Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi

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The genome of the bacterium *Borrelia burgdorferi* B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like *Mycoplasma genitalium*, it contains no genes for cellular biosynthetic reactions. Because *B. burgdorferi* and *M. genitalium* are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

In the mid-1970s, a geographic clustering of an unusual rheumatoid arthritis-like condition was reported in Connecticut¹. That cluster of cases focused attention on the syndrome that is now called Lyme disease. It was subsequently realized that a similar disorder had been known in Europe since the beginning of this century. Lyme disease is characterized by some or all of the following manifestations: an initial erythematous annular rash, 'flu-like symptoms, neurological complications, and arthritis in about 50% of untreated patients². In the United States, the disease occurs primarily in northeastern and midwestern states, and in western parts of California and Oregon. These regions coincide with the ranges of various species of *Ixodes* ticks, the primary vector of Lyme disease. Lyme disease is now the most common tick-transmitted illness in the United States, and has been reported in many temperate parts of the Northern Hemisphere.

It was not until the early 1980s that a new spirochaete, *Borrelia burgdorferi*³, was isolated and cultured from the midgut of *Ixodes* ticks, and subsequently from patients with Lyme disease^{4,5}. Analysis of genetic diversity among individual *Borrelia* isolates has defined a closely related cluster containing at least 10 tick-borne species of Lyme disease agents, called '*B. burgdorferi* (*sensu lato*)'. *B. burgdorferi* resembles most other spirochaetes in that it is a highly specialized, motile, two-membrane, spiral-shaped bacterium that lives primarily as an extracellular pathogen. *Borrelia* is fastidious and difficult to culture *in vitro*, requiring a specially enriched media and low oxygen tension⁶.

One of the most striking features of *B. burgdorferi* is its unusual genome, which includes a linear chromosome approximately one megabase in size^{7–10} and numerous linear and circular plasmids^{11–13}, with some isolates containing up to 20 different plasmids. The plasmids have a copy number of approximately one per chromosome^{10,14}, and different plasmids often appear to share regions of homologous DNA^{13,15,16}. Long-term culture of *B. burgdorferi* results in the loss of some plasmids, changes in protein expression profiles,

and a loss in the ability of the organism to infect laboratory animals, suggesting that the plasmids encode important proteins involved in virulence^{17–19}.

Because of its importance as a pathogen of humans and animals, and the value of complete genome sequence information for understanding its life cycle and advancing drug and vaccine development, we sequenced the genome of *B. burgdorferi* type strain (B31), using the random sequencing method previously described^{20–24}. Here we summarize the results from sequencing, assembly and analysis of the linear chromosome and 11 plasmids.

Chromosome analysis

The linear chromosome of *B. burgdorferi* has 910,725 base pairs (bp) and an average G+C content of 28.6%. Base pair one represents the first double-stranded base pair that we observed at the left telomere. Previous genome characterizations agree with the nucleotide sequence of the large chromosome^{10,25–28}. The 853 predicted coding sequences (open reading frames; ORFs) have an average size of 992 bp, similar to that observed in other prokaryotic genomes, with 93% of the *B. burgdorferi* genome representing

Figure 1 Linear representations of the *B. burgdorferi* B31 chromosome and plasmids. The location of predicted coding regions colour-coded by biological role, RNA genes, and tRNAs is indicated. Arrows represent the direction of transcription for each predicted coding region. Numbers associated with tRNA symbols represent the number of tRNAs at a locus. Numbers associated with GES represent the number of membrane-spanning domains according to the Goldman, Engelman and Steitz scale as calculated by TopPred⁴⁹. Only proteins with five or more GES are indicated. Members of paralogous gene families are identified by family number. Transporter abbreviations: mal, maltose; P, gly and bet, proline, glycine, betaine; glyc, glycerol; aa, amino acid; E, glutamate; fru, fructose; glu, glucose; s/p, spermidine/putrescine; pan, pantothenate; Pi, phosphate; lac, lactate; rib, ribose; ?, unknown.

coding sequence. Biological roles were assigned to 59% of the 853 ORFs using the classification scheme adapted from Riley²⁹ (Fig. 1), 12% of ORFs matched hypothetical coding sequences of unknown function from other organisms, and 29% were new genes. The average relative molecular mass ($M_{\rm r}$) of the chromosome-encoded proteins in *B. burgdorferi* is 37,529 ranging from 3,369 to 254,242, values similar to those observed in other bacteria including *Haemophilus influenzae*²⁰ and Mycoplasma genitalium²¹. The median isoelectric point (pI) for all predicted proteins is 9.7.

