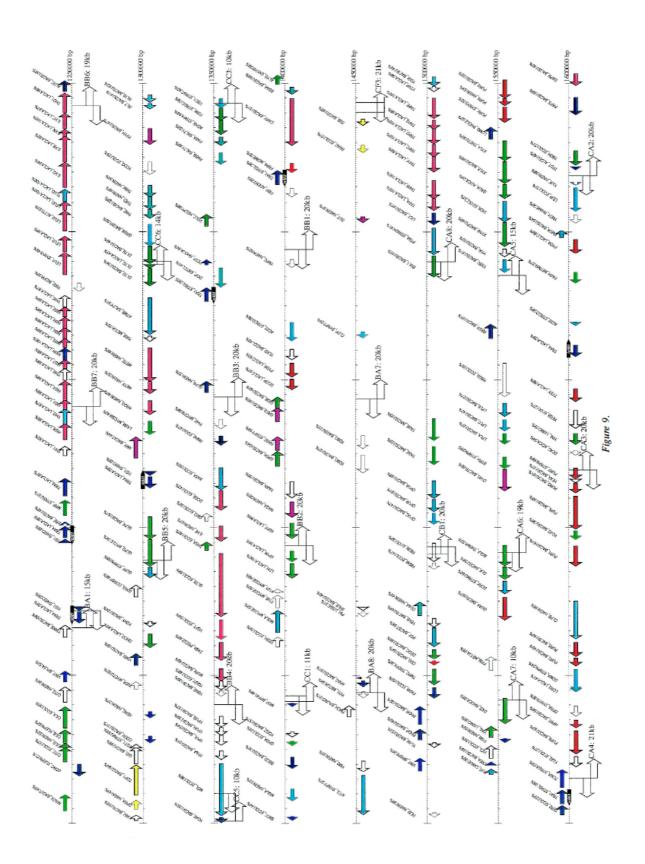
Figure 8. Distribution of chi-sites over the *L. lactis* genome. The distribution represents the number of chi sequences detected with a sliding window of 300 kb with a step of 10 kb, over the whole genome. Filled circles show total numbers of chi-sites in the window, open circles show the difference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

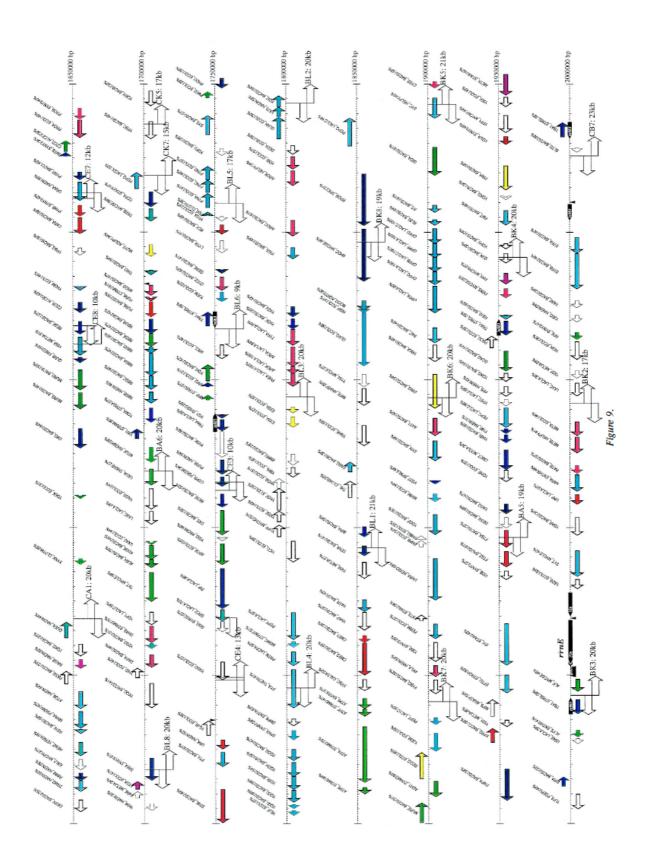
Figure 9. Linear representation of the Llactis IL1403 genome.

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.









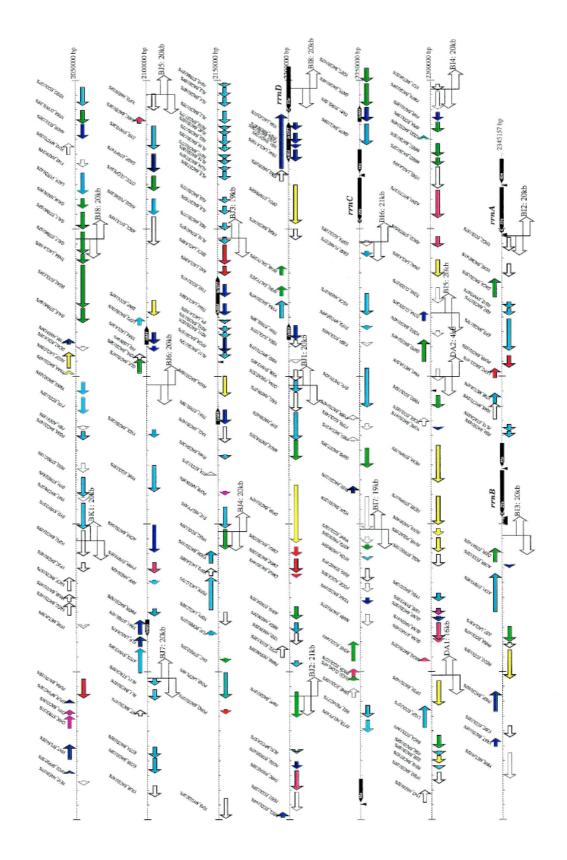
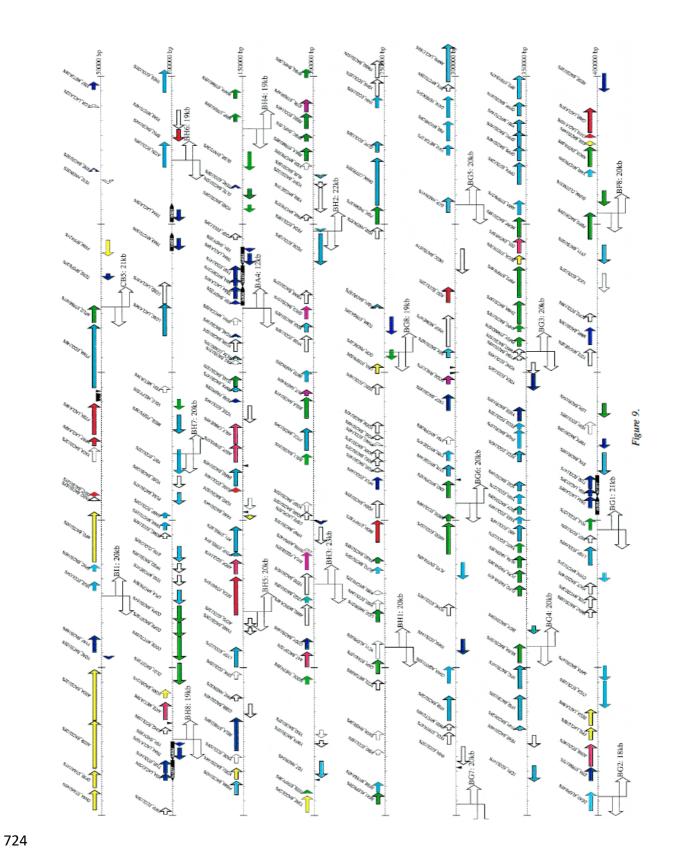


Figure 9.



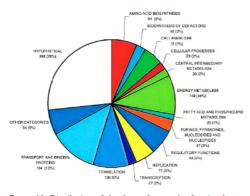


Figure 10. Distribution of the detected genes by functional categories. Colours designating different categories are defined in the legend of Figure 9. The number and the percentage of homology hits to SwissProt are indicated for each category. Classification method is presented in the text.

А

aaattttcggcttttttGTTACATTaactgAttaTTTgCGTATAgtct AG	TATG comGA
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consensus GTTACATTnnnnnAnnnTTTTCGTATAnnnn AGT	,
В	
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MITNFD	LYRWKKA
ctgacaaagctgtcagtaaaaaatGGAGGaattATGataacaaattttgatt	tatatcgttggaaaaaagct

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 λ -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 λ -clones	122
Average insert length (kb)	15.6
Number of gel readings from λ -inserts	622
Average read length (bp)	409
Total characters from λ -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 Genera			2 genes			
DHSS_SYNP1	29%	485	SOLUBLE HYDROGENASE, SMALL SUBUNIT (EC 1.12)			
PATB_BACSU	57%	1974	PUTATIVE AMINOTRANSFERASE B (EC 2.6.1)			
BI001.02 Aromatic amino-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-DEOXYHEPTONATE 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 (SOMERASE (EC 5.3.1.24)			
TRPC LACLA	100%	1495	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)			
TRPD LACLA	100%	1496	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)			
TRPG LACLA	998	1497	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)			
TRPE LACLA	100%	1498	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)			
AROD_BACSU	37%	1686	3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)			
PHEA_LACLA	100%	1780	PREPHENATE DEHYDRATASE (EC 4.2.1.51)			
AROK LACLA	100%	1781	SHIKIMATE KINASE (EC 2.7.1.71)			
AROA_LACLA	94%	1782	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYL/TRANSFERASE (EC 2.5.1.19)			
TYRA LACLA	90%	1783	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)			
AROC BACSU	61%	1790	CHORISMATE SYNTHASE (EC 4.6.1.4)			
AROB HELPY	398	1794	3-DEHYDROQUINATE SYNTHASE (EC 4.6.1.3)			
YDIB_ECOLI	37%	1795	HYPOTHETICAL 31.2 KD PROTEIN IN LPP-AROD INTERGENIC REGION			
AROG BACSU	32%	2261	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)			
Into Diroto	000	0001				
BIO01.03 Aspart			19 genes			
AAT2_METJA	36%	57	PUTATIVE ASPARTATE AMINOTRANSFERASE 2 (EC 2.6.1.1)			
ASSY_SYNY3	57%	125	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)			
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	88\$	1170	HOMOSERINE KINASE (EC 2.7.1.39)			
METF_HAEIN	32%	1279	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)			
METE_HAEIN	46%	1281	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATEHOMOCYSTEINE			
METHYLTRANSFER						
DAPB_BACSU	50%	1600	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)			
DAPA_BACSU	46%	1661	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)			
DHAS_STRMU	75%	1663	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)			
AAT1_BACSU	50%	1877	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)			
METB_HELPY	41%	1976	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)			
META_ECOLI	46%	1977	HOMOSERINE O-SUCCINYLTRANSFERASE (EC 2.3.1.46)			
PYRH_SYNY3	56%	2067	URIDYLATE KINASE (EC 2.7.4)			
THRC_PSEAE	38%	2153	THREONINE SYNTHASE (EC 4.2.99.2)			
ASNH_MYCTU	37%	2292	PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC			
6.3.5.4)						
BIC01.04 Branch	hed cha	in famil	y 11 genés			
ILVX_BACSU	52%	1199	ACETOLACTATE SYNTHASE (EC 4.1.3.18)			
LEU1_SYNY3	45%	1238	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)			
LEU3_LACLA	998	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)			
ILVD_LACLA	988	1244	DIHYDROXY-ACID DEHYDRATASE (EC 4.2.1.9)			
ILVB_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)			

ILVE_HAEIN	67%	1320	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
BIO01.05 Gluta	umate fa	mily	21 genes
ARLY CAMJE	45%	126	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
ARGE ECOLI	26%	557	ACETYLORNITHINE DEACETYLASE (EC 3.5.1.16)
ARGC_LACPL	48%	802	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
ARGJ BACSU	49%	803	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35)
ARGD_SYNY3	428	804	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
ARGB_METJA	42%	805	PROBABLE ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
AHRC_BACSU	378	880	ARGININE HYDROXIMATE RESISTANCE PROTEIN
MURI_BACSU	46%	1310	GLUTAMATE RACEMASE (EC 5.1.1.3)
	40%	1312	TABA PROTEIN
TABA_PSESZ			
YGFT_ECOLI	34%	1313	HYPOTHETICAL 69.7 KD PROTEIN IN KDUI-LYSS INTERGENIC REGION
GLTB_ECOLI	39%	1316	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
DCEB_ECOLI	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	46%	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 Histi	dine fa	mily	9 genes
PT1P_ECOLI	278	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)
H1SX_LACLA	98%	1229	
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			PROFESSION CARDENALITATION - 5-ANTINOTATION CONSTRUCTION CARDONALIDE REBOTIDE
HIS6_LACLA	988	1234	HIGE BROWEIN (CYCLAGE)
HISC_LACLA	998	1235	HISF PROTEIN (CYCLASE)
			PROSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19) /
PHOSPHORIBOSIL	-WIP PI	ROPHOSPH	OHYDROLASE (EC 3.6.1.31)
BIO01.07 Pyruv			2 genes
DDL_ENTHR	54%	339	D-ALANINED-ALANINE LIGASE (EC 6.3.2.4)
ALR_BACSU	43%	860	ALANINE RACEMASE (EC 5.1.1.1)
BIO01.08 Serin			10
	32%	¥ 463	12 genes
SERC_ECOLI			PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
GLYA_HELPY	30%	471	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
CYSK_BACSU	56%	524	CYSTEINE SYNTHASE (EC 4.2.99.8)
GLYA_BACSU	61%	589	SERINE HYDROXYMETHYLTRANSPERASE (EC 2.1.2.1)
SERC_BACCI	478	591	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
SERA_HAEIN	32%	592	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
SERB_HAEIN	42%		PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
CYSK_BACSU	53%	790	CYSTEINE SYNTHASE (EC 4.2.99.8)
CBH_CLOPE	34%	1147	
PFLA_HAEIN	50%		PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (EC 1.97.1.4)
CYSE_BACSU	58%	1900	
PKNS_MYCGE	35%	1936	PUTATIVE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1)
BTODO BTOOM	upoto o	E CORLOR	
BIOUZ. BIOSYNT	nESIS O	F COFACT	ORS, PROSTHETIC GROUPS, AND CARRIERS 40 genes
BIO02.01 Bioti	n		3 genes
BIOY BACSH		313	
BIOY_BACSH			
ACCD_SYNF7	53%	787	BIOY PROTEIN PRECURSOR ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA
(EC 6.4.1.2)	350		TABLE COMPATION CONDUCTION CONDUCT DISCONDERADE SUBURIT BETA
BIO02.02 Folic	acid		6 genes
HPPK_BACSU	42%	1164	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE
PYROPHOSPHOKIN	ASE (EC		
GCH1 BACSU		1164	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
DHPS_NEIME	34%		DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
FOLC_ECOLI	32%		FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
	40%		PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3)
PABA SALTY	50%	1346	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE
COMPONENT II (
BIC02.03 Heme	EC 4.1.3	3)	5 genes

none a 73% 42%	832 1151 1179 1605	NON-HAEM BROMOPEROXIDASE BPO-A1 (EC 1.11.1) PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC MAGNESIUM-PROTOPORPHYRIN IX MONOMETHYL ESTER OXIDATIVE CYCLASE FERROCHELATASE (EC 4.99.1.1)
26% 39% none a 73% 42%	1179	MAGNESIUM-PROTOPORPHYRIN IX MONOMETHYL ESTER OXIDATIVE CYCLASE
39% none ai 73% 42%		
39% none ai 73% 42%		
none a 73% 42%	1605	FERROCHELATASE (EC 4.99.1.1)
none a 73% 42%		
738 428		0 genes
738 428		
42%	732	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
	735	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE
/ 2-02		RATE DECARBOXYLASE (EC 4.1.1.71)
44%	1613	
70%	1714	PROBABLE MENAQUINONE BIOSYNTHESIS METHLYTRANSFERASE (EC 2.1.1
pterin		0 genes
enate		1 genes
138	1464	PANTOTHENATE KINASE (EC 2.7.1.33)
ine		0 genes
vin		5 genes
51%	1020	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4)
548	1021	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
50%	1022	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3.4-DIHYDROXY-2-BUTANONE
	1000	
		6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
585	T138	RIBOFLAVIN KINASE (EC 2.7.1.26)
		doxin, and glutathione 5 genes GLUTATHIONE REDUCTASE (EC 1.6.4.2)
		THIOREDOXIN REDUCTASE (EC 1.6.4.2)
36%	1691	THIOREDOXIN REDUCTASE (EC 1.6.4.5)
e		10 genes
26%	165	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
38%	483	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
12%	1092	
398		THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
88		PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7,4.7)
348		HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
		INDOLE-3-PYRUVATE DECARBOXYLASE (EC 4.1.1.74)
		HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
16% 10%	2109 2296	PYRUVATE OXIDASE (EC 1.2.3.3) HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION
55%	1107	
LOPE		73 genes
Ag. 14-	oprote	ins, and porins 29 genes
28 28	129	HYPOTHETICAL 30.7 KD LIPOPROTEIN IN GLNQ-ANSR INTERGENIC REGION
0.0	147	MIDAMINICE_DELEACEN DECOMPANY DECOMPOSE (136 VE CURRADE DECOMPANY)
		MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) WALL-ASSOCIATED PROTEIN PRECURSOR
		WALL-ASSOCIATED PROTEIN PRECURSOR TRYPSIN-RESISTANT SURFACE T6 PROTEIN PRECURSOR
		O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN REBA
		OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR (PLP3)
		OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)
88		28 KD OUTER MEMBRANE PROTEIN PRECURSOR
378	318	HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION
7%	370	HYPOTHETICAL 38.5 KD LIPOPROTEIN IN ADA-OMPC INTERGENIC REGION
10	412	ONDONE OF DUARTON DOORDEN & HOUSE OF
		CARBON STARVATION PROTEIN A HOMOLOG LIPOPROTEIN SPR PRECURSOR
		60 KD INNER-MEMBRANE PROTEIN
		CRTK PROTEIN
		PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99)
	pterin enate 13% ine vin 51% 54% 50% 58% 58% 58% 56% 56% 56% 56% 56% 56% 56% 56% 56% 56	chate 13% 1464 ine 1020 51% 1020 54% 1021 50% 1022 70% 963 56% 1022 70% 963 56% 1691 20 1464 103% 1022 70% 963 56% 1691 20 1400 56% 1691 20 148 1092 198 128 1292 138 1292 19% 1291 18% 1292 18% 1292 19% 1292 10% 2296 210% 107 COPE 228 128 129 19% 152 19% 152 19% 152 19% 152 19% 152 147

SPSE_MACSU 368 906 STAGE V STOQULATION PROFENT & SPST_MENU 318 121 MURAMIDABE-RELEASED PROFENT PRECURSOR (136 KD SURFACE PROFEIN) SURFACE 329 SURFACE CAVCORDERIN CLANNEL DENOIG PROTEINSOR ADMES_STREA 68 137 ADMESSITI S PRECURSOR (SALIVA-EINDING PROFEIN) DAMES_STREA 68 1347 ADMESSITI S PRECURSOR (SALIVA-EINDING PROFEIN) DIALES_STREA 68 1460 MURAMARE LLOPROFEIN INE PRECURSOR (MERDEAAME PROFEIN) DIERLEGOLI 318 1622 HYPOTHETICALI IS6.SKD LINOPERNEN IN HIPB-UXAB INTERGENIC DERION PRECURSOR (ORT) CATION FEFLUX SYSTEM PROTEIN C2CD CATION FEFLUX SYSTEM PROTEIN C2CD CALLACU 308 1646 CATION FEFLUX SYSTEM PROTEIN C2CD CATION FEFLUX SYSTEM PROTEIN C2CD CALACU 307 172 MURAMALDASE-RELEARED PROTEIN PROTEIN C3 MURAMARCSU CALACU 308 360 PENTICILLIN-BIDING PROTEIN C3 MURAMARCSU CALACU 398 340 UDP-N-ACETYLMURAMYL-D-GLUTAMYL-2, 6-DIAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMINOPINELATE-D-DAMIN	WAPA_STRMU	26%	682	WALL-ASSOCIATED PROTEIN PRECURSOR
UDST_GETUAL 328 915 FOUNTIVE POTABLINE CHANNEL PROFEDEN PROFEND RELEDING (13 6 NO SURFACE PROFEIN) CDSD_BEVIAL 318 1239 SURFACE GLYCOMPOTEIN CDSP HOMOLOG PROCESSION CDSD_BEVIAL 318 1239 SURFACE GLYCOMPOTEIN CDSP HOMOLOG PROCESSION CDSD_BEVIAL 318 1234 238 (STRAC) 764 1346 23 NO MEMBERARE REDICTION IN DEAL STREED (COLOR OF INTERCESSION CDSD_BEVIAL 313 1622 MICHANDER REDICTION IN DEAL STREED (COLOR OF INTERCESSION 136 1622 CALLAR LANSI 374 1723 MURANIDASE RELEASED PROFEIN CICCU 276 276 CALLAR LANSI 374 1723 MURANIDASE RELEASED PROFEIN CICCU 28 20 DEOLO, COLTANT SECURAS APPOLICUE/ON 2 20 20 20 20 MURA, ESTRA 374 172 MURANIDASE RELEASED PROFEIN SECURSOR (COLOR AND ADDING PROFEIN SECURSOR (COLOR ADDING PROFEIN SE	CAIC_ECOLI	26%	731	PROBABLE CROTONOBETAINE/CARNITINE-COA LIGASE (EC 6.3.2)
NHP_STRNU 318 121 MURANIDASE-RELEASED PROFEIN FRECURENC (136 KD SUKEACE PROFEIN) NHP_STRNA 324 129 SUKEACE GUIVEORHOETIC COSP HONDALD FRECURENC (NOFI) NHP_STRNA 634 137 ADMESIN B PRECURENC (SALIVA-DIKUNG PROFEIN) NHP_STRNA 634 1346 ADMESIN B PRECURENC (SALIVA-DIKUNG PROFEIN) NHP_STRNA 334 1260 MURANIDASE-RELEASED FRACURENC (SALIVA-DIKUNG PROFEIN) NHP_STRNA 334 1224 MURANIDASE-RELEASED PROFEIN (SALIVA-DIKUNG PROFEIN) NUBEL_COLL 334 1264 CATION FFLUX SYSTEM PROFEIN (SALIVA-DIKUNG PROFEIN) SKALANDARE 334 1264 ADMESIN B PRECURENC (SALIVA-DIKUNG PROFEIN) SKALANDARE 335 1264 ADMESIN B PRECURENC (SALIVA-DIKUNG PROFEIN) SKALANDARE 334 1346 PENICILLIN-BINDING PROFEIN A (PROFEIN 124 SKALANDARE 334 1346 PENICILLIN-BINDING PROFEIN A (PROFEIN) SKALANDARE 334 1346 PENICILLIN-BINDING PROFEIN A (PROFEIN) SKALANDARE 454 334 PENICILLIN-BINDING PROFEIN A (PROFEIN) SKALANDARE 454 <td></td> <td></td> <td></td> <td></td>				
CD9_BENGA 328 1299 SUBFACE GLVCOMPOTEIN CD9 HONOLOG PERCURSOR (GALLVA-EDUNIG POPULING PROTEIN) D29K_STRDC 764 1346 39 KU MEMBRANE PROTEIN IN PSA 5'REGION (GREI) D29K_STRDC 764 1346 39 KU MEMBRANE PROTEIN IN PSA 5'REGION (GREI) D29K_STRDC 764 1346 MEMBRANE PROTEIN INC THE CHECKLENGE (MEMBRANE PROTEIN CLUB INTER_COLL) D10K_STRDC 134 1174 1174 MEMBRANE PROTEIN CLUB APECURSOR (SALIVA-DINDING PROTEIN) C20L_ALGEDINGO (SALIVA-DINDING PROTEIN PROTEIN STRDGER (116 KU SURFACE PROTEIN) 30 30 314 B1003.02 MURCIE RECOLUS AND PROTEIN STRUCTURE COLUMNYL-2(A-DINDING PROTEIN) 315 1174 MEMBRANE ALL DUP-ARACEPTILALINGON (SALIVA-DINDING PROTEIN) B1003.02 MURCIE RECOLUS AND PROTEIN STRUCTURE COLUMNYL-2(A-DINDINDING PROTEIN) 316 PENICILLIN-BINDING PROTEIN 2 B1003.02 MURCIE RECOLUS AND STRUCTURE COLUMNYL-2(A-DINDINDING PROTEIN) 316 PENICILLIN-BINDING PROTEIN 2 B1003.02 MURCIE RECOLUS AND STRUCTURE COLUMNYL-2(A-DINDINDING PROTEIN) 316 PENICILLIN-BINDING PROTEIN 2 B1004.02 MURCIE RECOLUS AND STRUCTURE COLUMNYL PLANE				
ADDES_STRIAM 698 1347 ADDESTING PRECUMPOR (SALIVA-EINDING PROTEIN) PERSENTED 766 1347 ADDESTING PRECUMPORTEIN IN PERS PRECIM (ORFI) THEC_TREPA 366 1460 MERRENE LINDPROTEIN IN PERS PRECIM (ORFI) THEC_TREPA 366 1460 MERRENE LINDPROTEIN THEC PRECUMBER (MERRENE PROTEIN C) LINDPROTEIN LINDPROTEIN DEL FRECUMSOR THECENTIAL STRING 308 1460 MERRENE FRECUMSOR THECENTIAL STRING 308 1460 MERRENE LINDPROTEIN THE PRECUMBOR (136 KG SURFACE PROTEIN (SC ADDES STREA 308 1747 MERRENE LINDPROTEIN STRING (SC SURFACE PROTEIN (SC MERLETREN 308 1747 MERRENE ADD PPL/000 MERRENE (SC 23.1.7) BEODIO STREAM STREAM STREAM PROTEIN 22 BEODIO STREAM STR				
P29E_STROC 769 1349 29 KD NEMERARNE PROFENT IN DEAL STREETING (DEF) P29E_STROC 769 1349 1520 MERRENEL LIPOPROTEIN THRC THECONSON (MERRENE PROTEIN C) LPLA_BACSU 274 1526 LIPOPROTEIN LIPAL STREETING (DELTA) 156.5 DERE_STREE 374 1564 CATION EFFLUX SYSTEM PROTEIN CCCC MER_STREE 374 173 MUDANIDASE-BELARED PROTEIN CCCC MER_STREE 374 173 MUDANIDASE-BELARED PROTEIN CCCC MER_STREE 374 173 MUDANIDASE-BELARED PROTEIN CCCC STOD.20 MURCIE RECOLUS AND PROTEIN STREEMARD PROTEIN PROTEIN CARBOXYUNYLTERANSFERASE (EC 2.5.1.7) MURCEASU 391 100 DUP-N-ACCEYLINGANOVALANNINE 1-CARBOXYUNYLTERANSFERASE (EC 2.5.1.7) STRUE_STREE 316 PENCILLIN-BIDINE FROTEIN ACCENTANIC 4-DIALINODIMERASE (EC 2.5.1.7) MURCEASU 291 316 PENCILLIN-BIDINE FROTEIN ACCENTANIC 4-DIALINSFERASE (EC 2.5.1.7) PERP_STREE 228 316 PENCILLIN-BIDINE FROTEIN ACCA AUDICASING (EF 4.5.1.1.1) PERP_STREE 228 316 PENCILLIN-BIDINE FROTEIN ACCA AUDICASING (EF 4.5.1.1.1) PERP_STREE				
NHPC_TREPA 364 1460 MERNBARE LIFEOROTIN THE CHECKENSUE (MEMBERANE PROTEIN C) LIFLA LACU 374 1522 HYPOTHETICAL 136.5 KD LIFOPROTEIN IN HIFE-UKAD INTERGENIC BESCION FRECURSON (DRT) CALLARU 300 1646 CATION EFFLUX SYSTEM FROTEIN CCC BESCION FRECURSON (DRT) CALLARU 300 1646 CATION EFFLUX SYSTEM FROTEIN CCC BESCION FRECURSON (DRT) CALLARU 300 174 173 MURATIONAL SYSTEM FROTEIN CCC BESCION FRECURSON (DRT) DARES STREA 135 214 ADBESIN B PRECURSON (SALIVA-SINGHAR) DARES STREA 135 214 ADBESIN B PRECURSON (SALIVA-SINGHAR) DARES STREA 354 214 ADBESIN B PRECURSON (SALIVA-SINGHAR) DARES STREA 354 214 ADBESIN B PRECURSON (SALIVA-SINGHAR) DARES STREA 358 310 PROBACLE CUP-N-ACETYLGUIGONAMINE 1-CARBOXYVINILTRANSFERASE (EC 2.5.1.7) DREP, SARTEN 248 PENICILLIN-BIDINE FROTEIN 14 (PRECURSON (PRE 4) PERP, BACSU 288 940 UDP-N-ACETYLGUIGONAMINE 1-CARBOXYVINILTRANSFERASE (EC 2.5.1.7) MURA, ACICA 494 331 UDP-N-ACETYLGUIGONAMINE 1-CARBOXYVINILTRANSFERASE (EC 2.5.1.7) MURA, ACICA 494 328 PENICILLIN-BIDINGIN FROTEIN NGA </td <td></td> <td></td> <td></td> <td></td>				
LPLA_BACSU 278 1526 LIPOPROTEIN LPLA PECCUSOR UREK_EGOL 338 1626 HATOPORTEIN LPLA STSTEM PROTEIN IN HIPS-UXAD INTERGENIC REGION PRECURSOR (ORT) 378 1729 MURALIDASE-RELEASED PROTEIN FECUNSOR (136 KD SURFACE PROTEIN) RED_STRES 378 1379 MURALIDASE-RELEASED PROTEIN FECUNSOR (136 KD SURFACE PROTEIN) RED_STRES 358 116 ADRESING (SLALUA-BUNNING PROTEIN 32 RED_STREM 358 136 PROFILOSULIN-BIDING PROTEIN 32 RED_STREM 369 360 UDP-N-ACETYLGUCOSOMINE 1-CARBOXYUNYLTRANSFERASE (EC 2.5.1.7) RED_STREM 364 512 PRICILLIN-BIDING PROTEIN 40 (PB-2B) RED_STREM 348 360 PRICILLIN-BIDING PROTEIN 40 (PB-2B) RED_STREM 348 164 ROB STREM-DETERMINING PROTEIN 28 (PB-2.5.1.7) RED_STREM 348 169 PROCEILIN-BIDING PROTEIN 28 (PB-2.5.1.7) RED_ASTRO 548 120 PROCEILIN-BIDING PROTEIN 28 (PB-2.5.1.7) RED_ASTRO 548 140 PROCEILIN-BIDING PROTEIN 28 (PB-2.5.1.7.				
VIDER_ECOLI 338 162 HYPOTHETICAL 136.5 KD LIPOPROTEIN IN HIPB-UXAB INTERGENIC REGION FRECUNSOR (ORF) CATION EFFLUX SYSTEM PROTEIN CZCD CATION EFFLUX SYSTEM PROTEIN CZCD REP_STRU 178 173 MURALINASE-RELEASED PROTEIN PRECUNSOR (I36 KD SURFACE PROTEIN) BIODJ.02 Murcin seculus and peptidoglycan 23 genes BER_STRUM 593 111 PROMALE UDP-N-ACETYLALUCASMMILE 1-CARBOXYUNYULTRANSFERASE (EC 2.5.1.7) BER_STRUM 594 59 PENICILLIN-BIDINE PROTEIN 1A (PB-7.4) BER_STRUM 548 528 PENICILLIN-BIDINE PROTEIN 1A (PB-7.4) BER_STRUM 548 528 PENICILLIN-BIDINE PROTEIN 1A (PB-7.4) BER_STRUM 278 661 ROD SHARE-DETERMINING PROTEIN 1A (PB-7.4) BER_STRUM 278 662 PENICILLIN-BIDINE PROTEIN 1A (PB-7.4) BER_STRUM 278 662 PENICILLIN-BIDINE PROTEIN 2B BER_STRUM 278 678 PENICILLIN-BIDINE				
RESIGN FRECURSOR (ORFT) CCCL ALGEO OWER_STREM JOB Idda CATION EFFLUX SYSTEM PROTEIN C2CD MED_STREM JOB Idda ADESIM B PRECURSOR (JALCA DURING FROTEIN) BIOGJ.02 Murcin secculus and peptidoglycan 23 genes FROMARLE UDP-K-ACETYLOUCOSAMINE 1-CARBOXYLINULTRANSFERASE (EC. 2, 1, 1) BIOGJ.02 Murcin secculus and peptidoglycan 23 genes FROMARLE UDP-K-ACETYLOUCOSAMINE 1-CARBOXYLINULTRANSFERASE (EC. 2, 1, 1, 1) BINES.STREM JOB PROMARLE UDP-K-ACETYLOUCOSAMINE 1-CARBOXYLINULTRANSFERASE (EC. 2, 5, 1, 2) MURA_DASU JOB PROMARLE ULIN- BINDING PROTEIN 4 (EPE-1A) MURA_ALCIA 49 532 UDP-N-ACETYLULUNOSAMINE 1-CARBOXYLINULTRANSFERASE (EC. 2, 5, 1, 2) MURA_ALCIA 49 533 UDP-N-ACETYLULUNOSAMINE PROTEIN AD (EPE-1A) MURA_ALCIA 49 532 UDP-N-ACETYLULUNOSAMINE PROTEIN RODA MURA_BACSU 278 680 PENICILLIN-BINDING PROTEIN AD (EPE-1A) MURA_MARGUNU 44 6 680 PENICILLIN-BINDING PROTEIN AD (EPE-1A) MURA_MACULA 44 6 680 PENICILLIN-BINDING PROTEIN AD (EPE-1A) MURA_MACULA 44 700 SHAPE-OETERNINGMONTL-BACAGUNUTATIONAL (EPE-1A) MURA_MACULA 44 700 SHAPE-OETERNIN				
CZCU_ALACRU 30% 1646 CATION EFFLUX SYSTEM FOOTLIN CZCD KRE_ETRSU 37% 1729 MURANIDASE-RELEASED FAOTEIN FREEUNSOR (136 KD SURFACE FROTEIN) BIOD.302 Murcin secoluls and peptidoglycan 3 gencs MURA_BACSU 55% 311 FROGANEL UDP-N-ACETYLALUCOSAMINE 1-CARBOXYVINYLITANSFERASE (cc. 2.1.1.7) BED2_STRIN 64% 336 PENICILLIN-BINDING FROTEIN 28 MURA_BACSU 33% 300 UUD-N-ACETYLMURANOVIALANYL-D-GLUTANYL-2,6-DIAMINOPINELATED- LANYL-D-ALANYL LIGASE (cc. 3.2.3.1) BED2_STRIN 64% 336 PENICILLIN-BINDING FROTEIN 14 (FB-74) BED2_STRIN 24 318 PENICILLIN-BINDING FROTEIN 14 (FB-74) BED2_STRIN 32% 661 ROD SHARE-DETERNING FROTEIN 14 (FB-74) BERALEY 32% 661 ROD SHARE-DETERNING FROTEIN 14 (FB-74) BERALEY 32% 610 AUD-N-ACETYLEADINE FOOTEN 14 (FB-74) BERALEY 32% 160 AUD-N-ACETYLEADINE MONTALANYL-D-GLUTANYL-(FBYLAPEFTIDE) BERALEY 318 110 AUD-N-ACETYLEADINGENERAUS (FC 2.1.1.1)				HYPOTHETICAL 136.5 KD LIPOPROTEIN IN HIPB-UXAB INTERGENIC
NRP. STREM 37% 1729 MURAMIDASE-BELEASED FORTEIN PERCENSOR (136 KD SURFACE PROTEIN) BIOGJ.G2 MURSIM SECONDS 35% 2164 ADRESSING 53% 2164 ADRESSING 53% 2164 ADRESSING 53% 311 FROBARLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7) DIPP2_STREM 64% 336 PENICILLIN-BINDING FROTEIN 2B MURR. BACSU 28% 300 PRANCILLIN-BINDING FROTEIN 2B MURR_BACSU 28% 306 PENICILLIN-BINDING FROTEIN 1A (PBC-1A) PROLEASE (EC 2.5.1.7) MURR_ALCOSU 28% 300 PRANCILLIN-BINDING FROTEIN 1A (PBC-1A) (PBC-2.5.1.7) MURR_ALCOSU 28% 300 PRANCILLIN-BINDING FROTEIN 1A (PBC-1A) (PBC-2.5.1.7) MURR_ALCOSU 28% 306 PRANCILLIN-BINDING FROTEIN 1A (PBC-2.8.0.0.1.1.1.58) NURA-ACETYLGUEORAMILE 1-CARBOXYVINUTARASPERASE (EC 2.7.6.13 MURA_ALCOSU 27% 31% 160 PROTEIN PERCENSOR HILE 1-CARBOXYVINUTARASPERASE (EC 2.7.6.13 MURA_ALCOSU 38% 1400 AUTOLYSIN FRECURSOR (EC 3.5.1.23) NURA-ACETYLGUEORAMINE 1-CARBOXYLANING-CARBOXYLANING-(PBCTANING) MURR_BACSU 31% 151 UDP-N-ACETYLMURRAVYLANING-CAUTINASPERASE (EC 2.7.7.2)				
ADME_STREA 259 2164 ADMESIN B PRECURSOR (SALIVA-BINDING PROTEIN) BIO03.02 Murcin secolus and pepidoglycan 23 genes MURR_BACSU 559 311 PROBABL UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINVITRANSFERASE (EC 2.5.1.7) PEPL_STREM 669 336 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 289 340 UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINVITRANSFERASE (EC 2.5.1.7) PEPL_STREM 649 532 UDP-N-ACETYLGLUCOSAMINE (PED-14) PEPLASTRO 548 528 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 288 390 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 288 390 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 278 880 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 278 890 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 278 890 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 278 890 PENICILLIN-BIDING FROTEIN 28 MURR_BACSU 298 110 UDP-N-ACETYLGUCOSAMINEDACIMANTL-(PENIABSFERASE (EC 1.1.1.158) AUTOLISIN PRECURSOR (EC 3.5.1.28) MURG_BACSU 398 110 UDP-N-ACETYLGUCOSAMINEDACIMANTL-(PENIAPEPIDE) MURG_BACSU 398 110 UDP-N-ACETYLGUCOSAMINEDACIMANTL- LIGNSE (EC 6.3.2.9) MURG_BACSU 318 100 UDP-N-ACETYLGUCOSAMINEDACIMANCE-2.6-DIJTAMATL-(PENIAPEPIDE) MURG_BACSU 318 100 UDP-N-ACETYLGUCOSAMINEDACIMANCE-2.6-DIJTAMATL-(PENIAPEPIDE) MURG_BACSU 318 121 D-ALANTU-D-ALANINE CARDOYPEPIDIASE PERCURSOR (EC 3.4.1.6.4) MURG_BACSU 318 1258 PENICILLIN-BIDING FROTEIN MED MURE_BACSU 318 1258 PENICILLIN-BIDING FROTEIN MED MURE_BACSU 338 142 DIF FROTEIN MURC_BACSU 338 142 DIFF				
NUMBLE ACSU 23 genes MURA ACSU 55% 311 FROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7) DEP2_STREM 66% 36 DENICILLIN-BINDING FROTEIN 2B MURP EACSU 28% 300 DEP-N-ACETYMENROMYLALANYL-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-2, 6-DIAMINOPINELATE-D-GLUTANYL-1, 2, 6, 6, 2, 2, 1, 7, 7, 3, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7,				
MIRA_RACSU 558 311 FROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC. 2.5.1.7) TREP_STREM 668 366 FENICILLIN-BINDING FROTEIN 28 MIRR_BACSU 288 390 PENICILLIN-BINDING FROTEIN 4 PRECURSOR (PEP 4) PHOLBACSU 288 300 PENICILLIN-BINDING FROTEIN 1A (PEP-LA) MIRA_ACIGA 488 320 PEN-ACETYLGUCOSAMINE 1-CARBOXYUNJUTRANSFERASE (EC 2.5.1.7) PROD_BACSU 278 380 PENICILLIN-BINDING FROTEIN 1A (PEP-LA) MURA_ACIGA 488 320 UDP-N-ACETYLGUCOSAMINE PROTEIN RODA PEPELSACSU 278 380 PENICILLIN-BINDING FROTEIN RODA MURA_ACIGA 284 1629 PENICILLIN-BINDING FROTEIN RODA MURA_ACIGA 284 1629 PENICILLIN-BINDING FROTEIN RODA MURA_ACIGA 284 1629 UDP-N-ACETYLGUCOSAMINEACETYLMURAMYL-(PENIAPPFIDE) MURA_ACIGA 284 1630 UDP-N-ACETYLGUCOSAMINE-N-D-CUTMANTE-LGACE (EC 6.3.2.9) MURE_BACSU 314 1631 UDP-N-ACETYLGUCOSAMINE PENDEPRIDASE PROFENSIONE (EC 6.3.2.9) MURE_BACSU 134	ADHS_STRSA	35%	2164	ADHESIN B PRECURSOR (SALIVA-BINDING PROTEIN)
MIRA_RACSU 558 311 FROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC. 2.5.1.7) TREP_STREM 668 366 FENICILLIN-BINDING FROTEIN 28 MIRR_BACSU 288 390 PENICILLIN-BINDING FROTEIN 4 PRECURSOR (PEP 4) PHOLBACSU 288 300 PENICILLIN-BINDING FROTEIN 1A (PEP-LA) MIRA_ACIGA 488 320 PEN-ACETYLGUCOSAMINE 1-CARBOXYUNJUTRANSFERASE (EC 2.5.1.7) PROD_BACSU 278 380 PENICILLIN-BINDING FROTEIN 1A (PEP-LA) MURA_ACIGA 488 320 UDP-N-ACETYLGUCOSAMINE PROTEIN RODA PEPELSACSU 278 380 PENICILLIN-BINDING FROTEIN RODA MURA_ACIGA 284 1629 PENICILLIN-BINDING FROTEIN RODA MURA_ACIGA 284 1629 PENICILLIN-BINDING FROTEIN RODA MURA_ACIGA 284 1629 UDP-N-ACETYLGUCOSAMINEACETYLMURAMYL-(PENIAPPFIDE) MURA_ACIGA 284 1630 UDP-N-ACETYLGUCOSAMINE-N-D-CUTMANTE-LGACE (EC 6.3.2.9) MURE_BACSU 314 1631 UDP-N-ACETYLGUCOSAMINE PENDEPRIDASE PROFENSIONE (EC 6.3.2.9) MURE_BACSU 134	BIO03.02 Mureir	a saccu	lus and	peptidoglycan 23 genes
PRP2_STREPN 468 336 PENCILLIN-BINDING PROTEIN 28 WINF_BAGSU 398 336 UDP-N-ACETYLHURANVL-D-GLUTANVL-2,6-DIAMINOPINELATED- PALANVL-D-ALANVL LIGASE (EC 6.3.2.15) PEND_BAGSU 288 390 PENCILLIN-BINDING PROTEIN 4 PERCURSOR (PEP 4) PEND_BAGSU 288 390 PENCILLIN-BINDING PROTEIN 1A (PEP-1A) WIRA_ACIGA 498 532 UDP-A-ACETYLGUCOSAMINE 1-CARBOXVINITARNSFERASE (EC 2.5.1.7) PERD_BAGSU 278 586 PENCILLIN-BINDING PROTEIN 80 (PEP-2A) WIRA_ACIGA 498 532 UDP-A-ACETYLGUCOSAMINE PROTEIN RODA PERD_BAGSU 448 589 PENCENLING-PROTEINING PROTEIN RODA WIRA_ACIGA 498 531 UDP-A-ACETYLGUCOSAMINE REDUCTASE (EC 1.1.1.158) ALXS_ENTRM 398 1400 AUTOLYSIN PRECURSOR (EC 3.1.28) WIRA_BAGSU 398 1172 UDP-A-ACETYLGUCOSAMINE-N-ACETYLGUTANTER REDUCTASE (EC 1.1.1.158) ALXS_ENTRM 398 1400 AUTOLYSIN PRECURSOR (EC 3.1.28) WIRE_BAGSU 598 1630 UDP-A-ACETYLGUCOSAMINE-N-ACETYLGUTANTH-(PENTAPPFTIDE) PYROPHOSPHORYL-UNDECARFUND -N-ACETYLGUCOSAMINE REMOVERALANINE-2-6-GUTINANTE-2.6-OIMINOPINELATE LIGASE (EC 6.3.2.13) WIRE_BAGSU 598 1630 UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) ALXS_ENTRM 418 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.28) WIRE_BAGSU 598 1630 UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) ALXS_ENTRM 418 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.28) WIRE_SAUGU 548 1931 UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) ALXS_ENTRM 418 1956 RODINAL TANLE-D-ALANNOVILALANINED-GUTINANTE-2.6-OIMINOPINELATE LIGASE (EC 6.3.2.13) WIRE_BAGSU 318 1255 PENCICLIN-BINDING PROTEIN MRED MACA_ESTRMS 2152 SBACITARCI PROTEINS PROTEIN MRED MACA_ESTRMS 2152 SBACITARCI PROTEIN MRED WIRE_DAGSU 318 1255 PENCICLINE CANDONYPETIDASE PRECURSOR (EC 3.4.16.4) PERP_BAGSU 318 1255 BACITARCI PROTEIN MRED MACA_ESTRMS 315 1250 DDT-GLOBORHAMINSE 3.5-EPIMERASE (EC 2.7.7.39) MIRE_BAGSU 338 142 DLTE PROTEIN MIRE CANDONYL MARMATER 21000000000000000000000000000000000000	MURA_BACSU	55%	311	PROBABLE UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC
NURP_BACSU 349 340 UDP-H-ACSTYLMURANCYLALANYL-D-GLUTANYL-2, 6-DIAMINOPIMELATED- LANNYL-D, ALMYL LIGASE (EC 6.3.15) PRPA_STROR 288 390 PERICILLIN-BINDING PROTEIN 4 PRECURSOR (PR 4) PRPA_STROR 548 PERICILLIN-BINDING PROTEIN 1A (PRP-1A) MURA_ACICA 498 532 UDP-N-ACETYLGUCOSAMINE 1-CAREOXYUNUITERANSPERASE (EC 2.5.1.7) MURA_ACICA 498 532 UDP-N-ACETYLGUCOSAMINE 1-CAREOXYUNUITERANSPERASE (EC 2.7.6.13 MURA_ACSU 278 688 PERICILIN-BINDING PROTEIN 26 (PSP-26) MURB_ACSU 378 1400 AUTOLYSIN PRECURSOR (EC 3.5.1.78) MURB_ACSU 398 1400 AUTOLYSIN PRECURSOR (EC 3.5.1.78) MURG_BACSU 354 1631 UDP-N-ACETYLGUCOSAMINE -RANSPERASE (EC 2.4.11) MURB_BACSU 314 1851 UDP-N-ACETYLGUCOSAMINE -NACETYLMURANCYLLANTE-D-GLUTAMATE-1-2, 6-DIAMINOPINELATE MURC_BACSU 554 1911 UDP-N-ACETYLGUCOSAMINE PROVENAUET C.6.3.2.13) MURE_BACSU 354 2158 PERICILIN-BINDING PROTEIN MERC-0ECUTAMATE-1-2, 6-DIAMINOPINELATE MURC_BACSU 354 2158 PERICILUCOSAMINE- PROTEIN ME				
NLAMPL-D- ALAWYL LIGASE (EC 6.3.2.15) PERD_BASCU 284 396 PENICILLIN-BINDING PROTEIN 1A (PEP-LA) PERD_BASCU 284 528 PENICILLIN-BINDING PROTEIN 1A (PEP-LA) PERD_BASCU 274 661 ROD SHAPE-DETERNINKE PROTEIN NOAD PERD_BASCU 274 661 ROD SHAPE-DETERNINKE PROTEIN NOAD PERD_BASCU 274 686 PENICILLIN-BINDING PROTEIN 28 (PEP-28) REAX_BASCU 244 889 PENICILLIN-BINDING PROTEIN SODA WIREBASCU 394 1172 UDE-N-ACETYLMUCOSAMINE C.S. 1.1.28) WIREBASCU 354 1600 UDD-N-ACETYLMUCOSAMINE TAMSTERAE EC 2.11) WIREBASCU 314 1951 UDD-N-ACETYLMUCOSAMINE TAMSTERAE EC 2.11) WIREBASCU 315 1601 UDD-N-ACETYLMUCOSAMINE TAMSTERAE EC 2.11) WIREBASCU 315 1951 UDD-N-ACETYLMUCOSAMINE TAMSTERAE EC 2.11) WIREBASCU 314 1956 AUTOLYSIN PRECUESOR (EC 3.5.1.28) WIREBASCU 315 1951 UDD-N-ACETYLMUCOSAMINE PYNOPHOSEDHONIALSE (EC 4.10) WIREBASCU 315 1951 UDD-N-ACETYLMUCOSAMINE PYNOP	PBP2_STRPN			PENICILLIN-BINDING PROTEIN 2B
PREPLACEU 28% 390 PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PR 4) PRPA_STROR 54% 52% PRICILLIN-BINDING PROTEIN 1A (PRP-1A) MURA_ACICA 49% 532 UDP-N-ACETVILLIN-BINDING PROTEIN 1A (PRP-1A) MURA_ACICA 49% 532 UDP-N-ACETVILLIN-BINDING PROTEIN 260 (PRP-2B) MURA_BACSU 27% 686 PENICILIIN-BINDING PROTEIN 26 (PRP-2B) MURA_BACSU 24% 914 ROD SHAPE-DETERNITIONE PROTEIN 2600 MURE_BACSU 39% 1400 AUTOLYSIN PRECURSOR (PC 3.5.1.28) MURA_BACSU 35% 1630 UDP-N-ACETVILALCOSAMINE-M-ACEGTLAULCOSAMINE PROTEIN MACDATIANTL- (PENTAPEPTIDE) MURA_BACSU 55% 1631 UDP-N-ACETVILAUROSAMINE-M-ACEGULAUROSAMINE-CAUCHANATE - 2.6-DIAINNOPINELATE MURA_BACSU 55% 1631 UDP-N-ACETVILAUROSAMINE-M-ACEGULAUROSAMINE-CAUCHANATE - 2.6-DIAINNOPINELATE MURA_BACSU 55% 1631 UDP-N-ACETVILAURONOPINALAUROSAMINE-CAUCHANATE - 2.6-DIAINNOPINELATE MURE_BACSU 31% 151 UDP-N-ACETVILAURONOPINALAUROSAMINE-CAUCHANATE - 2.6-DIAINNOPINELATE MURE_BACSU 31% 125 AUTOLYSIN PRECURASAMINE C				
PHPA_STROR 54% 52% PENICILLIN-BINDING PROTEIN 1A (PEP-1A) NURA_ACIGA 49% 532 UDP-M-ACETYLGUCOSANINE - ICARBOXYUNUTRANSFERASE (EC 2.5.1.7) NURA_ACIGA 49% 661 ROD SHAPE-DETERVIENING PROTEIN NGOA PERE_BASCU 27% 661 ROD SHAPE-DETERVIENING PROTEIN NGOA NURA_ACSU 44% 869 PENGEHOLIN-BENDING PROTEIN NGOA NURA_ACSU 24% 1400 AUTOLYSIN FRECUENSOR (EC 3.5.1.28) NURS_BACSU 35% 1600 UDP-N-ACETYLGULOSANINE TAMSFERASE (EC 2.1.1.1.158) NURS_BACSU 35% 1631 UDP-N-ACETYLGULOSANINE TAMSFERASE (EC 2.1.1.0) WIRE_BACSU 31% 1631 UDP-N-ACETYLGULOSANINE TAMSFERASE (EC 2.1.1.0) WIRE_BACSU 31% 1951 UDP-N-ACETYLGULOSANINE TAMSFERASE (EC 2.1.1.0) WIRE_BACSU 31% 1951 UDP-N-ACETYLGULOSANINE TAMSFERASE (EC 2.1.1.0) WIRE_BACSU 31% 1951 UDP-N-ACETYLGULOSANINE TAMSFERASE (EC 2.1.1.0) WIRE_BACSU 31% 1956 AUTOLYSIN PRECUENSOR (EC 3.5.1.28) WIRE_BACSU 31% 1951 UDP-N-AC	ALANYL-D- ALANY	L LIGA	SE (EC 6	5.3.2.15)
MURA_ACTICA 49% 532 UDP-N-ACETYLLICUCGSAMINE 1-CREENTING PROTEIN RODA PRDA_HELTY 32% 661 ROD SHAPE-DETERMINING PROTEIN RODA PRDE_BAGGU 27% 686 PENICILIN-BINDING PROTEIN RODA RODA_HELTY 32% 680 PENICILIN-BINDING PROTEIN RODA RODA_ECOLI 28% 914 ROD SHAPE-DETERMINING PROTEIN RODA RUBE_BACGU 35% 1400 ANTOLYSIN PRECURSOR (EC 1.5.1.28) RUBE_BACGU 55% 1610 UDP-N-ACETYLEURORYFENDALMER TAMSFERASE (EC 2.4.1) WIRE_BACGU 55% 1610 UDP-N-ACETYLEURORYFENDAMIL-D-GUTTAMUTE LIGASE (EC 6.3.2.9) WIRE_BACGU 31% 1951 UDP-N-ACETYLEURORYFENDAMIL-CURTAMATE-2.4.01AMATE-1.4.0 WIRE_BACGU 55% 1611 UDP-N-ACETYLEURORYFENDAMIL-D-GUTAMATE LIGASE (EC 6.3.2.9) WIRE_BACGU 31% 1951 UDP-N-ACETYLEURORYFENDAMIL-D-GUTAMATE-1.4.0 SODALSTIN SOMANTL-D-GUTAMATE LIGASE (EC 6.3.2.9) MIRE_BACGU 34% SOLALSTINCE SOLALSTINCE SOLALSTINCE COLALANTLO-CULTAMATE SOLALANTLO-LIGASE (EC 6.3.2.1.6.1) MIRE_BACGU	PBPD_BACSU			PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PBP 4)
RODA_BELERY 32% 661 ROD SHAPP-OPTERNITING FROTEIN RODA PRPE_BACSU 27% 688 FENCILLIN-BIDING FROMEN X (PBP-2R) MRAX_BACSU 44% 689 FENCIPLIN-ACCETYLENDING FROMEN X (PBP-2R) MRAX_BACSU 39% 1172 UOP-N-ACCETYLENDING FROMEN ROTEIN RODA MURE_BACSU 39% 1172 UOP-N-ACCETYLENDING FROMENT RODA MURE_BACSU 55% 1600 UOP-N-ACCETYLENDING FROMENT-N-ACCETYLENDING FROMENTALSE MURE_BACSU 55% 1610 UOP-N-ACCETYLENDING FROMENTALSE (EC 2.4.1) MURE_BACSU 51% 1610 UOP-N-ACCETYLENDING FROMENTALSE (EC 2.4.1) MURE_BACSU 51% 1610 UOP-N-ACCETYLENDING FROMENTALSE (EC 2.4.1) MURE_BACSU 51% 1911 UOP-N-ACCETYLENDING FROMENTALSE (EC 2.4.1.6.4) PASTRERY 25% 2111 D-ALAXYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) PASTRERY 25% 224 204 ROD SHAPE-DETERMINING FROMEIN MED MRCA_BACSU 35% 2336 D-ALAXYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) PASTRAGU 35% 236 <td>PBPA_STROR</td> <td></td> <td></td> <td></td>	PBPA_STROR			
PRPE_BACGU 27% 888 PENTCILIN-GINDIG FROTEIN 28 (PB-28) PRAY_BACSU 24% 99 PENTCILIN-GINDIG FROTEIN ROLA RODA_ECOLI 28% 914 ROD SHAPE-OFTERNINEN FROTEIN ROLA RURE_BACSU 39% 1172 UDP-N-ACETYLENCORGANINE FROTEIN ROLA RURE_BACSU 39% 1172 UDP-N-ACETYLENCORGANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 55% 1630 UDP-N-ACETYLEUCOSANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 55% 1630 UDP-N-ACETYLEUCOSANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 55% 1631 UDP-N-ACETYLEUCOSANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 55% 1631 UDP-N-ACETYLEUCOSANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 15% 1501 UDP-N-ACETYLEUCOSANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 1561 UDP-N-ACETYLEUCOSANINE TRANSFERASE (EC 2.4.1) MURE_BACSU 155 100 100 100 MURE_BACSU 155 100 100 100 100 MURE_BACSU 25% 100 100 100 10				UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
<pre>NRAY_BACSU 44% 869 FEGORED-N-ACETYLMICAMOUL-PENTAPEPTIDE-TRANSFERASE (KC 2.7.8.13 KODA_ECOL 28% 914 ROD SHAPE-DETERMINIC POTEIN RODA MURB_BACSU 39% 1172 UDF-N-ACETYLENDLPYRUNOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158) AUYS_ENTH 39% 1400 AITOLYSIN FRECURSOR (EC 3.5.1.2) WIRD_BACSU 55% 1630 UDF-N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1) WIRD_BACSU 55% 1630 UDF-N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1) WIRD_BACSU 55% 1630 UDF-N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1) WIRD_BACSU 55% 1631 UDF-N-ACETYLGUCOSAMINE TRANSFERASE (EC 2.4.1) WIRD_BACSU 55% 1631 UDF-N-ACETYLGUCOSAMINE TRANSFERASE (EC 2.4.1) WIRD_BACSU 55% 1211 DF-N-ACETYLGUCOSAMINE TRANSFERASE (EC 2.7.7.23) AUYS_ENTH 41% 1956 AITOLYSIN FRECURSOR (EC 3.5.1.24) UDC_STREQ 25% 2111 DF-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) AUYS_ENTH 41% 1956 AITOLYSIN FRECURSOR (EC 3.5.1.24) UDC_STREQ 25% 2111 DF-ALAYIL-D-ALANINE CARDOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) PAFF_BACSU 31% 2255 ROLFHACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) UCC 2.7.1.660 WRED_BACSU 22% 2244 ROD SHAPE-DETERMINING PROTEIN MED WRED_BACSU 33% 2336 DF-ALAYYL-D-ALANINE CARDOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) BEOG.0.3 Surface polyseccharides, lipopolysecharides and antigens 21 genes DACA_BACSU 35% 2336 DF-ALAYYL-D-ALANINE CARDOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) BEOG.3.03 Surface polyseccharides, lipopolysecharides and antigens 21 genes DACA_BACSU 35% 217 GLUCERAL-J-PHOSPHARESE (EC 4.2.1.46) NFBG_SHIPL 36% 200 DTDP-RHAMNOSYL TRANSFERASE (EC 4.2.1.46) NFBG_SHIPL 36% 201 DTDP-RHAMNOSYL TRANSFERASE (EC 4.2.1.46) NFBG_SHIPL 36% 201 DTDP-RHAMNOSYL TRANSFERASE (EC 2.7.7.39) NACLBACSU 23% DF TELCHCIC ACID TRANSLOCATION PREREMESE FORTEIN TAGH NGG_BACSU 23% 917 TELCHCIC ACID TRANSLOCATION PRENEMASE (EC 1.7.7.39) NGG_BACSU 23% 917 TELCHCIC ACID TRANSLOCATION PRENEMASE FORTEIN TAGH NGG_BACSU 23% 917 TELCHCIC ACID TRANSLOCATION PRENEMASE FORTEIN TAGH NGG_BACSU 23% 917 TELCHCIC ACID TRANSLOCATION PRENEMASE FORTEIN TAGH NGG_BACSU 23% 914 TELCHCIC ACID TRANSLOCATION PRENEMASE FORTEIN</pre>				
RODA_ECOLI 28% 914 ROD_SHAPE-DETERNITING PROTEIN RODA RODA_ECOLI 28% 91172 UDDE-N-ACETYLENDLPFNUNDVIGLUCOSAMINE REDUCTASE (EC 1.1.1.158) ALYS_ENTER 39% 1400 AITOLYSIN FRECUESOR (EC 3.5.1.28) WIRE_DACSU 55% 1630 UDDE-N-ACETYLENDCOSAMINE TRANSFERASE (EC 2.4.1) WIRE_DACSU 55% 1630 UDDE-N-ACETYLENDCOSAMINE TRANSFERASE (EC 2.4.1) WIRE_DACSU 55% 1631 UDDE-N-ACETYLENDCOSAMINE TRANSFERASE (EC 2.4.1) WIRE_DACSU 55% 1631 UDDE-N-ACETYLENDCOSAMINE TRANSFERASE (EC 2.4.1) WIRE_DACSU 55% 1931 UDDE-N-ACETYLENDCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) ALYS_ENTHR 41% 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.28) ALCS_STREQ 25% PACITALINE CARBONYPEPTIDASE PRECURSOR (EC 3.4.16.4) PACA_ECOLI 34% 2156 PENICILLIN- EINDING PROTEIN IA (PDP-1A) MACA_ECOLI 34% 2255 BACITALIN ECARBONYPEPTIDASE PRECURSOR (EC 3.4.16.4) BTOJAGANCSU 35% 236 D-ALANYL-D-ALANINE CARBONYPEPTIDASE PENELMSON (EC 3.4.16.4) BTOJAGANCSU 35% 142 DLTE PROTEIN REC				
MURB_BACSU39%112UDP-N-ACETYLENOLPYRUVOYLGULGUSGAMINE REDUCTASE (EC 1.1.1.158) ALYS_ENTRMURS_BACSU45%1639UDP-N-ACETYLGUCOGAMINE-N-ACETYLMURAMOYLALANINED-GULTAMATE LIGASE (EC 6.3.2.9) MURD_BACSUMURD_BACSU55%1630UDP-N-ACETYLGUCOGAMINE-N-ACETYLMURAMOYLALANINED-GULTAMATE LIGASE (EC 6.3.2.9) MURD_BACSUMURD_BACSU55%1931UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) MURD_BACSUMURD_BACSU55%1931UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) MURD_BACSUMURD_BACSU55%1931UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) MURD_BACSUMURD_BACSU25%2111D-ALAYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) PAPEJANCSUMACS_DOLL34%2255BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) BACASCUBACSU22%224ROD SHAPE-DETERNINING PROTEIN MRED MRED_BACSU21BACSU31%235DO SHAPE-DETERNINING PROTEIN MRED MRED_BACSU21BACSU33%142DLTE PROTEIN MREDOKLANDOSE 3.5-EPIMERASE (EC 5.1.3.13) MRED_SCOLI35%BACSU33%142DLTE PROTEIN MCCASCU21BACSU33%142DLTE PROTEIN MCCASCU21BACSU33%142DLTE PROTEIN MCCASCU21BACSU33%142DLTE PROTEIN MCCASCU21BACSU33%142DLTE PROTEIN MCCASCU21BACSU33%142DLTE PROTEIN MCCASCU21BAC				PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.13
ALYS_ENTER 39% 1400 AUTOLYSIN FRECURSOR (EC 3.5.1.2.8) WIRG_BACSU 45% 1639 UDD-N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1) WIRG_BACSU 55% 1630 UDD-N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1) WIRE_BACSU 55% 1631 UDD-N-ACETYLGUCOSAMINE TRANSFERASE (EC 2.4.1) WIRE_BACSU 55% 1931 UDD-N-ACETYLGUCOSAMINE TRANSFERASE (EC 2.4.1) MURE_BACSU 55% 1931 UDD-N-ACETYLGUCOSAMINE TRANSFERASE (EC 2.7.7.23) ALYS_ENTHR 41% 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.28) ALSS_ENTHR 14% 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.2.8) ALXS_ENTHR 14% 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.2.8) ALYS_ENTHR 14% 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.2.8) ALYS_ENTHR 14% 1256 AUTOLYSIN PRECURSOR (EC 3.1.2.6) MEC_2.7.1.60 WRELBACSU 34% 2255 BACITACIN RESISTANCE PROTEIN MRED WRELBACSU 33% 142 DITE PROTEIN REC ALASIN MEC_2.7.1.61 WRELBACSU 35% 236 D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4)		28%		ROD SHAPE-DETERMINING PROTEIN RODA
<pre>MURG_BACSU 45% 1639 UDP-N-ACETYLGULCOSAMINE-M-ACETYLMURANTL-(PERTAPEPTIDE) PYROPHOSHMERVL-INDECAPRENDL N-ACETYLGULCOSAMINE THA-ACETYLMURANOYLALANINED-GLUTAMATE LIGASE (EC 6.3.2.9) MURE_BACSU 55% 1630 UDP-N-ACETYLMURANOYLALANINED-GLUTAMATE LIGASE (EC 6.3.2.9) MURE_BACSU 51% 1630 UDP-N-ACETYLMURANOYLALANINE-D-GLUTAMATE LIGASE (EC 6.3.2.9) MURE_BACSU 51% 1031 UDP-N-ACETYLMURANOYLALANIN-D-GUTAMATE-2.6-DIAMINOPIMELATE LIGASE (EC 6.3.2.13) CAD_BACSU 55% 1191 UDP-N-ACETYLMURANOYLALANIN-D-GUTAMATE-2.6-DIAMINOPIMELATE DAC_STRSQ 25% 2111 D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECUNSOR (EC 3.4.16.4) PARCABCOLI 34% 2255 BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66) WRED_BACSU 23% 2244 ROD SHAPE-DETERMINING PROTEIN MRED REC_BACSU 30% 2295 ROD SHAPE-DETERMINING PROTEIN MRED REC_BACSU 30% 122 DIFE PROTEIN MRED REC_BACSU 30% 1236 D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) RTO3.03 Surface polysecharides, lipopolysecharides and antigens 21 genes DITE_BACSU 30% 142 DIFE PROTEIN REC_BACSU 30% 142 DIFE PROTEIN REC_BACSU 30% 127 GLUCOSCE 4.6-DEMYDRATASE (EC 4.2.1.46) RTO3.03 SURface polysecharides, lipopolysecharides and antigens 21 genes DITE_BACSU 55% 217 GLUCEROL-3-PHOSPHATE CYTIDYLYTANSFERASE (EC 2.7.7.39) RAGE_BACSU 25% 1217 GLUCEROL-3-FONSPHATE CYTIDYLYTANSFERASE (EC 2.7.7.39) RAGE_BACSU 25% 1217 CLUCOSC ACID TRANSLOCATION PREMEASE PROTEIN TAGG RAGBACSU 23% 937 TEICHOIC ACID TRANSLOCATION PREMASE PROTEIN TAGG RAGBACSU 23% 1447 PROTEIN DLTD PRECU</pre>				UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
PYROPHOSHORYL-INDECARENOL N-ACETYLGLUCOSAMINE TRANSPERASE (EC 2.1.1.) WURD_BACSU 55% 1630 UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE (EC 6.3.2.9) WURD_BACSU 31% 1851 UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE (EC 6.3.2.9) WURD_BACSU 54% 1931 UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) ALYS_ENTHR 41% 1956 AUTOLYSIN PRECURSOR (EC 3.5.1.28) ALYS_ENTHR 41% 1956 AUTOLYSIN PRECURSOR (EC 3.4.16.4) PREP_BACSU 31% 2158 PENICILLIN-BINDING PROTEIN IA (PBP-IA) BACA_ECOLI 34% 2255 BACITACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66) WRED_BACSU 32% 2294 ROD SHAPE-DETERMINING PROTEIN MRED WRED_BACSU 33% 2235 ROD SHAPE-DETERMINING PROTEIN MRED WRED_BACSU 33% 2336 D-ALANYL-D-ALANINE CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) BIO03.03 Surface polysaccharides, lipopolysaccharides and atigens 21 genes DUTE_BACSU 33% 142 DIFE PROTEIN HED_SHILL 35% 196 DIDP-4-DEHYDROHARISE 3.5-SEPIMERASE (EC 5.1.3.13) REB2_ECOLI 46% 197 DIDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46) YEG_SHILL 35% 196 DIDP-4-DEHYDROHARISE 3.5-SEPIMERASE (EC 2.7.7.39) INCLHAEIN 31% 213 LICD PROTEIN RED_BACSU 55% 217 GLUCERCLOID TRANSLOCATION PREMASE PROTEIN TACH NGG_BACSU 29% 941 TEICHOIC ACID TRANSLOCATION PRIMESE PROTEIN TACH NGG_BACSU 29% 941 TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR INGE_BACSU 29% 941 TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR INGEBACSU 29% 941 TEICHOIC ACID BIOSYNTHESIS PROTEIN F NGGBBACSU 29% 941 TEICHOIC ACID BIOSYNTHESIS PROTEIN F NGGBBACSU 29% 941 TEICHOIC ACID BIOSYNTHESIS PROTEIN F NGGBBACSU 23% 1475 PROBABLE POLY(GLYCEROL-PHOSPHATE) ALPHA-GLUCOSYLTRANSPERASE (EC 2.4.1.52) INCLLACEULUAR PROCESSES 04 DITB PROTEIN P				
NURD_BACSU55%1630UDP-N-ACETYLAURAMOYLALANINE-D-GLUTAMATE LICASE (EC 6.3.2.9)NURD_BACSU31%1851UDP-N-ACETYLAURAMOYLALANINE-D-GLUTAMATE2,6-DLAMINOPIMELATELIGASE (EC 6.3.2.13)DCAD_BACSU54%1931UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)ALYS_ENTHR41%1956AUTOLYSIN PRECURSOR (EC 3.5.1.28)DAC_STRSQ25%2111D-ALANTL-D-ALANINE CARDOXYPEPTLDASE PRECURSOR (EC 3.4.16.4)PAPF_BACSU31%2255BACITRACIN RESISTANCE PROTEIN IA (PEP-1A)BACA_BCOLI34%2255BACITRACIN RESISTANCE PROTEIN MEDWEED_BACSU21%22%ROD SHAPE-DETERMINING PROTEIN MEDWEED_BACSU30%2295ROD SHAPE-DETERMINING PROTEIN MEDWEED_BACSU35%2136D-ALANIL-D-ALANINE CARBOXYPEPTLDASE PRECURSOR (EC 3.4.16.4)DACA_BACSU35%142DLTE PROTEINBACA_BACSU35%142DLTE PROTEINBACSU35%142DLTE PROTEINDITE_BACSU35%142DLTE PROTEINDITE_BACSU35%142DLTE PROTEINBACS_BACSU35%217GLYCEROL-3-PHORHARMOSE 3.5-EPIMERASE (EC 5.1.3.13)RNB_BACSU36%142DTD-F-HAMNOSYL TRANSPERASE (EC 2)LICD_BACSU35%217GLYCEROL-3-PHORHARSE (EC 2)LICD_BACSU35%217GLYCEROL-3-PHORHARSE (EC 2)LICD_BACSU29%937TEICHOIC ACID TRANSLOCATION ATP-BINDING PROTEIN TAGGRAGE_BACSU29%937TEIC				
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2.4.1.52) RFBU PROTEIN RFBU_SALTY 25% 2186 RFBU PROTEIN RFAK_SALTY 28% 2187 LIPOPOLYSACCHARIDE 1,2-N-ACETYLGLUCOSAMINETRANSFERASE (EC 2.4.1.56) (DTB_HAEIN 39% 2218 LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB 81003.04 Surface structures 0 genes 81004. CELLULAR PROCESSES 29 genes	FAGE_BACSU	23%	1477	PROBABLE POLY(GLYCEROL-PHOSPHATE) ALPHA-GLUCOSYLTRANSFERASE (E
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2.4.1.56) KDTB_HAEIN 39% 2218 LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB BIO03.04 Surface structures 0 genes BIO04. CELLULAR PROCESSES 29 genes				
BIO03.04 Surface structures 0 genes BIO04. CELLULAR PROCESSES 29 genes	2.4.1.56)			,
BIO04. CELLULAR PROCESSES 29 genes	CDTB_HAEIN	39%	2218	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB
	BIO03.04 Surfac	e struc	tures	0 genes
NTORA 01 Coll division 8 conce	31004. CELLULAR	PROCES	SES	29 genes
				0