Analysis of codon usage in *B. burgdorferi* reveals that all 61 triplet codons are used. When both AU- and GC-containing codons specify a single amino acid, there is a marked bias (from 2-fold to more than 20-fold, depending on the amino acid) in the use of AU-rich codons. The most frequently used codons are AAA (Lys, 8.1%), AAU (Asn, 5.9%), AUU (Ile, 5.9%), UUU (Phe, 5.7%), GAA (Glu, 5.0%), GAU (Asp, 4.2%) and UUA (Leu, 4.2%). The most common amino acids are Ile (10.6%), Leu (10.3%), Lys (10.2%), Ser (7.8%) and Asn (7.2%). The high value for Lys is in agreement with the median calculated isoelectric point of 9.7.

Plasmid analysis

Analysis of the nucleotide sequence and Southern analyses on B. burgdorferi DNA indicate that, in addition to the large linear chromosome, isolate B31 contains linear plasmids of the following approximate sizes: 56 kilobase pairs (kbp) (lp56), 54 kbp (lp54), four plasmids of 28 kbp (lp28-1, lp28-2, lp28-3 and lp28-4), 38 kbp (lp38), 36 kbp (lp36), 25 kbp (lp25) and 17 kbp (lp17); and circular plasmids of the following sizes: 9 kbp (cp9), 26 kbp (cp26) and five or six homologous plasmids of 32 kbp (cp32). These include all of the plasmids previously identified in this strain, but comparisons with other B31 cultures suggest that this isolate may have lost one 21 kbp linear and one or two 32 kbp circular plasmids during growth in culture since its original isolation 11-14,19,30. The sequences of all plasmids were assembled as part of this project. However, the assembled sequences of the cp32 and related lp56 plasmids could not be determined with a high degree of confidence because of DNA sequence similarity among them (≥99% in several regions of

Table 2 Gene identification numbers are listed with the prefix BB as in Fig. 2. Each gene identified is listed in its functional role category (adapted from Riley²⁹). The percentage of similarity and a two-letter abbreviation for genus and species for the best match are also shown. An expanded version of this table with additional information is available on the World-Wide Web at http://www.tigr.org/tdb/mdb/bbdb/bbdb/hbdb.htm. Abbreviations of gene ammes are: Ac, acetyl; BP, binding protein; biosyn, biosynthesis; cello, cellobiose; CPDase, carboxypeptidase; Dcase, decarboxylase; DHase, dehydrogenase; flgr, flagellar/flagellum; fru, fructose; GBP, glycine, betaine, L-proline; glu, glucose; Kase, kinase; mal, maltose; MC-methyl-accepting chemotaxis; MTase, methyltransferase; NAG, N-acetylglucosamine; OH, hydroxy; OP, oligopeptide; P, phosphate; PPTase, phosphotransferase; PPase, phosphatase; prt, protein; put, putative; RDase, reductase; RG, ribose/galactose; SAM, S-adenosyl-methionine; Sase, synthetase/synthase; SP, spermidine/putrescine; ss, single-stranded; sub, subunit; Tase, transferase.