DIVC_BACSU	31%	22	CELL DIVISION PROTEIN DIVIC
		27	
FTSH_LACLA	988		CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24)
SP0J_BACSU	448	96	STAGE 0 SPORULATION PROTEIN J
FTSY_BACSU	58%	823	CELL DIVISION PROTEIN FTSY HOMOLOG
	40%	997	CELL DIVISION ATP-BINDING PROTEIN FTSE
FTSE_ECOLI			
SP3E_BACSU	498	1701	STAGE III SPORULATION PROTEIN E
FTSZ BACSU	618	1918	CELL DIVISION PROTEIN FTSZ
FTSA_BACSU	37%	1919	CELL DIVISION PROTEIN FTSA
1101_01000			
BI004.02 Cell			3 genes
HLY3_BACCE	44%	495	HEMOLYSIN III (HLY-III)
YOXC_BACSU	60%	879	HYPOTHETICAL 29.7 KD PROTEIN IN FOLD-AHRC INTERGENIC REGION
FRPA_NEIME	30%	1394	IRON-REGULATED PROTEIN FRPA
FRIA_MELINE	200	*224	INON ADOUNTED FROTEIN FAIL
BIO04.03 Chape	erones		4 genes
SUGE ECOLI	468	122	SUGE PROTEIN
CH10_LACLA	100%	396	10 KD CHAPERONIN (PROTEIN CPN10)
CH60_LACLA	978	397	60 KD CHAPERONIN (PROTEIN CPN60)
DNAK_LACLA	998	977	DNAK PROTEIN (HEAT SHOCK PROTEIN 70)
BIO04.04 Deto	zificati	on	1 genes
SODM_LACLA	100%	410	SUPEROXIDE DISMUTASE (MN) (EC 1.15.1.1)
SODM_LACUA	1002	410	SUPEROATDE DISHUTASE (FIN) (AC 1.15.1.1)
BIO04.05 Prote	ein and	peptide s	secretion 5 genes
SECA STAAU	51%	115	PREPROTEIN TRANSLOCASE SECA SUBUNIT
	52%	534	
TIG_BACSU			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)
DBI G_DEGGG	410	2000	broken the theory
BIO04.06 Trans	sformati		8 genes
CMA2_BACSU	46%	729	COMA OPERON PROTEIN 2
CMF3_BACSU	37%	1094	COMF OPERON PROTEIN 3
CMF1_BACSU	37%	1095	COMF OPERON PROTEIN 1
CME3_BACSU	28%	1811	COME OPERON PROTEIN 3
CME1_BACSU	39%	1812	COME OPERON PROTEIN 1
CMG3 BACSU	448	2166	COMG OPERON PROTEIN 3 PRECURSOR
CMG2_BACSU	30%	2167	COMG OPERON PROTEIN 2
CMG1_BACSU	39%	2168	COMG OPERON PROTEIN 1
BIO04.07 Other			0 genes
			0 genes
BIO04.07 Other	r .		
	r .		
BIO04.07 Other BIO05. CENTRAL	r L INTERM		ETABOLISM 30 genes
BIO04.07 Other	r L INTERM		
BIO04.07 Other BIO05. CENTRAL	r L INTERM		ETABOLISM 30 genes
BIO04.07 Other BIO05. CENTRAL BIO05.01 Gener GRC3_BACSU	r L INTERM ral	EDIARY M	TABOLISM 30 genes 7 genes
BIO04.07 Other BIO05. CENTRAL BIO05.01 Gener GRC3_BACSU 2.5.1.30)	r L INTERM ral 31%	EDIARY M	TABOLISM 30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC
BI004.07 Other BI005. CENTRAL BI005.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR	r L INTERM 31% 42%	EDIARY M 184 198	State 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 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU	r L INTERM 31% 42% 47%	EDIARY M	7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANYLTRANSTRANSFERASE (EC 2.5.1.10)
BI004.07 Other BI005. CENTRAL BI005.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR	r L INTERM 31% 42%	EDIARY M 184 198	State 30 genes 7 genes probable heptaprenyl diphosphate synthase component II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133)
BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU	r L INTERM 31% 42% 47% 48%	184 198 878 985	30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANVLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION
BIO04.07 Other BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU	r L INTERM 31% 42% 47% 48% 44%	184 198 878 985 1185	30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.1.33) 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 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU	r L INTERM 31% 42% 47% 48%	184 198 878 985	30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANVLTRANSTRANSFERASE (EC 2.5.1.10) HYPOTHETICAL 55.8 KD PROTEIN IN SPOILQ-MTA INTERGENIC REGION
BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30)	r L INTERM 31% 42% 47% 42% 42% 35%	184 198 878 985 1185 1378	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
BIO04.07 Other BIO05. CENTRAL BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU	r L INTERM 31% 42% 47% 48% 44%	184 198 878 985 1185	30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.1.33) 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
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BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30)	r L INTERM 31% 42% 47% 48% 44% 35% 62%	EDIARY ME 184 198 878 985 1185 1378 1950	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
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BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU GRC3_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amine NYLA_PSES8	r L INTERM 31% 42% 47% 48% 44% 35% 62% 62% 0 sugars 32%	184 198 878 985 1185 1378 1950 167	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. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amine NYLA_PSES8 NODB_RHILV	r L INTERM 31% 42% 42% 42% 42% 42% 42% 55% 62% 50 sugarf 32% 32%	EDIARY M 184 198 878 985 1185 1378 1950 167 279	30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANVLTRANSTRANSFERASE (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)
BIO04.07 Other BIO05. CENTRAN BIO05.01 Gener 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	r L INTERM 31% 42% 47% 48% 44% 35% 62% 62% 0 sugars 32% 37% 36%	EDIARY ME 184 198 878 985 1185 1378 1950 167 279 1032	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. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amine NYLA_PSES8 NODB_RHILV	r L INTERM 31% 42% 47% 48% 44% 35% 62% 62% 0 sugars 32% 37% 36%	EDIARY ME 184 198 878 985 1185 1378 1950 167 279 1032	30 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) GERANVLTRANSTRANSFERASE (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)
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BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amine NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU NAGD_ECOLI YVYH_BACSU NAGD_HAEIN BIO05.03 Degra NAGD_HAEIN BIO05.04 Phosp DUT_HAEIN DUT_HAEIN	r L INTERM 31% 42% 47% 42% 42% 42% 42% 42% 42% 42% 42	EDIARY ME 184 198 878 985 1185 1378 1950 5 167 279 1032 5.1.16) 1154 1296 1371 1376 1611 of polyss 701 1275 1523 2007 2007 sompounds 179 456	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) HYDOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYDOTHETICAL 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-ANINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 3.5.1.25) UDP-GLUCOSE-1-PHOSPHATE USINERASE (EC 5.3.1.10) GUCOSAMINE-6-PHOSPHATE LSOMERASE (EC 5.3.1.10) BODULULANASE (EC 3.2.1.135) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.16) GLIGO-1, 6-GLUCOSIDASE (EC 3.2.1.10) EXOCHITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) CHITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) EXOLICITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) EXOLICITINASE 1 FRECURSOR (EC 3.2.1.16) EXOLUCIANASE (ES '-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener 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 Amina NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU NAGD_HAEIN BIO05.03 Degra NEPU_THEVU AMY_BACST O16_BACTR CHIX_STROI CHI1_BACCI BIO05.04 Phosp DUT_HAEIN	r L INTERM 42% 47% 42% 42% 42% 42% 42% 42% 42% 42	EDIARY M 184 198 878 985 1185 1378 1950 167 279 1032 5.1.16) 1154 1296 1371 1376 1611 of polysa 701 1275 1523 2007 2007 2007 2007	S0 genes 7 genes PROBABLE HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (EC DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.33) GERANYLTRANSTRANSFERASE (EC 2.5.1.10) HYDOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYDOTHETICAL 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-ANINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITODLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINEFRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 2.7.7.9) GLUCOSE-1-PHOSPHATE USUMERASE (EC 3.1.10) MCOPULULANASE (EC 3.2.1.135) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.16) OLIGO-1, 6-GLUCOSIDASE (EC 3.2.1.10) EXOCHTINASE I PRECURSOR (EC 3.2.1.10) EXOCULULANASE PRECURSOR (EC 3.2.1.10) EXOCHTINASE I PRECURSOR (EC 3.2.1.10) CHITONASE AI PRECURSOR (EC 3.2.1.12) CHITINASE AI PRECURSOR (EC 3.2.1.12) CHITINASE AI PRECURSOR (EC 3.2.1.12) CHITINASE AI PRECURSOR (EC 3.2.1.12) CHITIN
BIO04.07 Other BIO05. CENTRAI BIO05.01 Gener GRC3_BACSU 2.5.1.30) STRL_STRGR ISPA_BACSU YWNE_BACSU YWNE_BACSU YWNE_BACSU 2.5.1.30) METK_STAAU BIO05.02 Amine NYLA_PSES8 NODB_RHILV GLMS_MYCLE (ISOMERIZING) NAGD_ECOLI YVYH_BACSU NAGD_ECOLI YVYH_BACSU NAGD_HAEIN BIO05.03 Degra NAGD_HAEIN BIO05.04 Phosp DUT_HAEIN DUT_HAEIN	r L INTERM 31% 42% 47% 42% 42% 42% 42% 42% 42% 42% 42	EDIARY ME 184 198 878 985 1185 1378 1950 5 167 279 1032 5.1.16) 1154 1296 1371 1376 1611 of polyss 701 1275 1523 2007 2007 sompounds 179 456	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) HYDOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION HYDOTHETICAL 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-ANINOHEXANOATE-CYCLIC-DIMER HYDROLASE (EC 3.5.2.12) CHITOOLIGOSACCHARIDE DEACETYLASE (EC 3.5.1) PROBABLE GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE NAGD PROTEIN PUTATIVE UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (EC 5.1.3.14) N-ACETYLGUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 3.5.1.25) UDP-GLUCOSE-1-PHOSPHATE USINERASE (EC 5.3.1.10) GUCOSAMINE-6-PHOSPHATE LSOMERASE (EC 5.3.1.10) BODULULANASE (EC 3.2.1.135) ALPHA-AMYLASE PRECURSOR (EC 3.2.1.16) GLIGO-1, 6-GLUCOSIDASE (EC 3.2.1.10) EXOCHITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) CHITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) EXOLICITINASE 1 PRECURSOR (EC 3.2.1.14) CHITINASE AI PRECURSOR (EC 3.2.1.14) EXOLICITINASE 1 FRECURSOR (EC 3.2.1.16) EXOLUCIANASE (ES '-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 40% 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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WCAL_SALTY	35%	947	PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAL
DEOD_STRTR	72%	954	PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1)
LACC_STRMU	338	982	TAGATOSE-6-PHOSPHATE KINASE (EC 2.7.1)
3MGA_HAEIN	37%	1134	DNA-3-METHYLADENINE GLYCOSIDASE (EC 3.2.2.20)
GLPK_BACSU	61%	1270	GLYCEROL KINASE (EC 2.7.1.30)
THGA_ECOLI	40%	1319	GALACTOSIDE ACETYLTRANSFERASE (EC 2.3.1.18)
GIDB_BACSU	60%	1378	GLUCOSE INHIBITED DIVISION PROTEIN B
DEOC_BACSU	60%	1461	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)
BGL1_BACSU	56%	1488	BETA-GLUCOSIDASE (EC 3.2,1,21)
GLK_BACSU	34%	1517	GLUCOKINASE (EC 2.7.1.2)
BGLA_THEMA	33%	1518	BETA-GLUCOSIDASE A (EC 3.2.1.21)
STRH_STRPN	29%	1524	BETA-N-ACETYLHEXOSAMINIDASE PRECURSOR (EC 3.2.1.52)
XYNB_BACPU	48%	1540	BETA-XYLOSIDASE (EC 3.2.1.37)
GALM_ACICA	29%	1543	ALDOSE 1-EPIMERASE PRECURSOR (EC 5.1.3.3)
XYLB_BACSU	49%	1544	XYLULOSE KINASE (EC 2.7.1.17)
XYLA_THETU	50%	1545	XYLOSE ISOMERASE (EC 5.3.1.5)
XYNX_CLOTM	28%	1618	EXOGLUCANASE XYNX PRECURSOR (EC 3.2.1.91)
ALKH_BACSU	35%	1668	4-HYDROXY-2-OXOGLUTARATE ALDOLASE (EC 4.1.3.16)
UXAC_ECOLI	44%	1669	URONATE ISOMERASE (EC 5.3.1.12)
UXUA_THENE	578	1673	MANNONATE DEHYDRATASE (EC 4.2.1.8)
RBSK_BACSU	47%	1683	RIBOKINASE (EC 2.7.1.15)
ASCB_ECOLI GIDA BACSU	53% 61%	1718 1895	6-PHOSPHO-BETA-GLUCOSIDASE ASCB (EC 3.2.1.86) GLUCOSE INHIBITED DIVISION PROTEIN A
RPE_SYNY3	47%	1983	
	60%		RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
GALE_STRMU BGA2_ECOLI	34%	2034 2036	UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) EVOLVED BETA-GALACTOSIDASE ALPHA-SUBUNIT (EC 3.2.1.23)
THGA LACLA	100%	2036	GALACTOSIDE 0-ACETYLTRANSFERASE (EC 2.3.1.18)
GAL7_STRMU	52%	2039	GALACTOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.10)
GAL1_STRMU	588	2041	GALACTOKINASE (EC 2.7.1.6)
GALM_HAEIN	36%	2042	ALDOSE 1-EPIMERASE (EC 5.1.3.3)
GLK_BACSU	478	2081	GLUCOKINASE (EC 2.7.1.2)
GNTK_BACSU	498	2249	GLUCONOXINASE (EC 2.7.1.12)
YQEC_BACSU	53%	2250	HYPOTHETICAL 32.8 KD PROTEIN IN NUCB-AROD INTERGENIC REGION
BIO06.13 TCA	cycle		9 genes
CISY_THIFE	298	665	CITRATE SYNTHASE (EC 4.1.3.7)
ACON_BRAJA	51%	667	ACONITATE HYDRATASE (EC 4,2.1.3)
IDH_STRMU	60%	669	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
MLES_LACLA	98%	920	MALOLACTIC ENZYME (EC 1)
MAOX_BACST	49%	1201	MALATE OXIDOREDUCTASE (NAD) (EC 1.1.1.38)
CITC_ECOLI	378	1205	[CITRATE (PRO-3S)-LYASE] LIGASE (EC 6.2.1.22)
CILG_HAEIN	52%	1205	CITRATE LYASE ACYL CARRIER PROTEIN (CITRATE LYASE GAMMA CHAIN)
CILB_KLEFN	52%	1206	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
CILA_ECOLI	56%	1207	CITRATE LYASE ALPHA CHAIN (EC 4.1.3.6)
BTO07 BAUEN		BUOGBUO	LIPID METABOLISM 20 genes
BIOUV. FRIIT	ACID AND	rnosrno	LIFID MEINBODIOM 2V Genes
BIO07.01 Gene	ral		20 genes
LPLA_MYCPN	36%	65	PROBABLE LIPOATE-PROTEIN LIGASE A (EC 6)
PLSX_BACSU	478	71	FATTY ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX HOMOLOG
OT DO DEODE			PATTI ACID/PROSPROSITID SINTRESIS PROTEIN PESA ROMODOG
GLPQ_BACSU	33%	217	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
FABZ_ECOLI		217 558	
FAB2_ECOLI 4.2.1)	33% 42%	558	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-{ACYL CARRIER PROTEIN] DEHYDRATASE (EC
FAB2_ECOLI 4.2.1) FABI_HAEIN	33% 42% 42%	558 559	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-{ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9)
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA	338 428 428 248	558 559 653	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-{ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2)
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA	33% 42% 42% 24% 49%	558 559 653 662	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-{ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14)
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU	33% 42% 42% 42% 48% 49%	558 559 653 662 781	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39)
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU	33% 42% 24% 48% 48% 45% 45%	558 559 653 662 781 782	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU FABG_BACSU FABF_VIBHA	33% 42% 42% 48% 48% 45% 45% 46% 42%	558 559 653 662 781 782 783	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41)
PAB2_ECOLI 4.2.1) PABI_HAEIN DLTA_LACCA ACCC_METJA PAB0_BACSU PAB6_BACSU PABF_VIBHA BCCP_ANASP	33% 42% 24% 48% 48% 45% 45%	558 559 653 662 781 782	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-{ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
PAB2_ECOLI 4.2.1) PAB1_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2}	338 428 428 488 488 458 468 468 458	558 559 653 662 781 782 783 783 784	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC
FAB2_DCOLI 4.2.1) FAB1_HAEIN DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN	33% 42% 42% 48% 48% 45% 45% 46% 42%	558 559 653 662 781 782 783	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41)
PAB2_ECOLI 4.2.1) PAB1_HAEIN DLTA_LACCA DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN FAB2_HAEIN 4.2.1)	338 428 428 488 488 458 468 458 468 458 458 458 518	558 559 653 662 781 782 783 784 784 784	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU	33% 42% 24% 49% 45% 46% 42% 51% 50%	558 559 653 662 781 782 783 784 784 784 784	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE (II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14)
FAB2_BCOLI 4.2.1) FAB1_HAEIN DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN	338 428 428 448 458 468 468 518 508 598 498	558 559 653 662 781 782 783 784 784 784	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC
PAB2_DCOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA (EC 6.4	33% 42% 42% 48% 45% 46% 42% 51% 50% 59% 49%	558 559 653 662 781 782 783 784 784 784 784 786 788	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA {CC 6.4 KDGL_STRMU	33% 42% 42% 48% 46% 46% 42% 51% 50% 59% 49% .1.2) 68%	558 559 653 662 781 782 783 784 784 784 784 786 788 1093	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107)
FAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2} FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA {EC 6.4 KOCL_STRMU ATOB_HAEIN	33% 42% 42% 45% 45% 46% 42% 51% 50% 59% 49% .1.2) 66% 44%	558 559 653 662 781 782 783 784 784 784 786 788 1093 1608	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9)
PAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA {EC 6.4 KDCL_STRMU ATOB_HAEIN FABG_BACSU	33% 42% 42% 45% 45% 46% 42% 51% 50% 59% 49% .1.2) 66% 44% 39%	558 559 653 662 781 782 783 784 784 784 786 788 1093 1608 1824	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYMPHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
PAB2_DCOLI 4.2.1) PABI_HAEIN DLTA_LACCA DCCC_METJA PABD_BACSU PABG_BACSU PABF_VIBHA BCCP_ANASP 6.4.1.2) PAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ACCA_HAEIN ACCA_HAEIN PABG_BACSU PAC_BACSH	33% 42% 42% 48% 46% 42% 51% 50% 59% 49% 49% 49% 45%	558 559 653 662 781 782 783 784 784 784 784 786 788 1093 1608 1824 1883	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILLIN ACYLASE (EC 3.5.1.11)
PAB2_ECOLI 4.2.1) PABI_HAEIN DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA (EC 6.4 KDGL_STRMU ATOB_HAEIN FABG_BACSU PAC_BACSU PGSA_BACSU	338 428 428 458 458 468 428 518 508 598 498 498 498 448 438 438	558 559 653 662 781 782 783 784 784 784 784 784 786 788 1093 1608 1824 1883 2026	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILLIN ACYLASE (EC 3.5.1.11) CDP-DIACYLGLYCEROLGLYCEROL-3-PHOSPHATE 3-
PAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU FABG_BACSU FABG_BACSU FABG_BACSU FAB2_HAEIN 4.2.1} ACCC_BACSU ACCA_HAEIN ALCHA {EC 6.4 KDGL_STRMU ATOB_HAEIN FABG_BACSU PAC_BACSU PACSU PASA_BACSU PHOSPHATIDYLT	33% 42% 42% 45% 45% 46% 42% 51% 50% 59% 49% 1.1.2) 66% 44% 39% 45% 45% 43% 7RANSFERAS	558 559 653 662 781 782 783 784 784 784 784 786 788 1093 1608 1824 1824 1823 2826 555 (EC 2	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILLIN ACYLASE (EC 3.5.1.11) CDP-DIACYLGLYCEROLGLYCEROL-3-PHOSPHATE 3- .7.8.5)
PAB2_ECOLI 4.2.1) PABI_HAEIN DLTA_LACCA ACCC_METJA FAB0_BACSU FAB6_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA (EC 6.4 KDGL_STRMU ATOB_HAEIN FABG_BACSU PAC_BACSU PGSA_BACSU	338 428 428 458 458 468 428 518 508 598 498 498 498 448 438 438	558 559 653 662 781 782 783 784 784 784 784 786 788 1093 1608 1824 1824 1823 2826 555 (EC 2	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILLIN ACYLASE (EC 3.5.1.11) CDP-DIACYLGLYCEROLGLYCEROL-3-PHOSPHATE 3-
PAB2_ECOLI 4.2.1) PAB1_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABD_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA {EC 6.4 KDGL_STRMU ATOB_HAEIN FABG_BACSU PAC_BACSH PGSA_BACSU PHOSPHATIDYLT CDSA_PSEAE	33% 42% 42% 45% 45% 45% 45% 51% 50% 59% 49% 49% 49% 45% 43% 45% 43% 32%	558 559 653 662 781 782 783 784 784 784 784 786 788 1093 1608 1824 1883 2026 5E (EC 2 2179	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE II (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-[ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILLIN ACYLASE (EC 3.5.1.11) CDP-DIACYLGLYCEROLGLYCEROL-3-PHOSPHATE 3- .7.8.5)
PAB2_ECOLI 4.2.1) PABI_HAEIN DLTA_LACCA ACCC_METJA FABD_BACSU FABD_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA {EC 6.4 KDGL_STRMU ATOB_HAEIN FABG_BACSU PAC_BACSU PHOSPHATIDYLT CDSA_PSEAE	33% 42% 42% 45% 45% 45% 45% 51% 50% 59% 49% 49% 49% 45% 43% 45% 43% 32%	558 559 653 662 781 782 783 784 784 784 784 786 788 1093 1608 1824 1883 2026 5E (EC 2 2179	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE (I (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] SYNTHASE (I (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILIN ACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3- .7.8.5) PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41)
PAB2_ECOLI 4.2.1) FABI_HAEIN DLTA_LACCA DLTA_LACCA ACCC_METJA FABD_BACSU FABG_BACSU FABF_VIBHA BCCP_ANASP 6.4.1.2) FAB2_HAEIN 4.2.1) ACCC_BACSU ACCA_HAEIN ALPHA {EC 6.4 KDCL_STRMU ATOB_HAEIN FABG_BACSU PHOSPHATIDYLT CDSA_PSEAE BIO08. PURINE	33% 42% 42% 45% 45% 46% 42% 51% 50% 59% 49% 1.1.2) 66% 44% 39% 45% 43% 7RANSFERAS 32%	558 559 653 662 781 782 783 784 784 784 786 788 1093 1608 1824 1883 2026 2027 2179 IDINES,	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) D-ALANINE-ACTIVATING ENZYME (EC 6.3.2) BIOTIN CARBOXYLASE (EC 6.3.4.14) MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (EC 2.3.1.39) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) 3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE (I (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN] SYNTHASE (I (EC 2.3.1.41) BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (EC (3R)-HYDROXYMYRISTOYL-(ACYL CARRIER PROTEIN] DEHYDRATASE (EC BIOTIN CARBOXYLASE (EC 6.3.4.14) ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT DIACYLGLYCEROL KINASE (EC 2.7.1.107) ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9) 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) PENICILIN ACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3- .7.8.5) PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41)

BIO08.02 Nucle	otide an	nd nucleo	oside interconversions 4 genes
DGK2_LACAC	62%	491	DEOXYGUANOSINE KINASE (EC 2.7.1.113) / DEOXYADENOSINE KINASE
(BC 2.7.1.76)			
KITH_STRGC	798	583	THYMIDINE KINASE (EC 2.7.1.21)
DGK2_LACAC	55%	1168	DEOXYGUANOSINE KINASE (EC 2.7.1.113) / DEOXYADENOSINE KINASE
(EC 2.7.1.76)			
KCY_BACSU	49%	1740	PROBABLE CYTIDYLATE KINASE (EC 2.7.4.14)
BIO08.03 Purin			
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) /
			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	67%	1514	GMP_SYNTHASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.2)
PURK_SYNY3	338	1548	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC
4.1.1.21)			
PUR6_HAEIN	59%	1549	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC
4.1.1.21)			
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	66%	1574	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC
6.3.2.6)			
PUR8_BACSU	76%	1685	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
PUR8_STRMU	81%	1685	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
KGUA_SYNY3	48%	1946	GUANYLATE KINASE (EC 2.7.4.8)
PURA_BACSU	59%	2009	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
PURQ_BACSU	318	2107	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE I (EC 6.3.5.3)
KAD_LACLA	988	2137	ADENYLATE KINASE (EC 2.7.4.3)
			otide biosynthesis 10 genes
PYRG_BACSU	64%	486	CTP SYNTHASE (EC 6.3.4.2)
PYRE_BACSU	578.	1078	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
PYRC_LACLE	42%	1079	DIHYDROOROTASE (EC 3.5.2.3)
DCOP_LACLC	978	1380	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
PYDB_LACLC		1381	DIHYDROOROTATE DEHYDROGENASE B (EC 1.3.3.1)
CDD_BACSU	54%	1461	CYTIDINE DEAMINASE (EC 3.5.4.5)
TYSY_LACLA		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)	400		
PYRB_SYNY3	42%	1641	ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2)
BTOOR OF Calma			and musleakides
			s and nucleotides 11 genes
HPRT_LACLA	99%	25	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
KTHY_BACSU APT_ECOLI	48% 54%	621	THYMIDYLATE KINASE (EC 2.7.4.9) ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
KPRS_BACSU	66%	824	RIBOSE-PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7) RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1)
DEOB_BACSU	558	953	PHOSPHOPENTOMUTASE (EC 5.4.2.7)
XPT_BACSU	52%	1157	XANTHINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2)
HPRT_BACSU	56%	1557	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.*)
URK_HAEIN	52%	1705	URIDINE KINASE (EC 2.7.1.48)
KPRS_BACCL	26%	1906	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC 2.7.6.1)
UPP_LACLA	978	1972	
PURR BACSU	-50%	2331	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) PUR OPERON REPRESSOR
PURR_BACSU	20.6	5331	FUR OPERON REPRESSOR
BT008.06 Sugar	-110100	ide bice	wynthesis and interconversions 0 genes
broos.oo bugar	-nucreot	Ide bios	Synchesis and interconversions 0 genes
BIO09. REGULAT	ORV PING	TONO	94 genes
BIOUS. REGULAR	OKI FUNC	TIONS	24 genes
BIO09.01 Gener	•1		41 conor
YQAE_BACSU	35%	11.	41 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA
INTERGENIC REG.			HIPOTREFICAL TRANSCRIPTIONAL REGULATOR IN SPOILIC-CWLA
	50%		DEMARTING ODEN DEDDDECOND
XRE_BACSU RELA_STREQ	50% 66%	44 106	PUTATIVE PBSX REPRESSOR
	298		PUTATIVE GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
	348	128	TETRACYCLINE REPRESSOR PROTEIN CLASS H
YQAE_BACSU		133.	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOIIIC-CWLA
INTERGENIC REG.			TETERACYCI THE DEDDECCOP DECERTIN OF ACC D. (TRANSCROUCH WHICH
TER2_ECOLI	38%	143	TETRACYCLINE REPRESSOR PROTEIN CLASS B (TRANSPOSON TN10)

CODY_BACSU	49%	162	CODY PROTEIN (VEGETATIVE PROTEIN 286B)
MECB BACSU	518	549	NEGATIVE REGULATOR OF GENETIC COMPETENCE MECH
CTSR_BACSU	458	627	TRANSCRIPTIONAL REGULATOR CTSR
MECB BACSU	50%	629	NEGATIVE REGULATOR OF GENETIC COMPETENCE MECH
	34%	737	HYPOTHETICAL P20 PROTEIN
YP20_BACLI			
SLYA_SALTY	26%	747	TRANSCRIPTIONAL REGULATOR SLYA (SALMOLYSIN) HYPOTHETICAL P20 PROTEIN
YP20_BACLI	33%	795	
BLAI_BACLI	31%	843	PENICILLINASE REPRESSOR (REGULATORY PROTEIN BLAI)
DEGU_BACSU	39%	910	TRANSCRIPTIONAL REGULATORY PROTEIN DEGU (PROTEASE PRODUCTION
ENHANCER PROT			
HRCA_LACLA	99%	975	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
SORC_KLEPN	21%	1204	SORBITOL (SOR) OPERON REGULATOR
XRE_BACSU	42%	1220	PUTATIVE PBSX REPRESSOR
YQAE_BACSU	35%	1300	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOIIIC-CWLA
INTERGENIC RE			
Y186_HAEIN	39%	1506	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI0186
TER2_ECOLI	29%	1551	TETRACYCLINE REFRESSOR PROTEIN CLASS B (TRANSPOSON TN10)
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_ECOLI	31%	1730	ARSENICAL RESISTANCE OPERON REPRESSOR
GERE_BACSU	41%	1737	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	31%	1927	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI0186
BIRA BACSU	33%	1953	BIRA BIFUNCTIONAL PROTEIN (BIOTIN OPERON REPRESSOR)
RPC2 BPP22	30%	2003	REPRESSOR PROTEIN C2
Y186 HAEIN	3.48	2032	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI0186
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
YQAE_BACSU	418	2276	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SPOIIIC-CWLA
INTERGENIC RE	GION (OR		
FNR_BACSU	28%	2298	ANAEROBIC REGULATORY PROTEIN
ACRR_ECOLI	32%	2317	POTENTIAL ACRAB OPERON REPRESSOR
BI009.02 Two-	component		
RESE_BACSU	338	400	SENSOR PROTEIN RESE (EC 2.7.3)
YYCF_BACSU	69%	401	HYPOTHETICAL 27.2 KD SENSORY TRANSDUCTION PROTEIN IN ROCK-PURA
INTERGENIC RE			
DEGS_BACBR	40%	909	SENSOR PROTEIN DEGS (EC 2.7.3)
CZCR_ALCEU	39%	1028	
YEDV_ECOLI	28%	1030	PROBABLE SENSOR PROTEIN YEDV (EC 2.7.3)
PHOP_BACSU	40%	1456	ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY
PROTEIN PHOP			
PHOR_BACSU	32%	1457	ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHOR (EC 2.7.3)
RESE_BACSU	278	1633	SENSOR PROTEIN RESE (EC 2.7.3)
CZCR_ALCEU	43%	1635	TRANSCRIPTIONAL ACTIVATOR PROTEIN CZCR
RESE_BACSU	33%	1722	SENSOR PROTEIN RESE (EC 2.7.3)
COPR_PSESM	34%	1723	TRANSCRIPTIONAL ACTIVATOR PROTEIN COPR
YXDK_BACSU	33%	1784	HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3 REGION (EC
2.7.3)			
YXDJ_BACSU	428	1785	HYPOTHETICAL 26.6 KD SENSORY TRANSDUCTION PROTEIN IN IDH
3'REGION			
BIO09.03 LacI	-family :	regulato	ors 6 genes
CYTR_ECOLI	28%	728	TRANSCRIPTIONAL REPRESSOR CYTR
DDOD DDOOT		4633	RIBOSE OPERON REPRESSOR
RBSR_BACSU	318	1533	
RBSR_BACSU	318 428	1684	RIBOSE OPERON REPRESSOR
			RIBOSE OPERON REPRESSOR PROBABLE CATABOLITE CONTROL PROTEIN A
RBSR_BACSU	42%	1684	
RBSR_BACSU CCPA_STAXY PURR_HAEIN	42% 47%	1684 1692	PROBABLE CATABOLITE CONTROL PROTEIN A
RBSR_BACSU CCPA_STAXY	42% 47% 34%	1684 1692 1724	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION	42% 47% 34% 36%	1684 1692 1724 2196	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LyBR	42% 47% 34% 36%	1684 1692 1724 2196 regulato	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC MIS 4 genes
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION	42% 47% 34% 36% -family 25%	1684 1692 1724 2196 regulato 375	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC MARKET A genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LyBR WWFK_BACSU MLER_LACLA	42% 47% 34% 36% -family 25% 100%	1684 1692 1724 2196 regulato 375 893	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC MS 4 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC FERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LysR YWFR_BACSU	42% 47% 34% 36% -family 25%	1684 1692 1724 2196 regulato 375	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC MARKET A genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LysR YWFR_BACSU MLER_LACLA YWBI_BACSU REGION	42% 47% 34% 36% -family 25% 100% 29%	1684 1692 1724 2196 regulato 375 893 1261	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC 4 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC PERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN EPR-GALK INTERGENIC
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LyGR YWFK_BACSU MLER_LACLA YWBI_BACSU REGION YWBI_BACSU	42% 47% 34% 36% -family 25% 100% 29%	1684 1692 1724 2196 regulato 375 893 1261	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC MS 4 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC FERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR
RBSR_BACSU CCPA_STAXY PURR_HAEIN YYAG_BACSU REGION BIO09.04 LysR YWFR_BACSU MLER_LACLA YWBI_BACSU REGION	42% 47% 34% 36% -family 25% 100% 29%	1684 1692 1724 2196 regulato 375 893 1261	PROBABLE CATABOLITE CONTROL PROTEIN A PURINE NUCLEOTIDE SYNTHESIS REPRESSOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN TETB-EXOA INTERGENIC 4 genes HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PTA 3'REGION MALOLACTIC PERMENTATION SYSTEM TRANSCRIPTIONAL ACTIVATOR HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN EPR-GALK INTERGENIC