Abbrevation of genus and species are: Ah, Aeromonas hydrophila; Ar, Agrobacterium radiobacter; Al, Alteromonas sp.; Ab, Anabaena sp.; An, Anacystis nidulans; At, arabidopsis thaliana; Av, Azotobacter vinelandii; Bf, Bacillus firmus; Bl, Cacillus licheniformis; Bm, Bacillus megaterium; Bs, Bacillus stearothermophilus; Bs, Bacillus subtilis; Bb, Borrelia Bacillus megaletium, Bs, Bacillus steadurierimicipillus, Bs, Bacillus subulis, Bu, Burellus burgdorferi; Bc, Borrelia coriaceae; Bh, Borrelia hermsii; Ba, Buchnera aphidicola; Ca, Clostridium acetobutylicum; Cl, Clostridium longisporum; Cp, Clostridium perfringens; Cg, Corynegacterium glutamicum; Cb, Coxiella burnetii; Cp, Cyanophora paradoxa; Dd, Diotyostellum discoideum; Ec, Escherichia coli; Eh, Entamoeba histolytica; Ec, Enterobacter cloacae; El, Enterococcus faecalis; Eh, Enterococcus hirae; Ha, Haemophilus aegyptius; Hi, Haemophilus influenzae; Hp, Helicobacter pylori; Hs, Homo sapiens; La, Lactobacillus acidophilus; Ll, Lactococcus lactis; Li, Leptospira interrogans serovar lai; Mj, Methanococcus jannaschii; Mb, Methanosarcina barkeri; Ml, Mycobacterium leprae; Mt, Mycobacterium tuberculosis; Mc, Mycoplasma capricolum; Mg, Mycoplasma genitalium; Mh, Mycoplasma hominis; Mh, Mycoplasma hyorhinis; Mm, Mycoplasma mycoides; Mp, Mycoplasma pneumoniae; Mx, Myxococcus xanthus; Ng, Neisseria gonorrhoeae; Nm, Neisseria meningitidis; Os, Odontella sinensis; Pt, Paramecium tetraurelia; Pa, Pediococcus acidilactici; Pf, Plasmodium falciparum; Pg. Porphyromonas gingivalis; Pv, Proteus vulgaris; Pa, Pseudomonas aeruginosa; Pw, Pseudomonas mevalonii; Pp, Pseudomonas putida; Rm, Rhizobium meliloti; Rc, Rhodobacter capsulatus; Rs, Rhodobacter sphaeroides; Rp, Rickettsia prowazekii; Sc, Saccharomyces cerevisiae; Sc, Salmonella choleraesius; St, Salmonella typhimurium; Sh, Serpulina hyodysenteriae; Sd, Shigella dysenteriae; So, Spinacia oleracea; Sc, Staphylococcus camosus; Se, Staphylococcus epidermidis; Sp, Streptococcus pyogenes; Sc, Streptomyces coelicolor; Ss, Sulfolobus solfataricus; Syn, Synechococcus sp.; Sp, Synechocystis PCC6803; Tt, Thermoanaerobacterium thermosaccharolyticum; Tb, Thermophilic bacterium RT8.B4.; Ttv, Thermoproteus tenax virus; Tm, Thermotoga maritima; Tat, Thermus aquaticus thermophilus; Ta, Thermus aquaticus; Td, Treponema denticola; Tp, *Treponema pallidum*; Ta, *Triticum aestivum*; Tb, *Trypanosoma brucei* mitochondrion; Vc Vibrio cholerae; Vp, Vibrio parahaemolyticus; Zm, Zymomonas mobilis

3,000–5,000 bp per plasmid)^{13,16} (Table 1). Improved assembly strategies are being tested to achieve closure on these plasmids (G. Sutton, unpublished). Plasmid lp17 is identical to that of lp16.9 from Barbour *et al.*¹⁵.

The 11 plasmids we have described contain a total of 430 putative ORFs with an average size of 507 bp; plasmid G+C content ranges from 23.1% to 32.3%. Only 71% of plasmid DNA represents predicted coding sequences, a value significantly lower than that on the chromosome. This indicates that average intergenic distances are greater in the plasmids than in the chromosome, and that many potential ORFs contain authentic frameshifts or stops (see E29, for example), suggesting that they are decaying genes not encoding functional proteins. Of the 430 plasmid ORFs, only 70 (16%) could be identified and these include membrane proteins such as OspA-D, decorin-binding proteins, the VlsE lipoprotein recombination cassette, and the purine ribonucleotide biosynthetic enzymes GuaA and GuaB. We found that 100 ORFs (23%) match other hypothetical proteins from plasmids in this and related strains of B. burgdorferi 15,16,31; 10 ORFs (2.3%) match hypothetical proteins from species other than Borrelia; and 250 ORFs (58%) have no database match.