4 genes

BIO09.05 AraC-family regulators

CLAD LACED	30%	480	S-LAYER PROTEIN PRECURSOR (SURFACE LAYER PROTEIN)
SLAP_LACBR			
ADAA_BACSU	448	517	METHYLPHOSPHOTRIESTER-DNA ALKYLTRANSFERASE
LUMQ_PHOLE	32%	1547	PROBABLE TRANSCRIPTIONAL REGULATOR LUMO
TOXA_CLODI	30%	2284	TOXIN A
BIO09.06 GntR-	family	regulato:	rs 6 genes
YHHX_ECOLI	44%	261	HYPOTHETICAL 38.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION
(F345)			
TRER_BACSU	44%	434	TREHALOSE OPERON TRANSCRIPTIONAL REPRESSOR
FARR_ECOLI	30%	1459	FATTY ACYL RESPONSIVE REGULATOR (P30 PROTEIN)
YIN1 STRAM	30%	1676	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN INSTABLE DNA LOCUS
_	565	1010	Informatione management in another and accord
(ORF 1)			
YXAM_BACSU	24%	2215	HYPOTHETICAL 44.7 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION
YXAT_BACSU	18%	2305	HYPOTHETICAL 44.3 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION
TAA1_BACS0	10-8	2303	AIPOINDITCAL 44.5 KD PROIDIN IN GNIK-HIPG INTERGENIC REGION
		. .	-
BI009.07 DeoR-			
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
WW		341	PRODUDE ADC INMADIONIER DINDING PROTEIN IN IDA-DEOK INTERGENIC
REGION PRECURS			
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	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
YXEA_BACSU	398	1504	HYPOTHETICAL 13.0 KD PROTEIN IN IDH-DEOR INTERGENIC REGION
PRECURSOR			
BI009.08 MarR-	familv	regulato	rs 2 genes
YDEA ECOLI	32%		HYPOTHETICAL 42.5 KD PROTEIN IN UXAB-MARR INTERGENIC REGION
PETP_RHOCA	34%	1338	PETP PROTEIN
BI009.09 Bg1G-:	family	regulator	rs 1 genes
LICT_BACSU	418	1491	TRANSCRIPTION ANTITERMINATOR LICT
BI009.10 GTP-b:	inding	proteins	9 genes
YYAF_BACSU	68%	12	HYPOTHETICAL 40.1 KD GTP-BINDING PROTEIN IN RPSF-SPO0J
		14	HIPOTHETICAL 40.1 KD GIP-BINDING PROIEIN IN RPSP-SP003
INTERGENIC REG.	ION		
HFLX_ECOLI	448	222	GTP-BINDING PROTEIN HFLX
THE A CONTRACTOR	7.0 0	25.2	
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
YPHC_BACSU			
YPHC_BACSU REGION	62%	760	HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC
YPHC_BACSU			
YPHC_BACSU REGION LEPA_BACSU	62%	760	HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU	62% 77%	760 1116	HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX)	62% 77% 66%	760 1116 1163	HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA HYPOTHETICAL GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU	62% 77%	760 1116	HYPOTHETICAL 48.8 KD GTP-BINDING PROTEIN IN CMK-GPSA INTERGENIC GTP-BINDING PROTEIN LEPA
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU	62% 77% 66% 64%	760 1116 1163 1626	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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3	62% 77% 66% 64% 51%	760 1116 1163 1626 1654	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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU	62% 77% 66% 64%	760 1116 1163 1626	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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU	62% 77% 66% 51% 51% 60%	760 1116 1163 1626 1654	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 THDP
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3	62% 77% 66% 51% 51% 60%	760 1116 1163 1626 1654	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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA	62% 77% 66% 64% 51% 60% FION	760 1116 1163 1626 1654 2308	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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDF_BACSU BIO10. REPLICA BIO10.1 Degrad	62% 77% 66% 64% 51% 60% FION	760 1116 1163 1626 1654 2308 of DNA	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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA	62% 77% 66% 64% 51% 60% FION	760 1116 1163 1626 1654 2308	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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrac ADDB_BACSU	62% 77% 66% 51% 60% FION dation 28%	760 1116 1163 1626 1654 2308 of DNA 5	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 (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAY BIO10.01 Degrad ADDB_BACSU ADDA_BACSU	62% 77% 66% 51% 60% FION lation 28% 32%	760 1116 1163 1626 1654 2308 of DNA 5 7	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 (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA: BIO10.01 Degrac ADDB_BACSU ADDA_BACSU ADDA_BACSU	62% 77% 66% 51% 60% FION 28% 32% 33%	760 1116 1163 1626 1654 2308 of DNA 5 7 9	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 ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A ATP-DEPENDENT NUCLEASE SUBUNIT A
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAY BIO10.01 Degrad ADDB_BACSU ADDA_BACSU	62% 77% 66% 51% 60% FION lation 28% 32%	760 1116 1163 1626 1654 2308 of DNA 5 7	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 (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF 77 genes 11 genes ATP-DEPENDENT NUCLEASE SUBUNIT B ATP-DEPENDENT NUCLEASE SUBUNIT A
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDF_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU	62% 77% 66% 64% 51% 60% FION lation 28% 32% 33% 40%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555	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 THOP 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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Degrac ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH	62% 77% 66% 51% 60% FION 28% 32% 33% 40% 36%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619	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 (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THOF 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVNB_HAEIN RECJ_ERNCH EXOA_BACSU	62% 77% 66% 51% 60% FION lation 28% 32% 33% 40%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796	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 (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 ATP-DEPENDENT NUCLEASE SUBUNIT A EXCINUCLEASE ARC SUBUNIT B SINGLE-STRANEDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.01 Degrac ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH	62% 77% 66% 51% 60% FION 28% 32% 33% 40% 36%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619	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 (PIFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THOF 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA BIO10.1 Degrad ADDD_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU	62% 77% 66% 51% 60% FION 28% 32% 33% 40% 36% 54%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855	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 THOF 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) EXCINUCLEASE ABC SUBUNIT C
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDF_BACSU BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX7L_BACSU	62% 77% 66% 51% 60% FION 28% 32% 33% 40% 36% 54% 43%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876	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 THOP 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) EXCIDUCLEASE ABC SUBUNIT C EXCINUCLEASE ABC SUBUNIT C
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA BIO10.1 Degrad ADDD_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU	62% 77% 66% 51% 60% FION 28% 32% 33% 40% 36% 54%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855	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 THOP 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) EXCIDUCLEASE ABC SUBUNIT C EXCINUCLEASE ABC SUBUNIT C
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERNCH EXOA_BACSU UVRC_BACSU ENJ3_BACSU	62% 77% 66% 51% 60% FION 28% 32% 32% 32% 33% 40% 54% 40% 54% 50%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081	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 (PIFTY-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) EXOBEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXOBEOXYRIBONUCLEASE IARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXD3_BACSU EXD3_BACSU	62% 77% 66% 64% 51% 60% FION 28% 33% 40% 54% 40% 54% 40% 54% 53% 27%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777	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 CTP-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 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERNCH EXOA_BACSU UVRC_BACSU ENJ3_BACSU	62% 77% 66% 51% 60% FION 28% 32% 32% 32% 33% 40% 54% 40% 54% 50%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081	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 (PIFTY-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) EXOBEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXOBEOXYRIBONUCLEASE IARGE SUBUNIT (EC 3.1.11.6) PROBABLE ENDONUCLEASE III (EC 4.2.99.18)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA BIO10.01 Degrad ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU	62% 77% 66% 51% 60% FION 28% 32% 32% 30% 36% 40% 54% 43% 54% 54% 53%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778	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 (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-STRANED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBURIT C PUTATIVE EXODEOXYRIBONUCLEASE 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRE_HAEIN RECJ_ERNCH EXOA_BACSU UVRC_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU	62% 77% 66% 51% 60% FION 28% 32% 32% 30% 36% 40% 54% 43% 54% 54% 53%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778	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 CTP-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 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU	62% 77% 66% 51% 60% FION 28% 32% 32% 30% 36% 40% 54% 43% 54% 54% 53%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778	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 CTP-BINDING PROTEIN SIGNAL RECOGNITION PARTICLE PROTEIN (IFTY-FOUR HOMOLOG) POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THOF 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 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRE_HAEIN RECJ_ERNCH EXOA_BACSU UVRC_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU	62% 77% 66% 51% 60% FION 28% 32% 32% 30% 36% 40% 54% 43% 54% 54% 53%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778	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 (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-STRANED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBURIT C PUTATIVE EXODEOXYRIBONUCLEASE 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX7L_BACSU	62% 77% 66% 51% 60% FION 28% 32% 40% 54% 40% 54% 40% 54% 40% 54% 40% 52% 27% 32%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest	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 (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-STRANEED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (IC 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERNCH EXOA_BACSU UVRC_BACSU EXTA_BACSU	62% 77% 66% 64% 51% 60% 710N 814100 28% 32% 32% 33% 40% 54% 40% 54% 27% 32% 36% 40% 50% 27% 32%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2	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 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) EXISTICION, modification, recombination, and repair 66 CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX7L_BACSU	62% 77% 66% 51% 60% FION 28% 32% 40% 54% 40% 54% 40% 54% 40% 54% 40% 52% 27% 32%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest	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 (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-STRANEED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXODEOXYRIBONUCLEASE (IC 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)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU (ORFX) BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU BIO10.02 DNA re genes DNAA_STAAU DP3B_STAAU	62% 77% 66% 64% 51% 60% FION 84% 33% 40% 54% 40% 54% 40% 50% 27% 32% 80% 27% 32% 40% 50% 27% 32% 45% 45%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19	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 CTP-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) 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 POLYPEPT
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX7L_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA ra genes DNAA_STAAU DP3B_STAAU MPD_BACSU PRIM_BPP4	62% 77% 66% 51% 60% FION 8 ation 28% 32% 33% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 54% 54% 54% 54% 54% 54% 54% 54% 54	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38	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 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 V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE III (EC 4.2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCP) PUTATIVE F4-SPECIFIC DNA PRIMASE (EC 2.7.7)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU (ORFX) BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU EXTL_BACSU BIO10.02 DNA re genes DNAA_STAAU DP3B_STAAU	62% 77% 66% 64% 51% 60% FION 84% 33% 40% 54% 40% 54% 40% 50% 27% 32% 80% 27% 32% 40% 50% 27% 32% 45% 45%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19	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 CTP-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) 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 POLYPEPT
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX7L_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA ra genes DNAA_STAAU DP3B_STAAU MPD_BACSU PRIM_BPP4	62% 77% 66% 51% 60% FION 8 ation 28% 32% 33% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 54% 54% 54% 54% 54% 54% 54% 54% 54	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38	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 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 V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE III (EC 4.2.7.7.7) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCP) PUTATIVE F4-SPECIFIC DNA PRIMASE (EC 2.7.7)
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRE_BACSU UVRE_BACSU UVRE_BACSU EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI BIO10.2 DNA re genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXN_BACSU (ORF3)	62% 77% 66% 64% 51% 60% 710N 84tion 28% 32% 33% 40% 54% 43% 50% 27% 32% 40% 54% 43% 50% 27% 32% 40% 50% 27% 32% 45% 45% 41% 50% 21%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58	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-STRANBED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE IL (EC 4.2.99.18) EXODEOXYRIBONUCLEASE 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) EXISTICATION, 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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICA: BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA re genes DNAA_STAAU DP3B_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXU_BACSU YQEU_BACSU	62% 77% 66% 64% 51% 60% 28% 32% 32% 33% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 50% 27% 32% 40% 45% 45% 45% 45% 45% 45% 45% 45% 45% 45	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58 103	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 SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (IFTY-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) 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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRE_BACSU UVRE_BACSU UVRE_BACSU EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI BIO10.2 DNA re genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXN_BACSU (ORF3)	62% 77% 66% 64% 51% 60% 710N 84tion 28% 32% 33% 40% 54% 43% 50% 27% 32% 40% 54% 43% 50% 27% 32% 40% 50% 27% 32% 45% 45% 41% 50% 21%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58	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-STRANBED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE IL (EC 4.2.99.18) EXODEOXYRIBONUCLEASE 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) EXISTICATION, 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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAY BIO10.01 Degrad ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EXTL_BACSU EXTL_BACSU EXTA_BACSU EXTA_BACSU EXTA_BACSU EXTA_COLI BIO10.02 DNA re genes DNAA_STAAU DP3B_STAAU NPD_BACSU PRIM_BP4 YQXN_BACSU (ORF3) YQEU_BACSU	62% 77% 66% 51% 60% FION 8 ation 28% 32% 33% 40% 54% 40% 54% 40% 27% 32% 901icat 45% 41% 44%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58 103 120	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-STRANED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXOBOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE III (EC 4.2.99.18) EXOBEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA ra genes DNAA_STAAU DP3B_STAAU MPD_BACSU YRIM_BAPP4 YQXN_BACSU YAAK_BACSU YAAK_BACSU YAAK_BACSU	62% 77% 66% 64% 51% 60% 28% 32% 32% 33% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 54% 40% 50% 27% 32% 40% 45% 45% 45% 45% 45% 45% 45% 45% 45% 45	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58 103	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 SPOOB-ASSOCIATED GTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (IFTY-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) 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
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRE_BACSU UVRE_BACSU EX71_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA re genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXU_BACSU YAREBACSU YAREBACSU YAREBACSU YAREBACSU YAREBACCE 3.1.21.5)	62% 77% 66% 64% 51% 60% FION 28% 33% 40% 54% 40% 54% 40% 54% 40% 27% 32% 40% 27% 32% 40% 27% 32% 41% 31% 44% 44% 29%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58 103 120 151	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 CTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (IFTY-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) 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 III (EC 4.2.7.7.) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA PRIMASE (EC 2.7.7) HYPOTHETICAL 29.3 KD PROTEIN IN DEX-DNAG/DNAE INTERGENIC REGION HYPOTHETICAL 28.8 KD PROTEIN IN DNAJ-RPSU INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECR INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECR INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECR INTERGENIC REGION
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.01 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU ADDA_BACSU UVRB_HAEIN RECJ_ERWCH EXOA_BACSU UVRC_BACSU EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA ra genes DNAA_STAAU DP3B_STAAU MPD_BACSU YRIM_BAPP4 YQXN_BACSU YAAK_BACSU YAAK_BACSU YAAK_BACSU	62% 77% 66% 51% 60% FION 8 ation 28% 32% 33% 40% 54% 40% 54% 40% 27% 32% 901icat 45% 41% 44%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58 103 120	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-STRANED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1) EXOBOXYRIBONUCLEASE (EC 3.1.11.2) EXCINUCLEASE ABC SUBUNIT C PUTATIVE EXODEOXYRIBONUCLEASE III (EC 4.2.99.18) EXOBEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC 3.1.11.5) EXODEOXYRIBONUCLEASE V 67 KD POLYPEPTIDE (EC
YPHC_BACSU REGION LEPA_BACSU YSXC_BACSU (ORFX) OBG_BACSU SR54_SYNY3 THDP_BACSU BIO10. REPLICAN BIO10.1 Degrad ADDB_BACSU ADDA_BACSU ADDA_BACSU UVRE_BACSU UVRE_BACSU EX71_BACSU EX5A_ECOLI EX5A_ECOLI BIO10.02 DNA re genes DNAA_STAAU DP3B_STAAU MFD_BACSU PRIM_BPP4 YQXU_BACSU YAREBACSU YAREBACSU YAREBACSU YAREBACSU YAREBACCE 3.1.21.5)	62% 77% 66% 64% 51% 60% FION 28% 33% 40% 54% 40% 54% 40% 54% 40% 27% 32% 40% 27% 32% 40% 27% 32% 41% 31% 44% 44% 29%	760 1116 1163 1626 1654 2308 of DNA 5 7 9 555 619 796 855 876 1081 1777 1778 ion, rest 1 2 19 38 58 103 120 151	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 CTP-BINDING PROTEIN IN LONA-HEMA INTERGENIC REGION SIGNAL RECOGNITION PARTICLE PROTEIN (IFTY-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) 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 III (EC 4.2.7.7.) TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) PUTATIVE P4-SPECIFIC DNA PRIMASE (EC 2.7.7) HYPOTHETICAL 29.3 KD PROTEIN IN DEX-DNAG/DNAE INTERGENIC REGION HYPOTHETICAL 28.8 KD PROTEIN IN DNAJ-RPSU INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECR INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-RECR INTERGENIC REGION HYPOTHETICAL 11.8 KD PROTEIN IN DNAJ-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% 35%	395 . 402	SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III, DELTA' SUBUNIT (EC 2.7.7.7)			
HOLB_BACSU	438	423	DNA LIGASE (EC 6.5.1.2)			
DNLJ_RHOMR DNAC_ECOLI	278	454	DNA REPLICATION PROTEIN DNAC			
DP3A_HELPY	26%	494				
PRIM_LACLA	100%	542	DNA PRIMASE (EC 2.7.7)			
DFP_ECOLI	30%	565	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN			
TIR1_ECOLI	32%	640	TYPE I RESTRICTION ENZYME ECOR12411 R PROTEIN (EC 3.1.21.3)			
YC18_METJA	27%	644	HYPOTHETICAL PROTEIN MJ1218			
YABF_BACSU	47%	687	HYPOTHETICAL 20.7 KD PROTEIN IN METS-KSGA INTERGENIC REGION			
YAAJ_BACSU	51%	725	HYPOTHETICAL 17.8 KD PROTEIN IN SERS-DNAH INTERGENIC REGION			
DNAC_BACSU	56%	752	REPLICATIVE DNA HELICASE (EC 3.6.1)			
DNAB_BACSU	27%	756	REPLICATION INITIATION AND MEMBRANE ATTACHMENT PROTEIN			
DNAI_BACSU	388	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	99%	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	70%	1005	TOPOISOMERASE IV SUBUNIT B (EC 5.99.1) PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG			
DING_BACSU	38%	1007	TOPOISOMERASE IV SUBUNIT A (EC 5.99.1)			
PARC_STAAU	53% 41%	1009				
RADC_BACSU SSB_BACSU	618	1033	SINGLE-STRAND BINDING PROTEIN (SSB)			
DNAD. BACSU	378		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				
DYR_LACLA	87%	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	348	1689	DNA MISMATCH REPAIR PROTEIN			
			ATP-DEPENDENT DNA HELICASE RECQ (EC 3.6.1)			
RECQ_ECOLI	35%	1854				
RECQ_ECOLI DING_BACSU	348	1878	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG			
DING_BACSU DING_BACSU	34% 28%	1878 1880	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG			
DING_BACSU DING_BACSU PRIA_BACSU	34% 28% 58%	1878 1880 1944	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU	34% 28% 58% 49%	1878 1880 1944 2030	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC	34% 28% 58% 49% 99%	1878 1880 1944 2030 2031	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI	34% 28% 58% 49% 99% 42%	1878 1880 1944 2030 2031 2085	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REFLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU	34% 28% 58% 49% 99%	1878 1880 1944 2030 2031	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG)	34% 28% 58% 99% 42% 60%	1878 1880 1944 2030 2031 2085 2129	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU	34% 28% 58% 49% 99% 42% 60%	1878 1880 1944 2030 2031 2085 2129 2171	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN	34% 28% 58% 49% 99% 42% 60% 42% 68%	1878 1880 1944 2030 2031 2085 2129 2171 2192	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU	34% 28% 58% 49% 99% 42% 60%	1878 1880 1944 2030 2031 2085 2129 2171	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINF_ECOLI RADA_BACSU HOMOLOG DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU	34% 28% 58% 49% 99% 42% 60% 42% 68% 60% 42% 68% 60% 43%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) SINGLE-STRAND BINDING FROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DF3A_BACSU DP01_STRPN SSB_BACSU	34% 28% 58% 49% 99% 42% 60% 42% 68% 60% 43% 59%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) SINGLE-STRAND BINDING PROTEIN (SSB)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU DP3X_BACSU RUVB_PSEAE	34% 28% 58% 49% 99% 42% 60% 42% 68% 60% 43% 59%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269 2269	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBUNITS GAMMA AND TAU (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU DP3X_BACSU RUVB_PSEAE RUVA_HAEIN	34% 28% 58% 49% 99% 42% 60% 42% 68% 60% 43% 59% 40%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) 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			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU DP3X_BACSU RUVB_PSEAE RUVA_HAIN HEXB_STRPN	34% 28% 58% 49% 99% 42% 60% 42% 68% 60% 43% 59% 40% 57%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269 2269	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) 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			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU DOOLOG1 DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN	34% 28% 58% 49% 99% 42% 60% 42% 68% 60% 43% 59% 40% 57% 79%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269 2269 2271 2274	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) SINGLE-STRAND BINDING FROTEIN (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			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINF_ECOLI RADA_BACSU HOMOLOG DF3A_BACSU DF3A_BACSU DF3A_BACSU DF3A_BACSU DF3X_BACSU DF3X_BACSU RUVB_FSEAE RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI	34% 28% 58% 49% 99% 42% 60% 42% 60% 42% 60% 42% 59% 59% 57% 79% 99% 36%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269 2269 2269 2269 2274 2274	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DANAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE III (EC 2.7.7.7) 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)			
DING_BACSU DING_BACSU PRIA_BACSU YAAA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU DP3X_BACSU RUVB_PSEAE RUVA_HAEIN HEXA_STRPN DNAJ_LACLA	34% 28% 58% 49% 99% 42% 60% 42% 60% 42% 60% 42% 59% 59% 57% 79% 99% 36%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269 2269 2269 2269 2274 2274	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) 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 FROTEIN			
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DING_BACSU DING_BACSU PRIA_BACSU PRIA_BACSU PRIA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU DP3X_BACSU DP3X_BACSU RUVA_HAEIN HEXA_STRPN HEXA_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCR BIO11.01 Degra TRUA_ECOLI YACO_BACSU	34% 28% 56% 49% 99% 42% 60% 60% 60% 42% 60% 42% 60% 57% 40% 57% 99% 36% 81PTION 8dation 34% 26%	1878 1880 1944 2030 2031 2032 2129 2171 2192 2254 2259 2269 2271 2274 2287 2311 of RNA 482 595	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEINN ' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) SINGLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE II (EC 2.7.7.7) HOLLIDAY JUNCTION DNA HELICASE RUVB HOLLIDAY JUNCTION DNA HELICASE RUVA DNA MISMATCH REPAIR PROTEIN HEXB 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			
DING_BACSU DING_BACSU PRIA_BACSU PRIA_BACSU PRIA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DP3A_BACSU DP01_STRPN SSB_BACSU DP3X_BACSU DP3X_BACSU DP3X_BACSU RUVA_HAEIN HEXB_STRPN HEXA_STRPN DNAJ_LACLA RECG_ECOLI BIO11. TRANSCE BIO11.01 Degra TRUA_ECOLI	34% 28% 58% 99% 99% 42% 60% 42% 60% 42% 60% 42% 59% 59% 59% 36% 79% 99% 36% 81PTION 84dtion 4 34%	1878 1880 1944 2030 2031 2085 2129 2171 2192 2254 2259 2269 2269 2269 2271 2274 2287 2311 of RNA 482	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DANAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE III (EC 2.7.7.7) 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 18 genes PSEUDOURIDYLATE SYNTHASE I (EC 4.2.1.70)			
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DING_BACSU DING_BACSU DING_BACSU PRIA_BACSU PRIA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DF3A_BACSU DF3A_BACSU DF3X_BACSU DF3X_BACSU DF3X_BACSU DF3X_BACSU DF3X_BACSU DF3X_BACSU DF3X_BACSU DF3A_BACSU DF3A_BACSU PAS_BACSU DF3A_BACSU DF3	34% 28% 58% 99% 42% 60% 42% 60% 42% 60% 43% 59% 36% 36% 31% 32% 44% 37% 31% 32% 44% 37% 31% 39% 55% 47% 39% 26%	1878 1880 1944 2030 2031 2085 2129 2254 2259 2269 2274 2274 2287 2311 of RNA 482 595 613 807 965 1114 1138 1160 1250 1326 1326 1326 1326	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBURITS 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 AND HEXE (EC 4.1.1.5) RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) RIBONUCLEASE HII (EC 3.1.26.4) EXONUCLEASE SEDCH HOMOLOG (FRAGMENT) POLY (A) POLYMERASE (EC 4.1.1.5) RIBONUCLEASE SEDCH HOMOLOG (FRAGMENT) POLY (A) POLYMERASE (EC 3.1.26.4) EXONUCLEASE SEDCH HOMOLO			
DING_BACSU DING_BACSU PRIA_BACSU PRIA_BACSU PRIA_BACSU RECF_LACLC DINP_ECOLI RADA_BACSU HOMOLOG) DF3A_BACSU DF01_STRPN SSB_BACSU DF3A_BACSU	34% 28% 58% 99% 42% 60% 42% 60% 42% 60% 43% 59% 36% 79% 36% 32% 32% 31% 39% 31% 39% 35% 44% 37% 31% 39% 35% 42% 35% 39%	1878 1880 1944 2030 2031 2032 2129 2254 2259 2269 2269 2271 2274 2287 2311 0df RNA 482 595 613 807 965 1114 1138 1160 1250 1354 1598	PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PROBABLE ATP-DEPENDENT HELICASE DING HOMOLOG PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) HYPOTHETICAL 7.9 KD PROTEIN IN DNAN-RECF INTERGENIC REGION RECF PROTEIN DNA-DAMAGE-INDUCIBLE PROTEIN P DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7) DNA POLYMERASE I (EC 2.7.7.7) SINCLE-STRAND BINDING PROTEIN (SSB) DNA POLYMERASE III SUBURITS 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 AND HEXE (EC 4.1.1.5) RIBONUCLEASE III (EC 3.1.26.3) VACE PROTEIN HOMOLOG ALPHA-ACETOLACTATE DECARBOXYLASE PRECURSOR (EC 4.1.1.5) RIBONUCLEASE HII (EC 3.1.26.4) EXONUCLEASE SEDCH HOMOLOG (FRAGMENT) POLY (A) POLYMERASE (EC 4.1.1.5) RIBONUCLEASE SEDCH HOMOLOG (FRAGMENT) POLY (A) POLYMERASE (EC 3.1.26.4) EXONUCLEASE SEDCH HOMOLO			

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 Nucleopro	oteins	2 genes
DBH_BACST 67		DNA-BINDING PROTEIN II (HB)
DBH_VIBPR 37		DNA-BINDING PROTEIN HU
BIO12.04 Protein m CYPH_MYCTU 31		2 genes PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
CYPH_MYCTU 37		PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
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		synthesis and modification 55 genes
PRMA_BACSU 43		PROBABLE METHYLTRANSFERASE (EC 2.1.1)
RL34_COXBU 70 RL28 BACSU 56		50S RIBOSOMAL PROTEIN L34 50S RIBOSOMAL PROTEIN L28
RL28_BACSU 56 RS21_BACSU 87		30S RIBOSOMAL PROTEIN S21 (BS-B)
RS4_BACSU 62		30S RIBOSOMAL PROTEIN S4 (BS4)
R14H_BACSH 35	5% 306	30S RIBOSOMAL PROTEIN S14 HOMOLOG
DEAD_KLEPN 45		ATP-DEPENDENT RNA HELICASE DEAD
YVYD_BACSU 51		HYPOTHETICAL 22.0 KD PROTEIN IN FLIT-SECA INTERGENIC REGION
100 ·)0% 659 3% 751	50S RIBOSOMAL PROTEIN L33 50S RIBOSOMAL PROTEIN L9 (BL17)
RL9_BACST 52 YLX0_ENTFC 48		PROBABLE RIBOSOMAL PROTEIN IN INFB 5'REGION
RS1_BUCAP 32		305 RIBOSOMAL PROTEIN S1
RL19_BACST 73		50S RIBOSOMAL PROTEIN L19
RS14_SYNY3 41	\$ 908	30S RIBOSOMAL PROTEIN \$14
RL21_BACSU 67		50S RIBOSOMAL PROTEIN L21 (BL20)
RL27_BACSU 74 RL7_BACSU 61		50S RIBOSOMAL PROTEIN L27 (BL30) 50S RIBOSOMAL PROTEIN L7/L12 (BL9)
RL7_BACSU 61 RL7_STRPN 76		50S RIBOSOMAL PROTEIN L7/L12 (BLS) 50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT)
RL10_BACSU 63		50S RIBOSOMAL PROTEIN L10 (BL5)
RS16_BACSU 59		30S RIBOSOMAL PROTEIN S16 (BS17)
YKGM_ECOLI 45		HYPOTHETICAL 9.9 KD PROTEIN IN INTF-EACH INTERGENIC REGION
RL20_BACSU 69		50S RIBOSOMAL PROTEIN L20
RS15_BACSU 62 RL1_BACSU 67		30S RIBOSOMAL PROTEIN S15 (BS18) 50S RIBOSOMAL PROTEIN L1 (BL1)
RL1_BACSU 67 RL11_STACA 80		50S RIBOSOMAL PROTEIN L11
R14H_BACSH 30		30S RIBOSOMAL PROTEIN \$14 HOMOLOG
RL17_BACSU 72	2131	50S RIBOSOMAL PROTEIN L17 (BL15)
RS11_BACSU 82		30S RIBOSOMAL PROTEIN S11 (BS11)
RS13_BACSU 70 RL15_STAAU 67		30S RIBOSOMAL PROTEIN S13 (BS14) 50S RIBOSOMAL PROTEIN L15
RL15_STAAU 67 RS5_BACSU 77		30S RIBOSOMAL PROTEIN S5 (BS5)
RL6_BACST 63		50S RIBOSOMAL PROTEIN L6 (BL10)
RS8_BACSU 72	2142	30S RIBOSOMAL PROTEIN S8 (BS8)
RL5_BACST 80		50S RIBOSOMAL PROTEIN L5
RL24_BACST 62 RL14_BACSU 80		50s ribosomal protein L24 50s ribosomal protein L14
RS17_BACSU 77		30S RIBOSOMAL PROTEIN S17 (BS16)
RL16_BACSU 76		50S RIBOSOMAL PROTEIN L16
RS3_BACSU 73		30S RIBOSOMAL PROTEIN S3 (BS3)
RL22_BACSU 62		50S RIBOSOMAL PROTEIN L22
RS19_BACST 77 RL2_BACSU 76		30S RIBOSOMAL PROTEIN S19 (BS19) 50S RIBOSOMAL PROTEIN L2 (BL2)
RL4_BACSU 60		50S RIBOSOMAL PROTEIN L4
RL3_BACSU 69		50S RIBOSOMAL PROTEIN L3 (BL3)
RS10_STRMU 81		30S RIBOSOMAL PROTEIN \$10
RL33_MYCCA 57		50S RIBOSOMAL PROTEIN L33 30S RIBOSOMAL PROTEIN S2
RS2_PEDAC 71 RS2_BACSU 10	L% 2207)0% 2208	30S RIBOSOMAL PROTEIN SZ (BS1)
RS18_BACST 63		30S RIBOSOMAL PROTEIN S18 (BS21)
RS6_BACSU 58		30S RIBOSOMAL PROTEIN S6 (BS9)
RS9_BACSU 65		30S RIBOSOMAL PROTEIN S9 (BS10)
	3% 2327	50S RIBOSOMAL PROTEIN L13
RS7_ECOLI 64 RS7_BACSU 71	1% 2334 1% 2334	30S RIBOSOMAL PROTEIN S7 30S RIBOSOMAL PROTEIN S7 (BS7)
	7% 2335	305 RIBOSOMAL PROTEIN S12
BIO12.05 tRNA mod		8 genes
	5% 17 7% 129	PROBABLE PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) RIBONUCLEASE P PROTEIN COMPONENT (EC 3.1.26.5)
	2% 687	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1)
YGCA_HAEIN 30		HYPOTHETICAL RNA METHYL/TRANSFERASE HI0333 (EC 2.1.1)
TRMD_HAEIN 50		TRNA (GUANINE-N1)-METHYLTRANSFERASE (EC 2.1.1.31)
MDMC_STRMY 31		O-METHYLTRANSFERASE (EC 2.1.1)
FMT_BACSU 46 YGCA_HAEIN 27		METHIONYL-TRNA FORMYLTRANSFERASE (EC 2,1.2,9) HYPOTHETICAL RNA METHYLTRANSFERASE HI0333 (EC 2,1.1,-)
BIO12.07 Translat:		23 genes
YDGI_BACSU 30	0% 183	PUTATIVE NAD(P)H NITROREDUCTASE (EC 1)

RF3_SYNY3	478	349	PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)
RF2_HELPY	25%	451	PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)
IF2_ENTFC	36%	543	TRANSLATION INITIATION FACTOR IF-2
RF1_BACSU	54%	584	PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)
FLAV_DESVH	388	595	PLAVODOXIN
EFP_BACSU	48%	689	ELONGATION FACTOR P. (EF-P)
IF2 ENTFC	698	775	TRANSLATION INITIATION FACTOR IF-2
RBFA_BACSU	378	777	RIBOSOME-BINDING FACTOR A (P15B PROTEIN)
RF2 BACSU			
YDGI_BACSU	498	1500	PUTATIVE NAD(P)H NITROREDUCTASE (EC 1)
MVIM_ECOLI	348	1872	VIRULENCE FACTOR MVIM HOMOLOG
IF3_BACSU	61%	1892	TRANSLATION INITIATION FACTOR IF-3
EFTU_STROR	808	1909	ELONGATION FACTOR TU (EF-TU)
RRF_HAEIN	438	2066	RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR)
YIHK_ECOLI	55%	2073	65.4 KD GTP-BINDING PROTEIN IN GLNA-RBN INTERGENIC REGION
IF1_LACLA	100%	2134	TRANSLATION INITIATION FACTOR IF-1
FMNB_DESVM	39%	2161	FMN-BINDING PROTEIN
EFTS_HELPY	43%	2206	ELONGATION FACTOR TS (EF-TS)
EFTS_STRPN			ELONGATION FACTOR TS (EF-TS)
EFTS_BACSU	778	2207	ELONGATION FACTOR TS (EF-TS)
EFG_BACSU	728	2333	ELONGATION FACTOR G (EF-G)
EFG_THEMA	55%	2333	ELONGATION FACTOR G (EF-G)
BIO13. TRANSPOR	T AND B	INDING I	PROTEINS 185 genes

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% 28%	348 358	OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPF
CYCA_ECOLI AAPA_BACSU	478	360	D-SERINE/D-ALANINE/GLYCINE TRANSPORTER AMINO ACID PERMEASE AAPA
LYSP_ECOLI	49%	368	LYSINE-SPECIFIC PERMEASE
OPPA_BACSU	30%	523	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR
ALYS_ENTFA	35%	525	AUTOLYSIN (EC 3.5.1.28)
DEF_HELPY	39%	553	POLYPEPTIDE DEFORMYLASE (EC 3.5.1.31)
YQIX_BACSU	36%	556	PROBABLE AMINO-ACID ABC TRANSPORTER BINDING PROTEIN IN BMRU-
ANSR INTERGENI			
BRNQ LACDL	47%	683	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN
(BRANCHED- CHA			
DTPT LACLA	97%	703	DI-/TRIPEPTIDE TRANSPORTER
YDGF BACSU	33%	817	HYPOTHETICAL TRANSPORT PROTEIN IN EXPZ-DINB INTERGENIC REGION
OPUA BACSU	348	863	GLYCINE BETAINE TRANSPORT ATP-BINDING PROTEIN OFUAA
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	32%	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) (EC 6			NUMBER AND AND ADDRESS INTO AND ADDRESS DECEMBER
XASA_ECOLI	50%	1323	AMINO ACID ANTIPORTER (EXTREME ACID SENSITIVITY PROTEIN)
OPUC_BACSU	478	1471	GLYCINE BETAINE-BINDING PROTEIN PRECURSOR GLYCINE BETAINE TRANSPORT SYSTEM PERMEASE PROTEIN OPUAB
OPUB_BACSU	51% 58%	1471 1473	GLYCINE BETAINE TRANSPORT SISTEM PERMEASE PROTEIN OPUAB GLYCINE BETAINE TRANSPORT ATP-BINDING PROTEIN OPUAA
OPUA_BACSU PMSR_BACSU	54%	1590	PUTATIVE PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET
GLNH_ECOLI	36%	1797	GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (GLNBP)
YA79_HAEIN	38%	1798	HYPOTHETICAL AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN HI0179
YQIZ_BACSU	64%	1799	PROBABLE AMINO-ACID ABC TRANSPORTER ATP-BINDING PROTEIN IN
BMRU-ANSR INTE			TROBIDD TELLIO TRED TEL TRADICICIEN THE DENDING TROTDEN IN
GLNO ECOLI		1833	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
HISP_ECOLI	51%	1835	HISTIDINE TRANSPORT ATP-BINDING PROTEIN HISP
PEPT LACLC		1857	PEPTIDASE T (EC 3.4.11)
YDGF BACSU	35%	1870	HYPOTHETICAL TRANSPORT PROTEIN IN EXPZ-DINB INTERGENIC REGION
OPPA LACLA	90%	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 REG			
LYSP_ECOLI	ION PRECU 37%	URSOR 2257	LYSINE-SPECIFIC FERMEASE
	37%		
BI013.03 Anion	37% 8	2257	13 genes
BI013.03 Anion MEGL_PSEPU	37% 38%	2257	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11)
BI013.03 Anion	37% 8	2257	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI	37% 38% 28%	2257 77 95	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN	37% 38% 28% 25%	2257 77 95 180	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR	37% 38% 28% 25% 35%	2257 77 95 180 243	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN	37% 38% 28% 25% 35% 31% 34%	2257 77 95 180 243 298 546	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER)
BI013.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16)	37% 38% 28% 25% 35% 31%	2257 77 95 180 243 298	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLFT_BACSU MANA_STRMU ATKA_ENTFA	37% 38% 28% 25% 35% 31% 34%	2257 77 95 180 243 298 546	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI	37% 38% 28% 25% 35% 31% 34% 65% 41% 28%	2257 95 180 243 298 546 777 845 869	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 33%	2257 95 180 243 298 546 777 845 869 1098	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU	37% 38% 25% 35% 35% 31% 34% 65% 41% 28% 33% 62%	2257 77 95 180 243 298 546 777 845 869 1098 1516	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PRUCTOKINASE (EC 2.7.1.4)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLFT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 33% 62% 61%	2257 77 95 180 243 298 546 777 845 869 1098 1516 1516 1516	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) FRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU	37% 38% 25% 35% 35% 31% 34% 65% 41% 28% 33% 62%	2257 77 95 180 243 298 546 777 845 869 1098 1516	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PRUCTOKINASE (EC 2.7.1.4)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7	37% 38% 25% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28%	2257 77 95 180 243 298 546 777 845 869 1098 1516 1704 1756	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) FRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8)
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7	37% 38% 25% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28%	2257 77 95 180 243 298 546 777 845 869 1098 1516 1704 1756	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TSOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) FRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSPERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YPREN 3.1.4.16) GLFT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28% bydrates,	2257 77 95 180 243 298 546 777 845 869 1098 1516 1704 1516 1704 1756 , organi	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TRANSPORTING (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE S'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) FRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSPERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CNI6_YREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI	37% 38% 25% 35% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28% 35% bydrates, 35%	2257 77 95 180 243 298 546 777 845 845 845 845 1098 1516 1704 1756 , organi 245	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PROTASSIUM/COPPERTRANSPORTING ATPASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(III) DICITRATE TRANSPORT AYSTEM PERMEASE PROTEIN FECE
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI FECE_ECOLI	37% 38% 25% 35% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28% 35% bydrates, 35%	2257 77 95 180 243 298 546 777 845 869 1516 1704 1756 , organi 245 324	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATXA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI FECE_ECOLI FECE_ECOLI CITN_LACLA GLPF_STRPN	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 62% 61% 28% 42% 35% 42% 35% 42% 35%	2257 77 95 180 243 298 546 777 845 1098 1516 1704 1756 , organi 245 324 324 324 324 324 1756 921 1267	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1.3) PROBABLE S'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLITRANSFERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(111) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(111) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD CITRATE-SODIUM SYMPORT (CITRATE TRANSPORTER) GLYCEROL UPTAKE FACILITATOR PROTEIN
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI FECE_ECOLI FECE_ECOLI FECD_ECOLI CITN_LACLA GLPF_STRPN RBSB_HAEIN	37% 38% 25% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28% bydrates, 35% 42% 35% 42% 35% 48% 58% 45%	2257 77 95 180 243 298 546 777 845 869 1516 1704 1756 1704 1756 324 326 921 1267 1679	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSPERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN HON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECE IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD CITRATE-SODIUM SYMPORT (CITRATE TRANSPORTER) GLYCEROL UPTAKE FACILITATOR PROTEIN D-RIBOSE-BINDING PERIFLASMIC PROTEIN PRECURSOR
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YFREN 3.1.4.16) GLFT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI FECD_ECOLI FECD_ECOLI FECD_ECOLI CITN_LACLA GLPF_STRPN RBSB_HAEIN RBSC_BACSU	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 62% 61% 28% bydrates, 35% 42% 35% 42% 58% 45% 60%	2257 77 95 180 243 298 546 777 845 869 1098 1516 1704 1704 1756 324 326 921 1267 1680	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PROBABLE PHOSPHATE ACETYLTRANSPERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR IC alcohols and acids GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(III) DICITRATE TRANSPORT PROTEIN PRECURSOR IIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RESC
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CNI6_YREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI SNTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI GLPF_ECOLI GLPF_STRPN RBSC_BACSU RBSA_BACSU	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 62% 61% 28% 42% 35% 42% 58% 45% 60% 42%	2257 77 95 180 243 298 546 777 845 869 1098 1516 1704 17756 , organi 245 324 326 921 1267 1679 1680	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSILM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) FRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSPERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD CITRATE-SODIUM SYMPORT (CITRATE TRANSPORTER) GLYCEROL UPTAKE FACILITATOR PROTEIN D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR RLBOSE TRANSPORT SYSTEM PERMEASE PROTEIN FECD GLYCEROL UPTAKE FACILITATOR PROTEIN D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR RLBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC RLBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSA
BI013.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CN16_YEREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI 5NTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BI013.04 Carbol GLPF_ECOLI FECE_ECOLI FECE_ECOLI FECE_ECOLI CITN_LACLA GLPF_STRPN RBSB_HAEIN RBSC_BACSU RBSD_BACSU	37% 38% 25% 35% 31% 34% 65% 41% 28% 33% 62% 61% 28% 35% 42% 35% 42% 35% 42% 55% 45% 60% 56%	2257 77 95 180 243 298 546 777 845 1098 1516 1704 1756 , organi 245 324 324 324 324 324 1267 1679 1680 1681 1682	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSIUM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE S'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) PRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLITRANSFERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD CITRATE-SODIUM SYMPORT (CITRATE TRANSPORTER) GLYCEROL UPTAKE FACILITATOR PROTEIN PROBE-BINDING PERIFLASSIC PROTEIN PRECURSOR RIBOSE-BINDING PERIFLASSIC PROTEIN PRECURSOR RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
BIO13.03 Anion MEGL_PSEPU ATZN_ECOLI 5NTD_HAEIN DHAK_CITFR CNI6_YREN 3.1.4.16) GLPT_BACSU MANA_STRMU ATKA_ENTFA CADA_BACFI SNTD_HAEIN SCRK_STRMU PTA_BACSU SPHX_SYNP7 BIO13.04 Carbol GLPF_ECOLI GLPF_ECOLI GLPF_STRPN RBSC_BACSU RBSA_BACSU	37% 38% 28% 25% 35% 31% 34% 65% 41% 28% 62% 61% 28% 42% 35% 42% 58% 45% 60% 42%	2257 77 95 180 243 298 546 777 845 869 1098 1516 1704 17756 , organi 245 324 326 921 1267 1679 1680	13 genes METHIONINE GAMMA-LYASE (EC 4.4.1.11) ZINC-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) DIHYDROXYACETONE KINASE (EC 2.7.1.29) 2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE PRECURSOR (EC GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) POTASSILM/COPPER-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE A (EC 3.6.1.36) PROBABLE CADMIUM-TRANSPORTING ATPASE (EC 3.6.1) PROBABLE 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) FRUCTOKINASE (EC 2.7.1.4) PROBABLE PHOSPHATE ACETYLTRANSPERASE (EC 2.3.1.8) SPHX PROTEIN PRECURSOR ic alcohols and acids 13 genes GLYCEROL UPTAKE FACILITATOR PROTEIN IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD CITRATE-SODIUM SYMPORT (CITRATE TRANSPORTER) GLYCEROL UPTAKE FACILITATOR PROTEIN D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR RLBOSE TRANSPORT SYSTEM PERMEASE PROTEIN FECD GLYCEROL UPTAKE FACILITATOR PROTEIN D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR RLBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC RLBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSA

RBSA HAEIN	24%	2163	RIBOSE TRANSPORT ATP-BINDING PROTEIN RBSA
EBA2_FLAME	27%	2238	ENDO-BETA-N-ACETYLGLUCOSAMINIDASE F2 PRECURSOR (EC 3.2.1.96)
GNTP_BACLI	59%	2246	GLUCONATE PERMEASE
BI013.05 Catio	ns		18 genes
FEOB_ECOLI	398	188	FERROUS IRON TRANSPORT PROTEIN B
FEOA_ECOLI	388	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	42%	1148	NA (+) /H
PBUX_BACSU	48%	1158	XANTHINE PERMEASE
Y1B2_MYCTU	35%	1188	PUTATIVE CATION-TRANSPORTING ATPASE CY21C12.02 (EC 3.6.1)
ATCL_SYNP7	37%	1402	CATION-TRANSPORTING ATPASE PACE (EC 3.6.1)
FUR_CAMJE	308	1503	FERRIC UPTAKE REGULATION PROTEIN
UIDB_ECOLI	33%	1541	GLUCURONIDE CARRIER PROTEIN (GLUCURONIDE PERMEASE)
Y058_METJA	31%	1632	PUTATIVE AMMONIUM TRANSPORTER MJ0058
URAA_HAEIN	36%	1643	PROBABLE URACIL PERMEASE (URACIL TRANSPORTER)
FER_CLOTH	388		FERREDOXIN
NAPA_ENTHR	48%	1973	NA (+) /H
ATCS_SYNY3	36%	2002	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1)
ATA1_SYNY3	36%	2315	CATION-TRANSPORTING ATPASE PMA1 (EC 3.6.1)
			and pyrimidines 1 genes
PDP_BACST	56%	1463	PYRIMIDINE-NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.2)
BIO13.07 PTS s	ystem		13 genes
PTMA_ECOLI	46%	31	PTS SYSTEM, MANNITOL-SPECIFIC IIABC COMPONENT (EIIABC-MTL)
PTCC_BACSU	34%	175	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIC COMPONENT (EIIC-CEL)
PTCB_BACSU	52%	416	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIB COMPONENT (EIIB-CEL)
PTCA_BACSU	48%	417	PTS SYSTEM, CELLOBIOSE-SPECIFIC IIA COMPONENT (EIIA-CEL)
PTSA_STRMU	48%	435	PTS SYSTEM, SUCROSE-SPECIFIC IIABC COMPONENT (EIIABC-SCR)
FTSA_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 (SIIBC-FRU)
PTBA_BACSU	37%	1144	PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC HIABC COMPONENT (EHABC-
BGL)			
PTBA_ERWCH	418	1489	PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-
F TTOLE TO LEASE	37.9	1-203	The proving prime processing of the composition of the
BGL)	31.9	1405	The Statisty Shin-Sheessished-Statistic Timbe Convolute (Minde-
	418	1742	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN)
BGL) PTNA_ECOLI PTNC_ECOLI	41% 46%		
BGL) PTNA_ECOLI	41%	1742	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN)
BGL) PTNA_ECOLI PTNC_ECOLI	418 468 578	1742 1743 1744	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes
BGL) PTNA_ECOLI PTNC_ECOLI PTND_ECOLI	418 468 578	1742 1743 1744	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN)
BGL) PTNA_ECOLI PTNC_ECOLI PTND_ECOLI BI013.08 Multi	41% 46% 57% drug re	1742 1743 1744 sistance	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) 3 genes
BGL) PTNA_ECOLI PTNC_ECOLI PTND_ECOLI BI013.08 Multi BMR2_BACSU	41% 46% 57% drug re 46%	1742 1743 1744 sistance 123	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) 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)
BGL) PTNA_ECOLI PTNC_ECOLI PTND_ECOLI BI013.08 Multi BMR2_BACSU EMRB_ECOLI	41% 46% 57% drug re 46% 26% 36%	1742 1743 1744 sistance 123 930	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) 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
BGL) PTNA_ECOLI PTND_ECOLI PTND_ECOLI BIO13.08 Multi BNR2_BACSU EMRB_ECOLI MDL_ECOLI	41% 46% 57% drug re 46% 26% 36%	1742 1743 1744 sistance 123 930	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) 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
BGL) PTNA_ECOLI PTND_ECOLI PTND_ECOLI BI013.08 Multi BNR2_BACSU EMRB_ECOLI MDL_ECOLI BI013.09 Other	41% 46% 57% drug re 46% 26% 36%	1742 1743 1744 sistance 123 930 1302	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIIC-MAN) 3 genes MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL 37 genes
BGL) PTNA_ECOLI PTNC_ECOLI PTND_ECOLI BIO13.08 Multi BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Other YBJZ_ECOLI	41% 46% 57% 46% 26% 36% 34% 37% 32%	1742 1743 1744 sistance 123 930 1302 15	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) 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
BGL) PTNA_ECOLI PTNC_ECOLI PTND_BCOLI BIO13.08 Multi BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Other YBJZ_ECOLI YCHM_ECOLI	41% 46% 57% 46% 26% 36% 36% 34% 37%	1742 1743 1744 sistance 123 930 1302 15 53	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) 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 YEJZ HYPOTHETICAL 58.4 KD PROTEIN IN PTH-PRSA INTERGENIC REGION
BGL) PTNA_ECOLI PTND_ECOLI PTND_ECOLI BIO13.08 Multi BMR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Other YBJ2_ECOLI YCHM_ECOLI YHES_ECOLI YHH_ECOLI	41% 46% 57% drug re 46% 26% 36% 34% 37% 32% 35% 50%	1742 1743 1744 sistance 123 930 1302 15 53 74 100 248	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) 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 ABC TRANSPORTER ATP-BINDING PROTEIN YBJS HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJS HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES
BGL) PTNA_ECOLI PTNC_ECOLI PTND_BCOLI BIO13.08 Multi BMR2_BACSU EMRB_ECOLI MDL_ECOLI YBJ2_ECOLI YCHM_ECOLI YHIT_ECOLI YHIH_ECOLI YHIB_BACSU	41% 46% 57% 46% 26% 36% 34% 37% 32% 35%	1742 1743 1744 sistance 123 930 1302 15 53 74 100	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIIC-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 INTERGENIC REGION HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT
BGL) PTNA_ECOLI PTNA_ECOLI PTND_ECOLI BIO13.08 Multi BNR2_BACSU EMRB_ECOLI MDL_ECOLI BIO13.09 Other YBJZ_ECOLI YBIT_ECOLI YHES_ECOLI YHES_ECOLI YHIS_ECOLI YFIB_BACSU 3 'REGION	41% 46% 57% 46% 26% 36% 36% 37% 32% 35% 50% 39%	1742 1743 1744 sistance 123 930 1302 15 53 74 100 248 257	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIIC-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 YEJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJT HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES HYP
BGL) PTNA_ECOLI PTNA_ECOLI PTND_ECOLI BIO13.08 Multi BMR2_BACSU EMRB_BCOLI MDL_ECOLI BIO13.09 Other YBJZ_ECOLI YHEM_ECOLI YHEM_ECOLI YHEM_ECOLI YHEM_ECOLI YHEM_ECOLI YHEM_ECOLI YHIH_ECOLI YHIH_ECOLI YHIM_ECOLI YHIM_ECOLI YHIM_ECOLI YHIM_ECOLI YHIM_ECOLI	41% 46% 57% drug re 46% 36% 36% 34% 37% 32% 35% 50% 39% 44%	1742 1743 1744 sistance 123 930 1302 15 53 74 100 248 257 273	PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIIC-MAN) 3 genes MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2) MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE PROTEIN B MULTIDRUG RESISTANCE PROTEIN MDL 37 genes HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJZ HYPOTHETICAL 58.4 KD PROTEIN IN PTH-PRSA INTERGENIC REGION HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJZ HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJS 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
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Y796_METJA	48%	1108	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0796
YLUD_LACLA	100%	1242	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN LEUD
3 'REGION			
YSC1_STRGC	62%	1349	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN SCAA
5'REGION (ORF1			
YXBC_BACSU	51%	1538	HYPOTHETICAL METABOLITE TRANSPORT PROTEIN IN HTPG-IOLR
INTERGENIC REG		****	
YJEM_ECOLI	22%	1736	HYPOTHETICAL 56.3 KD PROTEIN IN GENX-PSD INTERGENIC REGION
(0514)	212.0	1,20	ATTOTAL SOLUTION AND PROTEIN IN GENERATOR THERE AND AND A
YEJF_ECOLI	278	1751	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YEJF
YQGJ_BACSU	60%	1751	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN ILOF
INTERGENIC REG			AIPOINEIICAL ABC IRANSPORTER AIP-BINDING PROTEIN IN SUDA-CONGA
YQGJ_BACSU	59%	1752	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN SODA-COMGA
			AFFOREITCAL ABC TRANSPORTER AFF-BINDING PROTEIN IN SUDA-CORGA
INTERGENIC REG		1789	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN IDH
YXDL_BACSU	49%	1/09	APPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN IDH
3 'REGION	439	1015	WHORE TAX AND DOLLARDONNS AND DISTRICT DOODLY
YATR_BACFI	43%	1815	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN
YJEM_ECOLI	39%	1855	HYPOTHETICAL 55.3 KD PROTEIN IN GENX-PSD INTERGENIC REGION
(0514)	3.5.0	2076	
YXDL_BACSU	35%	2076	HYPOTHETICAL ABC TRANSPORTER ATF-BINDING PROTEIN IN IDH
3'REGION			
YYBJ_BACSU	28%	2265	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN COTF-TETB
INTERGENIC REG			
Y796_MÉTJA	42%	2329	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0796
BIO14. OTHER C	ATEGORIE	s	94 genes
PTO14 01 Adapt			ical conditions 13 genes
CSP2_LACPL	82%	170	COLD SHOCK PROTEIN 2
TCMA_STRGA	28%	233	TETRACENOMYCIN C RESISTANCE AND EXPORT PROTEIN
MMR_BACSU	30%		METHYLENOMYCIN & RESISTANCE PROTEIN (MMR PEPTIDE)
	75%	515	COLD SHOCK PROTEIN CSPC
CSPC_BACSU			
TCMA_STRGA	25%	596	TETRACENOMYCIN C RESISTANCE AND EXPORT PROTEIN
VANZ_ENTFC	42%		VANZ PROTEIN
FSR_ECOLI	25%		FOSMIDOMYCIN RESISTANCE PROTEIN
ARSC_BACSU	51%		PUTATIVE ARSENATE REDUCTASE
TCMA_STRGA	29%	1553	
ALCONOM AND ADDRESS OF A			TETRACENOMYCIN C RESISTANCE AND EXPORT PROTEIN
TCMA_STRGA	278	1678	
CMCT_NOCLA	348	1925	CEPHAMYCIN EXPORT PROTEIN CMCT
CMCT_NOCLA FRI_LISIN	348 448	1925 2082	CEPHAMYCIN EXFORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN
CMCT_NOCLA	348	1925	CEPHAMYCIN EXPORT PROTEIN CMCT
CMCT_NOCLA FRI_LISIN MSCL_ECOLI	348 448 448	1925 2082 2150	CEPHAMYCIN EXFORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug	34% 44% 44% and anal	1925 2082 2150	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes
CMCT_NOCLA FRI_LISIN MSCL_ECOLI	348 448 448	1925 2082 2150	CEPHAMYCIN EXFORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA	34% 44% 44% and anal 100%	1925 2082 2150 og sens 1232	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage	34% 44% 44% and anal 100% related	1925 2082 2150 .og sens 1232 functi	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6	34% 44% 44% and anal 100% related 37%	1925 2082 2150 og sens 1232 functi 36	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA	34% 44% 44% and anal 100% related 37% 26%	1925 2082 2150 og sens 1232 functi 36 49	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METDA VINT_BPL54	34% 44% 44% not anal 100% related 37% 26% 25%	1925 2082 2150 og sens 1232 functi 36 49 445	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5	34% 44% 44% 100% related 37% 26% 25% 45%	1925 2082 2150 og sens 1232 functi 36 49 445 460	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64)
CMCT_NOCLA PRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7	34% 44% 44% 100% related 37% 26% 25% 45% 21%	1925 2082 2150 .og sens 1232 functi 36 49 445 460 464	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_MET0A VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7	34% 44% 44% 100% related 37% 26% 25% 45% 21% 31%	1925 2082 2150 .og sens 1232 functi 36 49 445 460 464 465	CEPHAMYCIN EXFORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VINT_BPL54	34% 44% 44% and anal 100% related 37% 26% 25% 45% 21% 31% 31%	1925 2082 2150 og sens 1232 functi 36 49 445 460 464 465 501	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VINT_BPL54 XERC_SALTY	34% 44% 44% and anal 100% related 37% 26% 25% 45% 21% 31% 31% 32%	1925 2082 2150 .og sens 1232 functi 36 49 445 460 464 465	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE/RECOMBINASE XERC
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VINT_BPL54	34% 44% 44% and anal 100% related 37% 26% 25% 45% 21% 31% 31%	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU	34% 44% 44% and anal 100% related 37% 26% 25% 45% 21% 31% 31% 32%	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE/RECOMBINASE XERC
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 TERS_BPSF6 V367_METJA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFD) TNPA_STAAU	348 448 448 and anal 1008 related 378 268 258 458 218 318 318 328 318 328	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SWALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) INTEGRASE INTEGRASE/RECOMBINASE XERC HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPHK7 VINT_BPL54 KERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7	348 448 448 and anal 1008 related 378 258 458 218 318 318 318 328 318	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons 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)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METDA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VIAT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2	348 448 448 and anal 1008 related 378 268 258 458 318 318 318 318 318 328 318 338	1925 2082 2150 og sens 1232 i functi 49 445 460 464 465 501 633 902 1034 1053 1064	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE 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)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VF4_BPHK7 VHC_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54	348 448 448 and anal 1008 related 378 258 458 258 318 318 328 318 328 338 338 338 328	1925 2082 2150 .og sens 1232 ! functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL 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
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 TERS_BPSF6 VJST_BPL54 VG64_BPML5 VP3_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGZ_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VINT_BPL54 CODV_BACSU	348 448 448 100% related 37% 26% 25% 45% 21% 31% 31% 32% 31% 45% 27% 33% 32% 31%	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SWALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (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/RECOMBINASE CODV
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug 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 COM_BACSU XERC_HABIN	348 448 448 1008 related 378 268 258 458 318 318 318 318 318 318 318 318 318 31	1925 2082 2150 og sens 1232 1 functi 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1257	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP64) 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 INTEGRASE/RECOMBINASE XERC
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 V367_METAA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VG13_BPFH2 VG13_BPFH2 VINT_BPL54 COV_BACSU VINT_BPL54 COV_BACSU	348 448 448 1008 related 378 258 458 258 318 318 318 328 318 328 318 328 338 328 338 328 338 328 338 328 338	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons 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 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
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 VB4_BPSF5 VG54_BPML5 VG64_BPML5 VG64_BPML7 VINT_BPL54 VG64_BPMK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HABIN SBCC_ECOLI MCP_BPF41	348 448 448 and anal 100% related 37% 25% 45% 21% 31% 31% 32% 31% 32% 31% 32% 31% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	1925 2082 2150 .og sens 1232 t functi 36 49 445 460 464 465 501 633 902 1034 1053 1063 1053 1053 1256 1257 1358	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SWALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL 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) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug 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 SBCC_ECOLI MCCP_BPF41 VINT_BPSF6	348 448 448 100% related 37% 26% 25% 45% 21% 31% 32% 31% 45% 27% 32% 31% 32% 32% 32% 32% 32% 32% 32% 32% 32% 32	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1256 1257 1350 1358 1454	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (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/RECOMBINASE XERC EXONUCLEASE SECC MAJOR CAPSID PROTEIN (MCP) INTEGRASE
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 VB367_METDA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VIAT_BPL54 VF4_BPHK7 VIAT_BPL54 XERC_SALTY VH4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA	348 448 448 1008 related 378 268 258 458 318 318 318 328 318 328 338 328 338 328 338 278 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 i functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1454	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 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 PROTEINSE (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
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA VG37_BPML5	348 448 448 1008 related 378 258 458 218 318 318 328 318 328 318 328 318 328 318 328 318 328 318 328 348 458 268 268 268	1925 2082 2150 .og sens 1232 ! functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1255 1350 1358 1454 1716 1873	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL PROTEIN (GP64) POTTAL VE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE INTEGRASE (A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTENSE (GP4) MORPHOGENESIS PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN GENE 37 PROTEIN (GP37)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 VB367_METDA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VIAT_BPL54 VF4_BPHK7 VIAT_BPL54 XERC_SALTY VH4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA	348 448 448 1008 related 378 268 258 458 318 318 318 328 318 328 338 328 338 328 338 278 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 i functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1454	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 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 PROTEINSE (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
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA VG37_BPML5	348 448 448 and anal 1008 related 378 258 458 318 318 318 328 318 328 318 328 338 328 338 328 378 448 488 968 488 258	1925 2082 2150 og sens 1232 i functi 36 445 460 464 465 501 633 902 1034 1053 1064 1210 1257 1350 1257 1350 1358 1454 1716 1873 2005	CEPHAMYCIN EXFORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP63) 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 PROTEINSE (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 GENE 37 PROTEIN (GP37) INTEGRASE
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 VIAT_BPL54 VG64_BPML5 VF3_BPHK7 VIAT_BPL54 VF4_BPHK7 VIAT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VF4_BPHK7 VG13_BPPH2 VIAT_BPL54 COV_BACSU XERC_HABIN SBCC_ECOLI MCP_BPF41 VIAT_BPSF6 PIP_LACLA VG3_BPML5 VIAT_BPL54	348 448 448 and anal 1008 related 378 258 458 318 318 318 328 318 328 318 328 338 328 338 328 378 448 488 968 488 258	1925 2082 2150 og sens 1232 i functi 36 445 460 464 465 501 633 902 1034 1053 1064 1210 1257 1350 1257 1350 1358 1454 1716 1873 2005	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) PORTAL PROTEIN (GP63) 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 INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN GENE 37 PROTEIN (GP37) INTEGRASE
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 V367_METAA VINT_BPL54 VG64_BPML5 VP4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VG13_BPPH2 VINT_BPL54 COV_BACSU (ORFB) TNPA_STAAU VG13_BPPH2 VINT_BPL54 COV_BPF41 VINT_BPSF4 VINT_BPF41 VINT_BPF41 VINT_BPF41 VINT_BPL54 BIO14.04 Transg	348 448 448 and anal 1008 related 378 258 458 258 318 318 318 328 318 328 318 328 318 328 318 328 318 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1455 1716 1873 2005	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SMALL SUBUNIT (G1P) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP63) 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 INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN GENE 37 PROTEIN (GP37) INTEGRASE
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPML5 VG64_BPML5 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA VG37_BFML5 VINT_BPL54 BIO14.04 Transy YI3A_LACJO	348 448 448 and anal 1008 related 378 258 458 258 318 318 328 318 328 318 328 318 328 318 328 318 328 318 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1454 1716 1873 2005	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL 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 CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN GENE 37 PROTEIN (GP37) INTEGRASE MASTRIANSE SPORENTIN 121223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA)
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPHL5 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VG13_BPPH2 VINT_BD54 COV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPL54 BIO14.04 Trans; YI3A_LACJO T150_ECOLI	348 448 448 100% related 37% 26% 25% 45% 21% 31% 31% 31% 32% 31% 32% 31% 32% 31% 32% 31% 26% 96% 48% 25% 96% rel 41%	1925 2082 2150 og sens 1232 i functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1256 1257 1350 1358 1454 1716 1873 2005 53 53	CEPHAMYCIN EXPORT PROTEIN CMCT NON-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP64) POTATIVE PROHEAD PROTEASE (GP4) INTEGRASE 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/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (GP37) INTEGRASE INSERTION BLEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 V367_METDA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VF4_BPHK7 VG13_BPFH2 VINT_BPL54 CODV_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU SBCC_ECOLI MCP_BPF41 VINT_BPL54 VINT_BPL54 BIO14.04 Transg Y13A_LACJO TSO_ECOLI TRA4_LACLA	348 448 448 1008 related 378 258 458 218 318 318 318 328 318 328 318 328 318 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1454 1716 1873 2005 14ted f 53 53 53	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP3) PUTATIVE PROHEAD PROTEASE (GP4) INTEGRASE INTEGRASE INTEGRASE (A CRANSPOSON TN554) PUTATIVE PROHEAD PROTEIN IN HEMY-GLTT INTERGENIC REGION TRANSPOSASE A (TRANSPOSON TN554) PUTATIVE PROHEAD PROTEIN 1 (LATE PROTEIN GP13) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN GENE 37 PROTEIN (GP37) INTEGRASE INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150 TRANSPOSASE FOR INSERTION SEQUENCE IS150
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 Y367_METJA VINT_BPL54 VG64_BPHK7 VINT_BPL54 VG64_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 COV_BACSU XERC_HAEIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA VG37_BPML5 VINT_BPL54 BIO14.04 Trans; YI3A_LACJO TIS6_ECOLI TRA4_LACLA YI91_SHIDY	348 448 448 and anal 1008 related 378 258 458 258 318 318 328 318 328 318 328 318 328 318 328 318 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1454 1716 1873 2005 18ted f 53 53 53 54 55	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SWALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL 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 INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE UNCTONS 59 genes INSERTION RLEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150 TRANSPOSASE FOR INSERTI
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 TERS_BPSF6 VP3_BPHK7 VP4_BPHK7 VP4_BPHK7 VINT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VP4_BPHK7 VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HABIN SBCC_ECOLI MCP_BPF41 VINT_BPSF6 PIP_LACLA VG37_BPML5 VINT_BPL54 BIO14.04 Trans; YI3A_LACJO T150_ECOLI TRA4_LACLA	348 448 448 and anal 1008 related 378 258 458 258 318 318 328 318 328 318 328 318 328 318 328 318 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 1 functi 36 49 445 460 464 465 501 633 902 1034 1053 1064 1210 1256 1257 1350 1358 1454 1716 1873 2005 18ted f 53 53 53 54 55	CEPHAMYCIN EXPORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 1 genes PROBABLE AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (EC 2.7.1.95) ons and prophages 21 genes TERMINASE SWALL SUBUNIT (GIP) PROBABLE INTEGRASE/RECOMBINASE PROTEIN MJ0367 INTEGRASE GENE 64 PROTEIN (GP64) POTAL PROTEIN (GP64) POTAL 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 INTEGRASE PROBABLE INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE UNCTONS 59 genes INSERTION RLEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150 TRANSPOSASE FOR INSERTI
CMCT_NOCLA FRI_LISIN MSCL_ECOLI BIO14.02 Drug KKIH_LACLA BIO14.03 Phage TERS_BPSF6 V367_METDA VINT_BPL54 VG64_BPML5 VP3_BPHK7 VIAT_BPL54 VF4_BPHK7 VIAT_BPL54 XERC_SALTY YHGE_BACSU (ORFB) TNPA_STAAU VG13_BPPH2 VINT_BPL54 CODV_BACSU XERC_HABIN SBCC_ECOLI MCP_BP41 VINT_BP5F6 PIP_LACLA VG37_BPML5 VINT_BPL54 SBCC_ECOLI MCP_BP45 VINT_BP5F6 PIP_LACLA VG37_BPML5 VINT_BPL54 SBC1_ECOLI TRA4_LACLA Y191_SHDY TRA9_MYCTU (ORFB)	348 448 448 1008 related 378 268 258 458 318 318 328 318 328 318 328 318 328 318 328 318 328 328 328 328 328 328 328 328 328 32	1925 2082 2150 og sens 1232 i functi 36 49 445 460 465 501 633 902 1034 1053 1064 1257 1350 1257 1350 1257 1350 1257 1350 1257 1350 1257 1350 1454 1716 1873 2005 i 455 53 53 53 54 55 89	CEPHAMYCIN EXFORT PROTEIN CMCT NOR-HEME IRON-CONTAINING FERRITIN LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL itivity 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 GENE 64 PROTEIN (GP64) PORTAL PROTEIN (GP63) 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 INTEGRASE/RECOMBINASE XERC EXONUCLEASE SBCC MAJOR CAPSID PROTEIN (MCP) INTEGRASE PROBABLE INTEGRASE/RECOMBINASE CODV INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN (MCP) INTEGRASE PHAGE INFECTION PROTEIN GENE 37 PROTEIN (GP37) INTEGRASE INSERTION ELEMENT IS1223 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 IS96