We found that 47 paralogous gene families containing from 2 to 12 members account for 39% (169 ORFs) of the plasmid-encoded genes with no known biological role (Fig. 1). Paralogue families 32 and 50, typified by previously identified *B. burgdorferi* plasmid genes cp32 orfC and cp8.3 orf2, respectively, have some similarities to proteins involved in replication, segregation and control of copy number in other bacterial systems^{16,31}. Previous studies have reported examples of plasmid gene duplication, but the extent of

Table 1 Genome features in Borrelia burgdorferi

Chromosome	910,725 bp (28.6% G+C)
Coding sequences (93%) RNAs (0.7%) Intergenic sequence (6.3%) 853 coding sequences 500 (59%) with identified database match 104 (12%) match hypothetical proteins 249 (29%) with no database match	

Plasmids	
cp9	9,386 bp (23.6% GC)
cp26	26,497 bp (26.3% GC)
lp17	16,828 bp (23.1% GC)
lp25	24,182 bp (23.3% GC)
lp28-1	26,926 bp (32.3% GC)
lp28-2	29,771 bp (31.5% GC)
lp28-3	28,605 bp (25.1% GC)
lp28-4	27,329 bp (24.4% GC)
lp36	36,834 bp (26.8% GC)
lp38	38,853 bp (26.1% GC)
lp54	53,590 bp (28.1% GC)
Coding sequences (71%)	
Intergenic sequence (29%)	
430 coding sequences	

Coding sequences (71%)
Intergenic sequence (29%)
30 coding sequences
70 (16%) with identified database match
110 (26%) match hypothetical proteins

250 (58%) with no database match	1
Ribosomal RNA 16S 23S 5S 23S 5S	Chromosome coordinates 444581-446118 438590-441508 438446-438557 435334-438267 435201-435312
Stable RNA	

tmRNA mpB

Transfer RNA 34 species (8 clusters, 14 single genes)

*The telomeric sequences of the nine linear plasmids assembled as part of this study were not determined; estimation of the number of missing terminal nucleotides by restriction analysis suggests that less than 1,200 bp is missing in all cases. Comparisons with previously determined sequences of lp 16.9 and one terminus of lp28-1 indicate that 25, 60 and 1,200 bp are missing, respectively.

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this redundancy has become even more apparent with the complete sequence of these 11 plasmids from isolate B31. Moreover, a preliminary search of 221 putative ORFs from the cp32s and lp56 indicates that at least 50% display ≥70% amino-acid similarity to ORFs from the other 11 plasmids presented here (data not shown). Although plasmid-encoded genes have been implicated in infectivity and virulence^{17–19}, the biological roles of most of these genes are not known. The significance of the large number of paralogous plasmid-encoded genes is not understood. These proteins may be expressed differentially in tick and mammalian hosts, or may undergo homologous recombination to generate antigenic variation in surface proteins. This hypothesis is supported by the identification of 63 plasmid-encoded putative membrane lipoproteins (Fig. 1).

Several copies of a putative recombinase/transposase similar to IS891-like transposases were identified in the *B. burgdorferi* plasmids. Linear plasmid 28-2 contains one full-length copy of this gene. Although no inverted repeats were found on either side of the transposase, there is a putative ribosome-binding site several nucleotides upstream of the apparent start codon, and a stemloop structure (-27 kcal mol⁻¹) 195 bp downstream of the stop codon in an area with no ORFs. This transposase might represent a functional gene important for the frequent DNA rearrangements that presumably occur in *Borrelia* plasmids. There are other partial or nearly complete copies of the transposase gene that contain frame-destroying mutations elsewhere in the genome: two copies on lp17, one on lp36, one on lp38, one on lp28-3, two on lp28-1, and one near the right end of the large linear chromosome.

Origin of replication

The replication mechanism for the linear chromosome and plasmids in *B. burgdorferi* is not yet known. Replication possibly begins at the termini, as has been proposed for the poxvirus hairpin telomeres³², or may begin from a single origin somewhere along the length of the linear replicon. Of the genes on the linear chromosome, 66% are transcribed away from the centre of the chromosome (Fig. 1), similar to the transcriptional bias observed for the genomes of *M. genitalium*²¹ and *M. pneumoniae*³³. It has been suggested that bacterial genes are optimally transcribed in the same direction as that in which replication forks pass over them, particularly for highly transcribed genes^{34,35}

Given the transcriptional bias observed in *B. burgdorferi*, it seems likely that the origin of replication is near the centre of the chromosome. Because bacterial chromosomal replication origins are usually near *dnaA*³⁶, it is intriguing to note that this gene (BB437) lies almost exactly at the centre of the linear *B. burgdorferi* chromosome^{10,27}. A centrally initiated, bi-directional replication fork would be equidistant from the two chromosome ends, and replication would traverse the rRNA genes in the same direction as transcription.

An analysis of GC skew, (G-C)/(G+C) calculated in 10-kilobase (kb) windows across the chromosome, shows a clear break at

the putative origin of replication. The GC-skew values are uniformly negative from 0 to 450 kb (minus strand), and uniformly positive (plus strand) from 450 kb to the end of the chromosome (Fig. 2). Additional evidence for the location of the origin of replication comes from our discovery of an octamer, TTGTTTTT, whose skewed distribution in the plus versus the minus strand of the chromosome matches the GC skew (Fig. 2). The biological significance of this octamer has not yet been determined, although it may be analogous to the Chi site in *Escherichia coli* that is implicated in *recBCD* mediated recombination. No GC skew was observed in any of the plasmids, although the heptamer ATTTTTT displays a skewed distribution in the plus versus the minus strand of lp28-4 that changes at the approximate midpoint of the plasmid (not shown).

Transcription and translation

Genes encoding the three subunits (α, β, β') of the core RNA polymerase were identified in *B. burgdorferi* along with σ^{70} and two alternative σ factors, σ^{54} and rpoS. The role and specificity of each of these σ factors in transcription regulation in *B. burgdorferi* are not known. The *nusA*, *nusB* and *rho* genes, which are involved in transcription elongation and termination, were also identified.

A region of the genome with a significantly higher G+C content (43%), located between nucleotides 434,000 and 447,000, contains the rRNA operon. As previously reported, the rRNA operon in *B. burgdorferi* contains a 16S rRNA–Ala-tRNA–Ile-tRNA–23S rRNA–5S rRNA–23S rRNA–5S rRNA–5S rRNA–37,38. All of the genes are present in the same orientation, except for that encoding Ile tRNA. Four unrelated genes, encoding 3-methyladenine glycosylase, hydrolyase and two with no database match, are also present in the rRNA operon. Three of these genes are transcribed in the same direction as the rRNAs.

We identified in the chromosome 31 tRNAs with specificity for all 20 amino acids (Fig. 1). These are organized into 7 clusters plus 13 single genes. All tRNA synthetases are present except glutaminyl tRNA-synthetase. A single glutamyl tRNA synthetase probably aminoacylates both tRNA^{Glu} and tRNA^{Gln} with glutamate followed by transamidation by Glu-tRNA amidotransferase, a heterotrimeric enzyme present in *B. burgdorferi* and several Gram-positive bacteria and archaea³⁰. The lysyl-tRNA synthetase (LysS) in *B. burgdorferi* is a class I type that has no resemblance to any known bacterial or eukaryotic LysS, but is most similar to LysS from the archaea⁴⁰.

Replication, repair and recombination

The complement of genes in *B. burgdorferi* involved in DNA replication is smaller than in *E. coli*, but similar to that in *M. genitalium*²¹. Three ORFs have been identified with high homology to four of the ten polypeptides in the *E. coli* DNA polymerase III: α , β and γ , and τ . In *E. coli*, the γ and τ proteins are produced by programmed ribosomal frameshifting. This observation suggests that DNA replication in *B. burgdorferi*, like that in *M. genitalium*, is accomplished with a restricted set of genes. *B. burgdorferi* has one