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YI91_SHIDY	25%	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	998	138	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YI91_SHIDY	25%	138	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
	23% 98%	371	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA4_LACLA			
YI3A_LACJO	30%	372	INSERTION ELEMENT IS1223 HYPOTHETICAL 20,7 KD PROTEIN (ORFA)
T150_ECOLI	41%	373	PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
TRA4_LACLA	100%	624	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YI91_SHIDY	26%	625	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
T150_ECOLI	418	626	PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
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 1S904
YI91_SHIDY	25%	834	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
T150_ECOLI	39%	835	PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE 1S150
YI3A LACJO	30%	836	INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA)
YI91_SHIDY	25%	836	INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
TRA4_LACLA	99%	837	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA1_STRSL	38%	955	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
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	39%	1273	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS905
YIS1_SHISO	28%	1274	INSERTION ELEMENT IS600 (ISO-S3) HYPOTHETICAL 11 KD PROTEIN
TRA1_STRSL	38%	1336	
TRA1_STRSL	38%	1394	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
			PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA4 LACLA	38%	1552	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE RLEMENT IS1161
	398	1582	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA4_LACLA	39%	1727	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
YIS1_SHISO	28%	1728	INSERTION ELEMENT IS600 (ISO-S3) HYPOTHETICAL 11 KD PROTEIN
TRA1_STRSL	38%	1734	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
			REALLY DESIGNATION AND DATE REALLY FROM AND
TRA1_STRSL	38%	1933	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL	38% 38%	1933 1958	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL	38% 38% 38%	1933 1958 1997	PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL	38% 38% 38% 42%	1933 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 TRA1_STRSL TRA1_STRSL TRA4_LACLA	38% 38% 42% 39%	1933 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 TRA1_STRSL TRA4_LACLA TRA1_STRSL	38% 38% 42% 39% 38%	1933 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 IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA	38% 38% 42% 39% 38% 96%	1933 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 IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TRA4_LACLA T150_ECOLI	38% 38% 42% 39% 38% 98% 41%	1933 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 IS904 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE LEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL	38% 38% 42% 39% 38% 96% 41% 38%	1933 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 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-LIKE SEQUENCE IS161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TRA4_LACLA T150_ECOLI	38% 38% 42% 39% 38% 98% 41%	1933 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 IS904 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE LEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS150
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL	38% 38% 42% 39% 38% 96% 41% 38%	1933 1958 1997 2063 2083 2127 2135 2136 2183	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-LIKE SEQUENCE IS161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA	38% 38% 42% 39% 38% 96% 41% 38% 100%	1933 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 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
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY	38% 38% 42% 38% 38% 98% 41% 38% 100% 25%	1933 1958 1997 2063 2083 2127 2135 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 ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE IS150 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TI 50_ECOLI TRA1_STRSL TRA4_LACLA YI 91_SSIDY YH21_HAEIN	38% 38% 42% 38% 38% 98% 41% 38% 100% 25% 47%	1933 1958 1997 2063 2083 2127 2135 2136 2136 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 SEQUENCE IS150 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 TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO	38% 38% 42% 38% 98% 98% 41% 38% 100% 25% 47% 31%	1933 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 IS150 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 H1721 INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA)
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO	38% 38% 42% 39% 41% 38% 41% 38% 41% 38% 41% 35% 47% 31%	1933 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 IS150 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 H1721 INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA)
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA YI91_STRDY YH21_HAEIN YI3A_LACJO TRA1_STRSL	38% 38% 42% 39% 41% 38% 41% 38% 41% 38% 41% 35% 47% 31%	1933 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 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 ELEMENT IS105 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN HI1721 INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA YI91_STRDY YH21_HAEIN YI3A_LACJO TRA1_STRSL	38% 38% 42% 39% 38% 96% 41% 38% 100% 25% 47% 31% 31%	1933 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 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 ELEMENT IS105 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS106 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN HI1721 INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA YI91_SSIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH	38% 38% 42% 39% 38% 96% 41% 38% 100% 25% 47% 31% 38% r ETICAL	1933 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 IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1061 O genes 315 genes
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA YI91_SHIDY YH21_HAEIN YH21_HAEIN YH3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene	38% 38% 42% 39% 38% 96% 41% 38% 100% 25% 47% 31% 38% r ETICAL ral	1933 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 SEQUENCE ELEMENT IS105 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 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 TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TI50_ECOLI TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU	38% 38% 42% 39% 41% 20% 41% 20% 25% 47% 38% r ETICAL cal 63%	1933 1958 1997 2063 2083 2127 2135 2136 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 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 0 genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA1_STRSL TRA4_LACLA T150_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU	38% 38% 42% 39% 38% 96% 41% 38% 100% 25% 47% 31% 38% r ETICAL Fal 63% 32%	1933 1958 1997 2063 2083 2127 2135 2136 2183 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 IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS105 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 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 MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HFT INTERCENIC REGION
TRA1_STRSL 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_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU	38% 38% 42% 39% 41% 20% 41% 20% 25% 47% 38% r ETICAL cal 63%	1933 1958 1997 2063 2083 2127 2135 2136 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 IS101 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 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 MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 5.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 5.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL PROTEIN HI1412
TRA1_STRSL 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_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU YACA_BACSU YACA_BACSU	38% 38% 42% 39% 38% 96% 41% 38% 100% 25% 47% 31% 38% r ETICAL Fal 63% 32%	1933 1958 1997 2063 2083 2127 2135 2136 2183 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 IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1061 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS105 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1061 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 MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HFT INTERCENIC REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU YE12_HAEIN	38% 38% 42% 39% 38% 98% 41% 38% 100% 25% 47% 31% 38% r ETICAL 63% 32% 35%	1933 1958 1997 2063 2083 2135 2135 2136 2183 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 IS101 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 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 MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 5.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 5.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL PROTEIN HI1412
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TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA Y191_SHIDY YH21_HAEIN Y13A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU YACA_BACSU YAFP_ECOLI	38% 38% 42% 39% 42% 90% 41% 38% 25% 47% 31% 38% r ETICAL 63% 32% 35% 36%	1933 1958 1997 2063 2083 2127 2135 2136 2196 2196 2196 2197 2248 21 24 43 50	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 O genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 5.1. KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 5.1. KD PROTEIN IN SPOILE-HFT INTERGENIC REGION HYPOTHETICAL 57.6 KD PROTEIN IN DINP-PRFH INTERGENIC REGION
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TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU YACA_BACSU YAFP_ECOLI (F181) Y293_MYCGE	36% 38% 42% 39% 42% 39% 41% 38% 100% 25% 47% 31% 38% r ETICAL 63% 32% 35% 36% 29% 41%	1933 1958 1997 2063 2083 2127 2135 2136 2183 2196 2196 2196 2197 2248 21 24 43 50 56 66	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 O 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 HIT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE HIT INTERGENIC REGION HYPOTHETICAL 9.7 KD PROTEIN IN SPOILE HT 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 PECI-FIMB INTERCENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN PECI-FIMB INTERCENIC REGION HYPOTHETICAL 9.0 KD PROTEIN IN PECI-FIMB INTERCENIC REGION HYPOTHETICAL PROTEIN MG293
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TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA1_STRSL TRA4_LACLA TI50_ECOLI TRA1_STRSL TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU YACA_BACSU YE12_HAEIN YAFP_ECOLI (P181) Y293_MYCGE YC9Q_BACSU YCSE_BACSU	38% 38% 42% 39% 41% 38% 25% 41% 38% 25% 47% 31% 38% r ETICAL 63% 32% 35% 36% 29% 41% 35% 29%	1933 1958 1997 2063 2083 2127 2135 2136 2183 2196 2196 2197 2248 2196 2197 2248 2196 2197 2248 2196 2197 2248 2196 2197 224 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 IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS101 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS100 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN HYPOTHETICAL TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS904 HYPOTHETICAL TRANSPOSASE-LIKE PROTEIN HI1721 INSERTION ELEMENT IS123 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) PROBABLE TRANSPOSASE FOR INSERTION-LIKE SEQUENCE ELEMENT IS1161 O genes 315 genes HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION HYPOTHETICAL 55.1 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 9.7.6 KD PROTEIN IN SPOILE-HPT INTERGENIC REGION HYPOTHETICAL 7.6 KD PROTEIN IN DINP-PRFH INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN PECI-FIMB INTERGENIC REGION HYPOTHETICAL 20.0 KD PROTEIN IN SEA-LIVD INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SEA-LIVD INTERGENIC REGION HYPOTHETICAL 24.1 KD PROTEIN IN SIPU 3'REGION
TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA1_STRSL TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA TRA4_LACLA YI91_SHIDY YH21_HAEIN YI3A_LACJO TRA1_STRSL BIO14.05 Othe BIO15. HYPOTH BIO15.01 Gene YAB0_BACSU YACA_BACSU YACA_BACSU YAFP_ECOLI (F181) Y293_MYCGE YGQ_BACSU YCSE_BACSU YCSE_BACSU	38% 38% 42% 39% 38% 42% 38% 41% 38% 100% 25% 47% 31% 38% F ETICAL 63% 32% 35% 36% 29% 41% 35% 29% 34%	1933 1958 1997 2063 2083 2135 2136 2183 2196 2196 2196 2197 2248 21 24 43 50 56 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 IS104 PROBABLE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS004 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS104 INSERTION ELEMENT IS911 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 55.1 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 SEA-ILVD INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SIDU 3'REGION HYPOTHETICAL 24.1 KD PROTEIN IN SIDU 3'REGION HYPOTHETICAL 26.1 KD PROTEIN IN SIDU 3'REGION HYPOTHETICAL 27.1 KD PROTEIN IN SIDU 3'REGION HYPOTHETICAL 27.1 KD PROTEIN IN SIDU 3'REGION HYPOTHETICAL PROTEIN MJO531
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YQKD_BACSU	32%	121	HYPOTHETICAL 34.6 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION
YCEE_ECOLI	448	127	HYPOTHETICAL 43.9 KD PROTEIN IN MSYB-WTRB INTERGENIC REGION
	446	127	HIPOTRETICAL 43.9 KD PROTEIN IN ASIB-HIRB INTERGENIC REGION
(ORF1)	200		
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 INTERGENTC 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	27%	185	HYPOTHETICAL 33.8 KD PROTEIN IN DAE-TYRZ INTERGENIC REGION
Y448 MYCPN	57%	190	HYPOTHETICAL PROTEIN MG448 HOMOLOG
Y369_MYCGE	318	192	HYPOTHETICAL PROTEIN MG369
YQHY_BACSU	32%	193	HYPOTHETICAL 14.7 KD PROTEIN IN ACCC-FOLD INTERGENIC REGION
Y320_MYCPN	26%	194	HYPOTHETICAL PROTEIN MG320 HOMOLOG
YIBD_ECOLI	30%	204	HYPOTHETICAL 40.5 KD PROTEIN IN SECB-TDH INTERGENIC REGION
Y4GN_RHISN	28%	205	HYPOTHETICAL 45.0 KD PROTEIN ¥4GN
YC22_METJA	28%	209	HYPOTHETICAL PROTEIN MJ1222
YC11_KLEPN	20%	211	HYPOTHETICAL 55.0 KD PROTEIN IN CPS REGION (ORF11)
YIBD_ECOLI	34%	214	HYPOTHETICAL 40.5 KD PROTEIN IN SECB-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
YQEI_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
		226	
YQEL_BACSU	468		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 H10003
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
YQHE_ECOLI	45%	264	HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION
Y181_MYCPN	35%	275	HYPOTHETICAL PROTEIN MG181 HOMOLOG (GT9_ORF434)
YHGF_NEIME	47%	283	HYPOTHETICAL 83.1 KD PROTEIN IN REGION E
YKQC_BACSU	61%	287	HYPOTHETICAL 61.5 KD PROTEIN IN ADEC-PDHA INTERGENIC REGION
YEAB_BACSU	46%	305	HYPOTHETICAL 31.8 KD PROTEIN IN GABP-GUAA INTERGENIC REGION
(ORFX)			
YQHE_ECOLI	45%	330	HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION
YYBR_BACSU	498	331	HYPOTHETICAL 14.7 KD PROTEIN IN COTF-TETB INTERGENIC REGION
YWKD BACSU	50%	331	HYPOTHETICAL 14.8 KD PROTEIN IN TOK-PRFA INTERGENIC REGION
	38%	364	
YWAC_BACSU	2016		
	208		HYPOTHETICAL 24.6 KD PROTEIN IN DAE-TYRZ INTERGENIC REGION
Y128_MYCGE	30%	364	HYPOTHETICAL PROTEIN MG128
YHCT_BACSU	40%	365	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI	40% 33%	365 369	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI	40% 33% 28%	365 369 376	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE	40% 33% 28% 32%	365 369 376 381	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI	40% 33% 28%	365 369 376	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549)	40% 33% 28% 32% 37%	365 369 376 381 386	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI YJ72_MYCGE YJCE_ECOLI (O549) YAAT_BACSU	40% 33% 28% 32% 37%	365 369 376 381 386 403	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 56.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549)	40% 33% 28% 32% 37%	365 369 376 381 386	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI YJ72_MYCGE YJCE_ECOLI (O549) YAAT_BACSU	40% 33% 28% 32% 37%	365 369 376 381 386 403	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 56.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI YJ72_MYCGE YJCE_ECOLI (O549) YAAT_BACSU Y552_HELPY	40% 33% 28% 32% 37% 44% 35%	365 369 376 381 386 403 404	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 56.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION HYPOTHETICAL PROTEIN HP0552
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3	40% 33% 28% 32% 37% 44% 35% 37%	365 369 376 381 386 403 404 409	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN SLL1556
YHCT_BACSU YIEF_ECOLI YEH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU	40% 33% 28% 32% 37% 44% 35% 37% 40%	365 369 376 381 386 403 404 409 419	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL PROTEIN HPO552 HYPOTHETICAL 37.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCPN YW11_MYCTU	40% 33% 28% 32% 44% 35% 40% 35% 38%	365 369 376 381 386 403 404 409 419 431 438	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 30.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 66.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 47.6 KD PROTEIN CY39.11C
YHCT_BACSU YIEF_ECOLI YEH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCPN YW11_MYCTU Y097_MYCTU	40% 33% 28% 32% 44% 35% 40% 30% 36% 38% 39%	365 369 376 381 386 403 404 409 419 431 438 442	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN SL1556 HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL PROTEIN MG105 HOMOLOG HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 18.2 KD PROTEIN CY78.07
YHCT_BACSU YIEF_ECOLI YEIF_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCPN YW11_MYCTU LYTF_BACSU	40% 33% 28% 37% 44% 35% 40% 35% 38% 39% 31%	365 369 376 381 386 403 404 409 419 431 438 442 443	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL PROTEIN HPO552 HYPOTHETICAL 37.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 47.6 KD PROTEIN MG105 HOMOLOG HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 18.2 KD PROTEIN CY38.07 MEMBRANE-BOUND PROTEIN LYTR
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU LYTR_BACSU YQAK_BACSU	40% 33% 328% 337% 445% 45% 45% 337% 45% 839% 345% 391% 46%	365 369 376 381 386 403 409 419 431 438 442 443 443	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 26.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 66.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SPAC-ABRB INTERGENIC REGION HYPOTHETICAL PROTEIN HP0552 HYPOTHETICAL 71.6 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY38.07 MEMBRANE-BOUND PROTEIN LYTR HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCPN YW11_MYCTU Y097_MYCTU YQ97_MYCTU LYTR_BACSU YQAK_BACSU YMCP_BPF41	40% 33% 28% 32% 44% 35% 40% 38% 38% 38% 38% 31% 27%	365 369 376 381 386 403 404 409 419 431 438 442 443 451 471	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 30.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 26.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN MG105 HOMOLOG HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 18.2 KD PROTEIN CY30.07 MEMBRANE-BOUND PROTEIN LYTR HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL PROTEIN IN MCP 3' REGION (FRAGMENT)
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCPN YW11_MYCTU Y097_MYCTU LYTR_BACSU YMCP_BPF41 YQB0_BACSU	40% 33% 282% 37% 44% 35% 40% 35% 39% 31% 46% 25%	365 369 376 381 386 403 404 409 419 431 438 442 443 451 471 473	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.5 KD PROTEIN SLL1556 HYPOTHETICAL 77.5 KD PROTEIN SLL1556 HYPOTHETICAL 77.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 77.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY78.07 MEMBRANE-BOUND PROTEIN LYTR HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI YJ72_MYCGE YJ7E_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU YWBA_BACSU Y05_MYCFN YW11_MYCTU UYTR_BACSU YQAK_BACSU YWCP_BFF41 YQB0_BACSU YWCB_BACSU	40% 33% 222% 425% 425% 4357% 4358% 3391% 455% 3467% 3467% 348% 3467% 348% 3467% 348% 3467% 348%	365 369 376 381 386 403 404 404 404 404 431 431 431 431 431 431 451 471 473 484	HYPOTHETICAL 9ROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 30.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 40.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 9ROTEIN HP0552 HYPOTHETICAL 70.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN SPR-GALK INTERGENIC REGION HYPOTHETICAL 45.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 34.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 34.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 34.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION
YHCT_BACSU YIET_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCTN Y105_MYCTN Y07_MYCTU LYTR_BACSU YQAK_BACSU YMCP_BPF41 YQBO_BACSU DEGU_BACSU DEGU_BACSU	40% 33% 232% 445% 357% 455% 338% 338% 338% 346% 27% 358% 346% 27% 358% 346% 34%	365 369 376 381 386 403 404 409 419 431 438 442 443 451 471 471 473 484 496	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 26.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 66.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION HYPOTHETICAL PROTEIN HP0552 HYPOTHETICAL 77.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN SLL1556 HYPOTHETICAL PROTEIN MG105 HOMOLOG HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL PROTEIN IN MCP 3' REGION (FRAGMENT) HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION DEGV PROTEIN
YHCT_BACSU YIEF_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU Y097_MYCTU YQAK_BACSU YMCP_BPF41 YQB0_BACSU YMCG_BACSU YPMC_BACSU	40% 33% 2827 4257 4257 4257 4257 8399 3168 8278 4275 8399 2358 8298 2988 298 298	365 369 376 381 386 403 404 409 419 431 438 442 443 451 471 471 473 484 496 497	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 70.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN IN SPAC-ABRB INTERGENIC REGION HYPOTHETICAL 7.5 KD PROTEIN SL1556 HYPOTHETICAL 7.5 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 7.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 18.2 KD PROTEIN CY39.11C HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 37.1 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 17.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 17.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN LVA 3'REGION
YHCT_BACSU YIET_ECOLI YEIH_ECOLI YJ72_MYCGE YJ7E_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCPN YW11_MYCTU Y097_MYCTU Y097_MYCTU LYTR_BACSU YQAK_BACSU YMCP_BPF41 YQB0_BACSU YMCG_BACSU YMCG_BACSU YMCG_BACSU	40% 33% 2327 4576% 3333457 4576% 3339167 588% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8%	365 369 376 381 386 403 404 409 431 438 443 451 471 473 484 497 499	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 30.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL G0.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL G0.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 9ROTEIN HPO552 HYPOTHETICAL 9ROTEIN HPO552 HYPOTHETICAL 47.6 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN SPR-GALK INTERGENIC REGION HYPOTHETICAL 47.6 KD PROTEIN CY39.11C HYPOTHETICAL 45.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY38.07 MEMBRANE-BOUND PROTEIN LYTR HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN LVA 3'REGION HYPOTHETICAL 70.6 KD PROTEIN IN LVA 3'REGION PRECURSOR (ORF1)
YHCT_BACSU YIET_ECOLI YEIH_ECOLI YJ72_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCFU Y097_MYCFU YW11_MYCFU YQAK_BACSU YQAK_BACSU YWCP_BFF41 YQB0_BACSU YWCP_BACSU DEGV_BACSU YBBD_BACSU YBBD_BACSU	40% 33% 2327 425% 43576% 43578 4358% 839167 588% 839167 588% 8495% 43295% 43295% 43295% 43295% 43295%	365 369 376 381 386 403 404 409 419 431 431 431 431 431 451 471 473 484 496 497 499 526	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 26.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 66.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.5 KD PROTEIN IN SPAC-ABRB INTERGENIC REGION HYPOTHETICAL 70.6 KD PROTEIN SLL1556 HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 22.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 71.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILA-GLYC INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILA STREGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILA STREGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILA STREGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOIL STREGION PRECURSOR (ORF1) HYPOTHETICAL 23.2 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YHCT_BACSU YIET_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU YH05_MYCFN YW11_MYCFU Y097_MYCFU LYTR_BACSU YMCP_BPF41 YQB0_BACSU YWCP_BPF41 YQB0_BACSU YMCP_BACSU YMCP_BACSU YPMR_BACSU YBMR_BACSU YB0A_BACSU YGQX_BACSU YQQX_BACSU	40% 332233 445% 455% 455% 33233 316% 8%% 8%% 8%% 8%% 8%% 8%% 8%% 8%% 8%% 8	365 369 376 381 386 403 404 409 419 431 431 438 442 443 451 471 473 484 496 497 526 529	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TMAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL A6.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 31.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 37.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL PROTEIN MG105 HOMOLOG HYPOTHETICAL 18.2 KD PROTEIN CY39.11C HYPOTHETICAL 18.2 KD PROTEIN CY30.11C HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 23.2 KD PROTEIN IN PEUA 5'REGION PRECURSOR (ORF1) HYPOTHETICAL 23.1 KD PROTEIN IN PONA 5'REGION
YHCT_BACSU YIET_ECOLI YEIH_ECOLI Y372_MYCGE YJCE_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU Y097_MYCTU YQAK_BACSU YMCP_BPF41 YQB0_BACSU YMCP_BPF41 YQB0_BACSU YMCP_BACSU YMCB_BACSU YPMR_BACSU YBBD_BACSU YPMR_BACSU YPAS_BACSU	43223 33427745 43705899167758449543 43333342224430 4430588888888888888888888888888888888888	365 369 376 381 386 403 404 409 431 438 443 451 471 473 484 497 499 526 529 530	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.5 KD PROTEIN IN SPAC-ABRB INTERGENIC REGION HYPOTHETICAL 77.5 KD PROTEIN SLL1556 HYPOTHETICAL 77.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 77.6 KD PROTEIN IN EPR-GALK INTERGENIC REGION HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 77.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 17.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.1 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.1 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.1 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SONA-COMGA INTERGENIC REGION HYPOTHETICAL 21.1 XD PROTEIN IN COTD-KDUD INTERGENIC REGION
YHCT_BACSU YIET_ECOLI YEIH_ECOLI YJ72_MYCGE YJ72_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU LYTR_BACSU YQAK_BACSU YQAK_BACSU YWLG_BACSU YWLG_BACSU YBBD_BACSU YBBD_BACSU YQGX_BACSU YPOA_STROR YPSA_BACSU YQGZ_BACSU	40% 33% 2327 4570 4530 4570 4530 16758 4954 88% 88% 88% 88% 88% 88% 88% 88% 88% 88	365 369 376 381 386 403 404 404 409 419 431 431 431 431 431 431 443 443 451 473 484 497 499 526 529 530	HYPOTHETICAL 28.9 KD PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL G0.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL G0.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 70.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 70.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN N PR-GALK INTERGENIC REGION HYPOTHETICAL 45.8 KD PROTEIN CY38.11C HYPOTHETICAL 45.8 KD PROTEIN CY38.11C HYPOTHETICAL 45.8 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 70.6 KD PROTEIN IN SPOIL-GUA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOIL-GUA INTERGENIC REGION HYPOTHETICAL 70.6 KD PROTEIN IN SPOIL-GUA INTERGENIC REGION HYPOTHETICAL 23.2 KD PROTEIN IN SPOILA-COMGA INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SODA-COMGA INTERGENIC REGION HYPOTHETICAL 14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YHCT_BACSU YIET_BCOLI YEIH_ECOLI YJ72_MYCGE YJ7E_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU LYTR_BACSU YQAK_BACSU YMCP_BPF41 YQBO_BACSU YWCP_BPF41 YQBO_BACSU YWCP_BACSU YWRCBACSU YPMR_BACSU YPMR_BACSU YQGZ_BACSU YPOA_STROR YPSA_BACSU YNG2_BACSU YNG2_BACSU YNG2_BACSU	40% 33% 2327 445% 3374 3327 445% 3327 4358% 8327 4358% 8329 3467% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8%	365 369 376 381 386 403 404 409 419 431 431 431 431 431 431 451 471 473 496 497 499 526 529 530 530 530	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 26.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 66.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.6 KD PROTEIN SLL1556 HYPOTHETICAL 74.6 KD PROTEIN SLL1556 HYPOTHETICAL 74.6 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 71.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 21.2 KD PROTEIN IN SOLA-COMGA INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SOLA-COMGA INTERGENIC REGION HYPOTHETICAL 14.8 KD PROTEIN IN NAGH 5'REGION (ORPH)
YHCT_BACSU YIET_ECOLI YEIH_ECOLI YJ72_MYCGE YJ72_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU LYTR_BACSU YQAK_BACSU YQAK_BACSU YWLG_BACSU YWLG_BACSU YBBD_BACSU YBBD_BACSU YQGX_BACSU YPOA_STROR YPSA_BACSU YQGZ_BACSU	40% 33% 2327 4570 4530 4570 4530 16758 4954 88% 88% 88% 88% 88% 88% 88% 88% 88% 88	365 369 376 381 386 403 404 404 409 419 431 431 431 431 431 431 443 443 451 473 484 497 499 526 529 530	HYPOTHETICAL 28.9 KD PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL PROTEIN MG372 HYPOTHETICAL G0.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL G0.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 70.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 70.5 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN SLL1556 HYPOTHETICAL 47.6 KD PROTEIN N PR-GALK INTERGENIC REGION HYPOTHETICAL 45.8 KD PROTEIN CY38.11C HYPOTHETICAL 45.8 KD PROTEIN CY38.11C HYPOTHETICAL 45.8 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 19.4 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 70.6 KD PROTEIN IN SPOIL-GUA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOIL-GUA INTERGENIC REGION HYPOTHETICAL 70.6 KD PROTEIN IN SPOIL-GUA INTERGENIC REGION HYPOTHETICAL 23.2 KD PROTEIN IN SPOILA-COMGA INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SODA-COMGA INTERGENIC REGION HYPOTHETICAL 14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION
YHCT_BACSU YIET_BCOLI YEIH_ECOLI YJ72_MYCGE YJ7E_ECOLI (0549) YAAT_BACSU Y552_HELPY YF56_SYNY3 YWBA_BACSU Y105_MYCFN YW11_MYCTU Y097_MYCTU LYTR_BACSU YQAK_BACSU YMCP_BPF41 YQBO_BACSU YWCP_BPF41 YQBO_BACSU YWCP_BACSU YWRCBACSU YPMR_BACSU YPMR_BACSU YQGZ_BACSU YPOA_STROR YPSA_BACSU YNG2_BACSU YNG2_BACSU YNG2_BACSU	40% 33% 2327 445% 3374 3327 445% 3327 4358% 8327 4358% 8329 3467% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8% 8%	365 369 376 381 386 403 404 409 419 431 431 431 431 431 431 451 471 473 496 497 499 526 529 530 530 530	HYPOTHETICAL PROTEIN MG128 HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION HYPOTHETICAL 36.9 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION HYPOTHETICAL 26.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION HYPOTHETICAL 66.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.2 KD PROTEIN IN SOXR-ACS INTERGENIC REGION HYPOTHETICAL 71.6 KD PROTEIN SLL1556 HYPOTHETICAL 74.6 KD PROTEIN SLL1556 HYPOTHETICAL 74.6 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN CY39.11C HYPOTHETICAL 145.8 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 32.2 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 71.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 28.9 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGION HYPOTHETICAL 21.2 KD PROTEIN IN SOLA-COMGA INTERGENIC REGION HYPOTHETICAL 23.1 KD PROTEIN IN SOLA-COMGA INTERGENIC REGION HYPOTHETICAL 14.8 KD PROTEIN IN NAGH 5'REGION (ORPH)

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YJAB_ECOLI (F147)	419	569	HYPOTHETICAL	16.4 KD	PROTEIN	IN RRFE-META INTERGENIC REGION
Y369_MYCGE	28%	572	HYPOTHETICAL	PROTEIN	MG369	
DEGV BACSU	30%	573	DEGV PROTEIN			
YQJW_BACSU	35%	578				IN GLNQ-ANSR INTERGENIC REGION
YF63_METJA	31%	581	HYPOTHETICAL			
YWCG_BACSU YAT3_STAAU	41% 28%	585 587				IN QOXD-VPR INTERGENIC REGION IN ATL 5'REGION (ORF3)
YWLC_BACSU	33%	588				IN SPOILR-GLYC INTERGENIC REGION
Y553_METJA	40%	594	HYPOTHETICAL			IN STOTIK ODIC INTERGENTE REGION
YWCD_BACSU	33%	601	HYPOTHETICAL	14.3 KD	PROTEIN	IN EPR-GALK INTERGENIC REGION
Y085_MYCGE	338	603	HYPOTHETICAL			
YQFU_BACSU	29%	612				IN CCCA-SODA INTERGENIC REGION
Y119_MYCTU YQJK_BACSU	25% 51%	615 617	HYPOTHETICAL			IN GLNQ-ANSE INTERGENIC REGION
YCEG_ECOLI	30%	623				IN PABC-HOLB INTERGENIC REGION
YZ42_METJA	32%	642	HYPOTHETICAL			
Y0A5_MYCTU	228	651	HYPOTHETICAL			
Y553_SYNY3	47%	658	HYPOTHETICAL			
YCEE_ECOLI (ORF1)	42%	659	HYPOTHETICAL	43.9 KD	PROTEIN	IN MSYB-HTRB INTERGENIC REGION
YRG2_LACLA	95%	660	HYPOTHETICAL	PROPETN	IN RPMC	3'REGION (ORF2)
YQGZ_BACSU	38%	672				IN SODA-COMGA INTERGENIC REGION
YCDQ_ECOLI	35%	678				IN PHOH-CSGG INTERGENIC REGION
YADE_ECOLI	28%	680	HYPOTHETICAL	46.3 KD	PROTEIN	IN HPT-PAND INTERGENIC REGION
PRECURSOR	250					
YJDJ_ECOLI (090A)	35%	684	HYPOTHETICAL	10.5 KD	PROTEIN	IN DCUB-LYSU INTERGENIC REGION
YJDI_ECOLI	56%	684	HYPOTHETICAL	8.6 KD F	ROTEIN I	IN DCUB-LYSU INTERGENIC REGION
(076)		004	MIL OTTALLCRID	0.0 10 1	NOTEIN 1	W BOOD-MIDD INTERDIATE ADDION
YABD_BACSU	43%	685	HYPOTHETICAL	29.2 KD	PROTEIN	IN METS-KSGA INTERGENIC REGION
YQHY_BACSU	39%	690				IN ACCC-FOLD INTERGENIC REGION
YXJH_BACSU	43%	722				IN PEPT-KATB INTERGENIC REGION
YICI_ECOLI YFBB_HAEIN	33% 26%	727 734	HYPOTHETICAL			IN GLTS-SELC INTERGENIC REGION
Y188_METJA	248	739	HYPOTHETICAL			
Y371_MYCGE	28%	740	HYPOTHETICAL			
YCSE_BACSU	40%	742	HYPOTHETICAL	28.1 KD	PROTEIN	IN SIPU 3'REGION
YYBT_BACSU	38%	750				IN RPLI-COTF INTERGENIC REGION
Y347_MYCPN YCND_BACSU	26%	754 758	HYPOTHETICAL			
YHCS_BACSU	36% 31%	768				IN PHRC-GDH INTERGENIC REGION IN CSPB-GLPP INTERGENIC REGION
YWBG_BACSU	368	770				IN EPR-GALK INTERGENIC REGION
YWBH_BACSU	27%	770				IN EPR-GALK INTERGENIC REGION
YLXS_BACSU	38%	771				IN NUSA 5'REGION (P15A)
YLXR_BACSU	518	773	HYPOTHETICAL	10.4 KD	PROTEIN	IN NUSA-INFB INTERGENIC REGION
(ORF3) YHI3_RHOCA	448	779	HYPOTHETTCAL	33 7 KD	PROVETN	IN HIMA 5'REGION (ORF3)
Y06B_MYCTU	31%	809				I CY338.11C PRECURSOR
YQGS_BACSU	34%	813				IN SODA-COMGA INTERGENIC REGION
YIDA_ECOLI	38%	821				IN IBPA-GYRB INTERGENIC REGION
Y143_HAEIN	25%	828	HYPOTHETICAL			
Y456_METJA YCFB_ECOLI	24% 58%	848 850	HYPOTHETICAL			IN PURB-ICDA INTERGENIC REGION
(ORF-15)	201	050	HIPOTHETICAL	42.0 ND	PROTEIN	IN FURB-ICDA INTERGENIC REGION
	31%	864	HYPOTHETICAL	32.6 KD	PROTEIN	IN MOLR-BGLX INTERGENIC REGION
PRECURSOR						
YHAD_HAEIN	50%	877	HYPOTHETICAL			_
YLXA_BACSU	64% 45%	885				IN FTSL 5'REGION (ORFB)
YWAC_BACSU YCDQ_ECOLI	45% 28%	894 897				IN DAE-TYRZ INTERGENIC REGION IN PHOH-CSGG INTERGENIC REGION
	37%	900	HYPOTHETICAL			IN PROA-COGG INTERGENIC REGION
	25%	907	MEMBRANE-BOUN			
	278	911				IN SIPU 3'REGION
	318	912				IN DIVIC-SPOILE INTERGENIC REGION
	34%					IN SELC-NLPA INTERGENIC REGION
	35% 33%		HYPOTHETICAL HYPOTHETICAL			IN SECB-TDH INTERGENIC REGION
	40%					IN ASPS-BISZ INTERGENIC REGION
	52%	986				IN CRH-TRXB INTERGENIC REGION
	46%		HYPOTHETICAL	34.7 KD	PROTEIN	IN CRH-TRXB INTERGENIC REGION
	36%		HYPOTHETICAL			
						IN ASPS-BISZ INTERGENIC REGION
YLYB_BACSU (ORF-X)	59%	1024	HIPOTRETICAL	33.7 KD	PROTEIN	IN LSP-PYRR INTERGENIC REGION
	42%	1027	HYPOTHETICAL	36.7 KD	PROTEIN	SLL0501
	41%					IN SPOIIIC-CWLA INTERGENIC REGION

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	
YQGZ_BACSU	42%	1070	HYPOTHETICAL 14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION	
YQFN_BACSU	44%	1082	HYPOTHETICAL 23.7 KD PROTEIN IN CCCA-SODA INTERGENIC REGION	
YQKB_BACSU	358	1083	HYPOTHETICAL 11.8 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION	
YIDA_ECOLI	448	1084	HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION	
YWFO_BACSU	52%	1085	HYPOTHETICAL 51.0 KD PROTEIN IN PTA 3'REGION	
YSXB_BACSU	388	1088	HYPOTHETICAL 12.3 KD PROTEIN IN RPLU-RPMA INTERGENIC REGION	
(ORF X)	100	1000		
YDAR_BACSU	40%	1090	HYPOTHETICAL 45.7 KD PROTEIN IN MUTT-GSIB INTERGENIC REGION	
YQFG_BACSU	46%	1092 1096	HYPOTHETICAL 17.8 KD PROTEIN IN PHOH-DGKA INTERGENIC REGION	
YVYE_BACSU	54% 25%	1098	HYPOTHETICAL PROTEIN IN DEGS-TAGO INTERGENIC REGION (FRAGMENT	0
YXIQ_BACSU YADO_ECOLI	29%	1103	HYPOTHETICAL 45.5 KD PROTEIN IN BGLS-KATB INTERGENIC REGION	
YQEJ_BACSU	46%	1103	HYPOTHETICAL 46.0 KD PROTEIN IN HEML-PFS INTERGENIC REGION HYPOTHETICAL 22.2 KD PROTEIN IN AROD-COMER INTERGENIC REGION	
Y03F_MYCTU	36%	1104	HYPOTHETICAL 52.2 KD PROTEIN IN AROD-COMER INTERGENIC REGION HYPOTHETICAL 54.3 KD PROTEIN CY130.15C	
YFEU_HAEIN	52%	1142	HYPOTHETICAL PROTEIN HI0754	
YFIA_BACSU	26%	1145	HYPOTHETICAL 29.3 KD PROTEIN IN GLVG-GLVBC INTERGENIC REGION	
YBDN_ECOLI	338	1149	HYPOTHETICAL 47.8 KD PROTEIN IN GENG-GENGE INTERGENIC REGION	
YBDM_ECOLI	46%	1150	HYPOTHETICAL 23.9 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION	
YHCJ_HAEIN	36%	1189	HYPOTHETICAL PROTEIN HI0145	
YNGB_CLOPE	338	1190	HYPOTHETICAL 31.2 KD PROTEIN IN NAGH 5'REGION (ORFB)	
YPTB_CLOAB	51%	1194	HYPOTHETICAL PROTEIN IN PTB 5'REGION (ORF1)	
Y912_HAEIN	28%	1195	HYPOTHETICAL PROTEIN HI0912	
YPIA BACSU	278	1197	HYPOTHETICAL 48.3 KD PROTEIN IN OCRA 5'REGION	
YWKB_BACSU	26%	1213	HYPOTHETICAL 33.6 KD PROTEIN IN TOK-PRFA INTERGENIC REGION	
YHI1 LACLA	92%	1225	HYPOTHETICAL PROTEIN IN HISC 5'REGION (ORF1)	
YHI6_LACLA	98%	1230	HYPOTHETICAL 30.7 KD PROTEIN IN HISD-HISB INTERGENIC REGION	
(ORF6)	200	1050	ALL AND AL	
YHIC_LACLA	978	1235	HYPOTHETICAL 31.3 KD PROTEIN IN HISIE 3'REGION (ORF13)	
YABJ_BACSU	53%	1250	HYPOTHETICAL 13.7 KD PROTEIN IN PURR-SPOVG INTERGENIC REGION	
(ORF2)		2000		
YGT1 STRMU	65%	1255	HYPOTHETICAL PROTEIN 1 IN GTFB REGION (FRAGMENT)	
YODS_MYCTU	32%	1259	HYPOTHETICAL 69.9 KD PROFEIN CY1A11.08	
YQHY_BACSU	24%	1263	HYPOTHETICAL 14.7 KD PROTEIN IN ACCC-FOLD INTERGENIC REGION	
Y568_METJA	35%	1283	HYPOTHETICAL PROTEIN MJD568	
YCDO ECOLI	25%	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	
(ORFX13)			AND AND AND AN AN AND ANOT AN ANALY AND	
YPUH BACSU	39%	1306	HYPOTHETICAL 22.0 KD PROTEIN IN RIBT-DACB INTERGENIC REGION	
(ORFX8)				
YPUG BACSU	37%	1307	HYPOTHETICAL 29.6 KD PROTEIN IN RIBT-DACB INTERGENIC REGION	
(ORFX7)				
YSNB_BACSU	39%	1309	HYPOTHETICAL 19.2 KD PROTEIN IN RPH-ILVB INTERGENIC REGION	
YGGV_ECOLI	48%	1309	HYPOTHETICAL 21.0 KD PROTEIN IN CSHB-ANSB INTERGENIC REGION	
(0197)				
YBIO_ECOLI	32%	1321	HYPOTHETICAL 86.8 KD PROTEIN IN DING-GLNQ INTERGENIC REGION	
Y442_MYCPN	36%	1327	HYPOTHETICAL PROTEIN MG442 HONOLOG	
YQGZ_BACSU	378	1356	HYPOTHETICAL 14.8 KD PROTEIN IN SODA-COMGA INTERGENIC REGION	
YEBH_ECOLI	348	1362	HYPOTHETICAL 30.4 KD PROTEIN IN MANZ-CSPC INTERGENIC REGION	
(ORF30)				
Y120_MYCGE	30%	1365	HYPOTHETICAL PROTEIN MG120	
Y121_MYCGE	48%	1366	HYPOTHETICAL PROTEIN MG121	
YAAN_BACSU	50%	1373	HYPOTHETICAL 43.8 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION	
YLXD_BACCL	46%	1382	HYPOTHETICAL 27.6 KD PROTEIN IN PYRAB-PYRD INTERGENIC REGION	
(ORF2)				
YMFC_HAEIN	62%	1388	HYPOTHETICAL PROTEIN HI0694	
Y882_HAEIN	35%	1404	HYPOTHETICAL PROTEIN HI0882	
Y531_METJA	34%	1409	HYPOTHETICAL PROTEIN MJ0531	
YQBO_BACSU	278	1424	HYPOTHETICAL 171.0 KD PROTEIN IN SPOILIC-CWLA INTERGENIC REGI	
YQBO_BACSU	29%	1426	HYPOTHETICAL 171.0 KD PROTEIN IN SPOIIIC-CWLA INTERGENIC REGI	ON
YE22_HAEIN	398	1451	HYPOTHETICAL PROTEIN HI1422	
YLXM_BACSU	53%	1455	HYPOTHETICAL 13.2 KD PROTEIN IN FFH 5'REGION	
YBXB_BACSU	448	1464	HYPOTHETICAL 22.5 KD PROTEIN IN RPLL-RPOB INTERGENIC REGION	
(P23)	4.75.6	1467	INFORMERTON DO A NO DOARDAN TH CORE DODA NUMBERONICE	
YBDM_ECOLI	478	1467	HYPOTHETICAL 23.9 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION	
YBDN_ECOLI	32%	1468	HYPOTHETICAL 47.8 KD PROTEIN IN CSTA-DSBG INTERGENIC REGION	
YTRP_LACLA	99%	1500	HYPOTHETICAL 13.3 KD PROTEIN IN TRPE 5'REGION	
YICL_ECOLI	34%	1505	HYPOTHETICAL 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	
YYAI_BACSU	33%	1539	HYPOTHETICAL 20.2 KD PROTEIN IN TETB-EXOA INTERGENIC REGION	
(ORFG)	0.74	1654	INDODUDUTINE OF A NO DOMDEN IN STAT DESS THERESING SECTOR	
YJJG_ECOLI YEXA_BACSU	27%	1554	HYPOTHETICAL 25.3 KD PROTEIN IN RIMI-PRFC INTERGENIC REGION	
YEXA_BACSU YEGB_ECOLI	378 278	1573 1577	HYPOTHETICAL 9.7 KD PROTEIN IN PUR OPERON	
" EVOD_ECOD1	4/5	7911	HYPOTHETICAL 50.9 KD PROTEIN IN ALKA-BAES INTERGENIC REGION	

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YMO1_RHIME (ORF334)	30%	1591	HYPOTHETICAL 36.4 KD PROTEIN IN MOCC-MOCA INTERGENIC REGION
DEGV_BACSU	35%	1601	DEGV FROTEIN
YOKD_BACSU	25%	1612	HYPOTHETICAL 34.6 KD PROTEIN IN GLNG-ANSR INTERGENIC REGION
YPBG_BACSU	30%	1639	HYPOTHETICAL 28.6 KD PROTEIN IN RECO-CMK INTERGENIC REGION
PRECURSOR	200	1000	THE PLAN IN THE PLAN INTERPLANT IN THE PLAN INTERPLANT IN THE PLAN INTERPLANT IN THE PLAN INTERPLANT INTERPLA
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	0.05	1031	RIPOINEIICAE 45.5 KD PROIEIN IN COID-KDOD INTERGENIC REGION
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 PROTEIN IN RNPA 3'REGION
YVDK_BACSU	60%	1726	HYPOTHETICAL 88.3 KD PROTEIN IN CLPP-CRH INTERGENIC REGION
LYTR_BACSU	31%	1739	MEMBRANE-BOUND PROTEIN LYTR
YFGA_ECOLI	23%	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	31%	1773	Hypotherical 31.1 kd protein in each-beta intergenic region
YBHL_ECOLI	35%	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
Y456_METJA	27%	1817	HYPOTHETICAL PROTEIN MJ0456
YNHE_ECOLI	39%	1825	HYPOTHETICAL 56.3 KD PROTEIN IN LPP-AROD INTERGENIC REGION
Y154_MYCLE	27%	1830	HYPOTHETICAL 42.2 KD PROTEIN U1496A/B1496_C1 154
YYBO BACSU	52%	1859	HYPOTHETICAL 34.0 KD PROTEIN IN COTF-TETE INTERGENIC REGION
Y260_SYNY3	35%	1862	HYPOTHETICAL 49.2 KD PROTEIN SLL0260
YAT3_STAAU	34%	1864	HYPOTHETICAL 16.6 KD PROTEIN IN ATL 5'REGION (ORF3)
YHBQ_ECOLI	35%	1869	HYPOTHETICAL 11.3 KD FROTEIN IN SOHA-MTR INTERGENIC REGION
(0100)	550	1000	NICHDRENE 110 NO INCIDIN IN COMPANY INCIDENCE INCIDE
YRKA_BACSU	48%	1882	HYPOTHETICAL 49.0 KD PROTEIN IN BLTD-TRKA INTERGENIC REGION
Y531_METJA	26%	1907	HYPOTHETICAL PROTEIN MJ0531
Y556_SYNY3	378	1917	HYPOTHETICAL 24.0 KD PROTEIN SLR0556
DEGV_BACSU	28%	1920	DEGV PROTEIN
YQHE_ECOLI	378	1924	HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION
YPEC_LACLC	888	1928	HYPOTHETICAL PROTEIN IN PEPC 5'REGION (ORF 2)
YQKG_BACSU	54%	1930	HYPOTHETICAL 21.0 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION
YQHY_BACSU	248	1939	HYPOTHETICAL 14.7 KD PROTEIN IN GENG-ANSK INTERGENIC REGION
		1939	
YQKG_BACSU	34%		HYPOTHETICAL 21.0 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION
AIEK ECOFI	40%	1949	HYPOTHETICAL 23.3 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION
YLP3_PSEPU	40%	1951	HYPOTHETICAL 44.7 KD PROTEIN IN LPD-3 5'REGION (ORF3)
YADS_ECOLI	33%	1966	HYPOTHETICAL 22.1 KD PROTEIN IN HEML-PFS INTERGENIC REGION
YDAR_BACSU	30%	1970	HYPOTHETICAL 45.7 KD PROTEIN IN MUTT-GSIB INTERGENIC REGION
Y837_METJA	28%	1980	HYPOTHETICAL PROTEIN MJ0837
YIGN_ECOLI	22%	1982	HYPOTHETICAL 54.7 KD PROTEIN IN UDP-UBIE INTERGENIC REGION
PRECURSOR			
YJEQ_HAEIN	29%	1984	HYPOTHETICAL PROTEIN HI1714
YABE_BACSU	39%	1985	HYPOTHETICAL 47.7 KD PROTEIN IN METS-KSGA INTERGENIC REGION
YE12_HAEIN	31%	2002	HYPOTHETICAL PROTEIN HI1412
YF56_METJA	38%	2013	HYPOTHETICAL PROTEIN MJ1556
YACC_BACSU	45%	2014	HYPOTHETICAL 31.8 KD PROTEIN IN FTSH-CYSK INTERGENIC REGION
YWJB_BACSU	40%	2015	HYPOTHETICAL 19.6 KD PROTEIN IN ACDA 5'REGION
YACF_BACSU	57%	2016	HYPOTHETICAL 37.1 KD PROTEIN IN FOLK-LYSS INTERGENIC REGION
YPJC_BACSU	45%	2017	HYPOTHETICAL 23.6 KD PROTEIN IN QCRC-DAPB INTERGENIC REGION
YQFU_BACSU	29%	2019	HYPOTHETICAL 32.5 KD PROTEIN IN CCCA-SODA INTERGENIC REGION
YHIT_MYCPN	378	2022	HYPOTHETICAL 16.1 KD PROTEIN HIT-LIKE PROTEIN
Y143_HAEIN	24%	2044	HYPOTHETICAL PROTEIN HI0143
YU12_MYCTU	30%	2045	HYPOTHETICAL 34.9 KD PROTEIN CY339.12C
YXJB_BACSU	40%	2052	HYPOTHETICAL 31.5 KD PROTEIN IN KATB 3'REGION
YQHL_BACSU	38%	2081	HYPOTHETICAL 14.6 KD PROTEIN IN GCVT-SPOILIAA INTERGENIC REGION
YJFG_HAEIN	298	2099	HYPOTHETICAL PROTEIN HI0121
Y018_MYCGE	36%	2101	HYPOTHETICAL HELIČASE MG018
YDP1_LACLC	95%	2114	HYPOTHETICAL 30.9 KD PROTEIN IN PEPX 5'REGION (ORF1)
YDP3_LACLA	88%	2117	HYPOTHETICAL 18.7 KD PROTEIN IN PEPX 3'REGION (ORF3)
YACL BACSU	42%	2126	HYPOTHETICAL 40.9 KD PROTEIN IN MECB-GLTX INTERGENIC REGION
YEEO_ECOLI	28%	2151	HYPOTHETICAL 60.1 KD PROTEIN IN AMN-CBL INTERGENIC REGION
YCEC_ECOLI	38%	2161	HYPOTHETICAL 36.0 KD PROTEIN IN RNE-RPMF INTERGENIC REGION
(ORFX)			
YEBI_HAEIN	28%	2162	HYPOTHETICAL PROTEIN HI0407
YAEL_HAEIN	278	2178	HYPOTHETICAL PROTEIN HI0918

Y506_SYNY3	46%	2180	UNDORUBRICANT 20 0 VD DOCRETN CT10504
YOBD_MYCTU	31%	2180	HYPOTHETICAL 28.8 KD PROTEIN SLL0506 HYPOTHETICAL 13.0 KD PROTEIN CY227.13 PRECURSOR
YBEA_ECOLI	31%	2182	HYPOTHETICAL 17.3 KD PROTEIN IN MRDA-PHPB INTERGENIC REGION
YABB BACSU	47%	2190	HYPOTHETICAL 28.3 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION
Y003_HAEIN	28%	2194	HYPOTHETICAL PROTEIN HI0003
YBHE_ECOLI	28%	2209	HYPOTHETICAL 36.3 KD PROTEIN IN MODC-BIOA INTERGENIC REGION
YQJV_BACSU	25%	2221	HYPOTHETICAL 44.7 KD PROTEIN IN GLNQ-ANSE INTERGENIC REGION
Y661_METJA	31%	2226	HYPOTHETICAL PROTEIN MJD661
YTFG_ECOLI	458	2227	HYPOTHETICAL 29.7 KD PROTEIN IN RPLI-CPDB INTERGENIC REGION
(F286)			
YYBR_BACSU	42%	2227	HYPOTHETICAL 14.7 KD PROTEIN IN COTF-TETB INTERGENIC REGION
YJBR_ECOLI	40%	2232	HYPOTHETICAL 13.5 KD PROTEIN IN APHA-UVRA INTERGENIC REGION
Y143_HAEIN	308	2252	HYPOTHETICAL PROTEIN HI0143
YPBG_BACSU	26%	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)	38%	2280	HYPOTHETICAL PROTEIN MJ0441
Y441_METJA YQEG_BACSU	428	2283	HYPOTHETICAL PROTEIN MJ0441 HYPOTHETICAL 20.1 KD PROTEIN IN NUCB-AROD INTERGENIC REGION
YWFA_BACSU	28%	2299	HYPOTHETICAL 20.1 KD PROTEIN IN ROCE-AROD INTERGENIC REGION
Y531_METJA	32%	2300	HYPOTHETICAL PROTEIN MJ0531
Y800_METJA	28%	2304	HYPOTHETICAL PROTEIN MJ0800
YJBC_ECOLI	30%	2306	HYPOTHETICAL 32.5 KD PROTEIN IN PEPE-LYSC INTERGENIC REGION
YOA5_MYCTU	248	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)
YHCC_ECOLI	37%	2339	HYPOTHETICAL 34.6 KD PROTEIN IN ARCB-GLTB INTERGENIC REGION
BIO16. UNKNOWN			83 genes
BIO16.01 Gener	a 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	0.0.0	2262	SECRETED 45 KD PROTEIN PRECURSOR
	99%	2293	SECRETED 45 KD PROTEIN PRECURSOR
_		2295	
BIO16.02 Uncla	ssified		78 genes
LCIA_LACLA	ssified 33%	48	78 genes Lactococcin a immunity protein
LCIA_LACLA OSMC_ECOLI	ssified 33% 48%	48 69	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C
LCIA_LACLA OSMC_ECOLI LCND_LACLA	ssified 33% 48% 97%	48 69 85	78 genes LACTOCOCCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCCIN A SECRETION PROTEIN LCND
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU	ssified 33% 48% 97% 45%	48 69 85 107	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI	ssified 33% 48% 97% 45% 33%	48 69 85 107 113	78 genes LACTOCOCCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU	ssified 33% 48% 97% 45% 33% 31%	48 69 95 107 113 131	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 (SPOIIIJ ASSOCIATED PROTEIN)
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA	ssified 33% 48% 97% 45% 33% 31% 48%	48 69 85 107 113 131 164	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)
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU	ssified 33% 48% 97% 45% 33% 31%	48 69 95 107 113 131	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 (SPOILIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU	ssified 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)
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI	ssified 33% 48% 97% 45% 33% 31% 48% 62% 42%	48 69 95 107 113 131 164 166 168	78 genes LACTOCOCCIN A IMMUNITY PROTEIN OSMOTICALLY INDUCIBLE PROTEIN C LACTOCOCCIN A SECRETION PROTEIN LCND CSBB PROTEIN ACVL 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)
LCIA_LACLA OSMC_ECOLI LCND_LACLA CSBB_BACSU ACPD_ECOLI JAG_BACSU AMID_MORCA YZDD_BACSU HYIN_AGRVI PHNO_ECOLI	ssified 33% 48% 97% 45% 33% 31% 48% 62% 42% 40%	48 69 95 107 113 131 164 166 168 225	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 (SPOIIIJ ASSOCIATED PROTEIN) PUTATIVE AMIDASE (EC 3.5.1.4) PET112-LIKE PROTEIN INDOLEACETAMIDE HYDROLASE (EC 3.5.1) PHNO PROTEIN
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GID_BACSU	69%	1255	GID PROTEIN (FRAGMENT)
2DKG_CORSP	46%	1266	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1)
FIBP_ADEB3	29%	1393	FIBER PROTEIN
FMCH_BACNO	31%	1408	POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMC (SEROGROUP H1)
P60_LISSE	31%		PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN)
XHLB_BACSU	40%	1414	HOLIN
DFRA_SYNY3	30%	1558	PUTATIVE DIHYDROFLAVONOL-4-REDUCTASE (EC 1.1.1.219)
DC4C_ACICA	34%	1575	
ESL2_MYCPN	278	1604	PUTATIVE ESTERASE/LIPASE 2 (EC 3.1)
PKSG_BACSU	338	1610	PUTATIVE POLYKETIDE BIOSYNTHESIS PROTEIN PKSG
F4RE_METJA	348	1652	PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1)
LAXC_LACLA	29%	1671	LACX PROTEIN, CHROMOSOMAL
RGG_STRGC	27%	1713	RGG PROTEIN
ARCL_ECOLI	40%	1732	CARBAMATE KINASE-LIKE PROTEIN 1
SMPB_ENTFA	63%	1757	SMALL PROTEIN B HOMOLOG
BMRU_BACSU	28%	1775	BMRU PROTEIN
DEDA_ECOLI	39%	1796	DEDA PROTEIN (DSG-1 PROTEIN)
XYNC_CALSA	338	1809	ACETYL ESTERASE (EC 3.1)
THL CLOAB	338	1823	ACETYL-COA ACETYLTRANSFERASE (EC 2.3.1.9)
PHPB_ECOLI	348	1869	PHPB PROTEIN
PFS_HAEIN	438	1929	PFS PROTEIN HOMOLOG
PROC_ECOL1	38%	1933	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
SUN_BACSU	33%	1938	SUN PROTEIN (FRAGMENT)
YFF1_MYCMY	448	1947	HYPOTHETICAL PROTEIN MG130
LAXC_LACLA	36%	1979	LACX PROTEIN, CHROMOSOMAL
BLTD_BACSU	338	1996	TRANSACETYLASE BLTD (EC 2.3.1)
RGG_STRGC	198	2024	RGG PROTEIN
FIB1_ADE41	308	2027	FIBER PROTEIN 1
DC4C_ACICA	35%	2032	4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44)
HIT_BACSU	418	2057	HIT PROTEIN
ARCL_ECOLI	458		CARBAMATE KINASE-LIKE PROTEIN 1
STA_ECOLI			STREPTOTHRICIN ACETYLTRANSFERASE (EC 2.3)
NARA_BACSU	278	2213	NARA PROTEIN
PQQE_ACICA	30%	2216	COENZYME PQQ SYNTHESIS PROTEIN E (COENZYME PQQ SYNTHESIS
PROTEIN III)			
RGG_STRGC	31%	2217	RGG PROTEIN
YHHF_ECOLI	30%	2219	21.7 KD PROTEIN IN FTSY-NIKA INTERGENIC REGION
GSPA_ECOLI	28%	2239	PUTATIVE GENERAL SECRETION PATHWAY PROTEIN B.
RGG_STRGC	19%	2268	RGG PROTEIN
TOXB_CLODI	27%	2285	TOXIN B.
PHNA_ECOLI	47%	2312	PHNA PROTEIN
	1495 g	jenes	

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

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

[#]For the strain mg1363 with the plasmid pMG820. *Presumably a trehalose specific system.