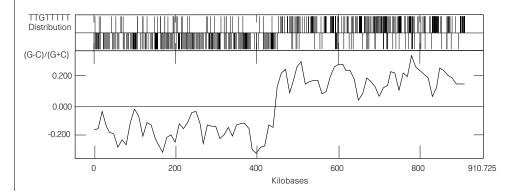


Figure 2 Distribution of TTGTTTT and GC skew in the *B. burgdorferi* chromosome. Top, distribution of the octamer TTGTTTT. The lines in the top panel represent the location of this octamer in the plus strand of the sequence, and those in the second panel represent the location of this oligomer in the minus strand of the sequence. Bottom, GC skew.



type I topoisomerase (*topA*) and two type II topoisomerases (gyrase and topoisomerase IV) for DNA topology management and chromosome segregation, despite its linear chromosomal structure. This suggests that topoisomerase IV may be required for more than the separation of circular DNAs during segregation.

The DNA repair mechanisms in *B. burgdorferi* are similar to those in *M. genitalium*. DNA excision repair can presumably occur by a pathway involving endonuclease III, PolI and DNA ligase. The genes for two of three DNA mismatch repair enzyme (*mutS*, *mutL*) are

present. The apparent absence of *mutH* is consistent with the lack of GATC (*dam*) methylation in strain B31 (S. Casjens, unpublished). Also present are genes for the repair of ultraviolet-induced DNA damage (*uvrA*, *uvrB*, *uvrC* and *uvrD*) (Table 2).

B. burgdorferi has a complete set of genes to perform homologous recombination, including recA, recBCD, sbcC, sbcD, recG, ruvAB and recJ. 3'-Exonuclease activity associated with sbcB in E. coli may be encoded by exoA (exodeoxynuclease III). Although recA is present, we found no evidence for lexA, which encodes the repressor that

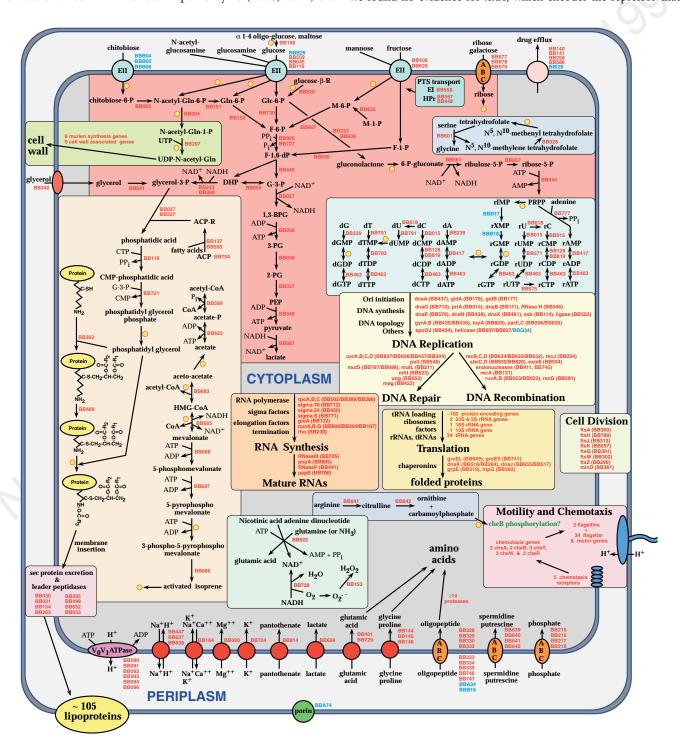


Figure 3 Solute transport and metabolic pathways in *B. burgdorferi*. A schematic diagram of a *B. burgdorferi* cell providing an integrated view of the transporters and the main components of the metabolism of this organism, as deduced from the genes identified in the genome. The ORF numbers correspond to those listed

in Table 2 (red indicates chromosomal and blue indicates plasmid ORFs). Presumed transporter specificity is indicated. Yellow circles indicate: places where particular uncertainties exist as to the substrate specificity, subcellular location or direction of catalysis: or expected activities that were not found.

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regulates SOS genes in *E. coli*. No genes encoding DNA restriction or modification enzymes are present.

Biosynthetic pathways

The small genome size of *B. burgdorferi* is associated with an apparent absence of genes for the synthesis of amino acids, fatty acids, enzyme cofactors, and nucleotides, similar to that observed with *M. genitalium*²¹ (Fig. 3, Table 2). The lack of biosynthetic pathways explains why growth of *B. burgdorferi in vitro* requires serum-supplemented mammalian tissue-culture medium. This is also consistent with previous biochemical data indicating that *Borrelia* lack the ability to elongate long-chain fatty acids, such that the fatty-acid composition of *Borrelia* cells reflects that present in the growth medium⁶.

Transport

The linear chromosome of *B. burgdorferi* contains 46 ORFs and the plasmids contain 6 ORFs that encode transport and binding proteins (Fig. 3, Table 2). These gene products contribute to 16 distinct membrane transporters for amino acids, carbohydrates, anions and cations. The distribution of transporters between the four categories of functions in this section is similar to that observed in other heterotrophs (such as *Haemophilus influenzae*, *M. genitalium* and *H. pylori*), with most being dedicated to the import of organic compounds.

There are marked similarities between the transport capacity of *B*.

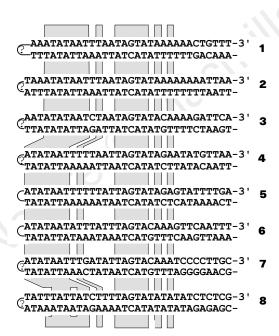


Figure 4 Telomere nucleotide sequences from *Borrelia* species. Nucleotide sequences are shown for known *Borrelia* telomeres as indicated: 1,*B. burgdorferi* Sh-2-82 chromosome left end; 2, *B. burgdorferi* B31 chromosome left end; 3, *B. afzelii* R-IP3 chromosome right end; 4, *B. burgdorferi* B31 chromosome right end; 5, *B. burgdorferi* B31 plasmid lp17 left end; 6, *B. burgdorferi* B31 plasmid lp17 right end; 7, *B. hermisii* plasmids bp7E and pb21E right ends; 8, *B. burgdorferi* B31 plasmid lp28-1 right end. In each case the telomere is at the left. Question marks (?) indicate locations where S1 nuclease was used to open terminal hairpins during the sequence determinations. Stippled areas highlight regions that appear to have been most highly conserved among these telomeres; no strong sequence conservation has been found near the right of the terminal 26 bp among the different sequences listed, except between the chromosomal left ends from strains B31 and Sh-2-82 (see text). The telomeric sequences of the strain B31 chromosome were determined in this report; the others are from references 14, 28, 30, 45, 46.

burgdorferi and M. genitalium. Both genomes have a limited number of recognizable transporters, so it is not clear how they can sustain diverse physiological reactions. Several of the identified transporters in both genomes exhibit broad substrate specificity, exemplified by the oligopeptide ABC transporter (opp operon) or the glycine, betaine, L-proline transport system (proVWX). Therefore, these organisms probably compensate for their restricted coding potential by producing proteins that can import a wide variety of solutes. This is important because B. burgdorferi is unable to synthesize any amino acids de novo. We were unable to identify any transport systems for nucleosides, nucleotides, NAD/NADH or fatty acids, although they are likely to be present.

Glucose, fructose, maltose and disaccharides seem to be acquired by the phosphoenolpyruvate:phosphotransferase system (PTS). The two nonspecific components, enzyme 1 (ptsI) and Hpr (ptsI), are associated in one operon with an apparently glucose-specific, phosphohistidine-sugar phosphotransferase enzyme IIA (crr). Separate from this operon are four permeases (enzyme IIBC), fruA in two copies (fructose), ptsG (glucose) and malX (glucose/maltose) (Fig. 3, Table 2). The fructose-specific enzyme IIA is induced in the ORF with IIBC (fruA), as has been observed in M. $genitalium^{41}$. Ribose may be imported by an ATP-binding cassette transporter (rbsAC). The rbsAC genes are transcribed in an operon with a methyl-accepting chemotaxis protein that may respond to β -galactosides, suggesting that movement of the organisms towards sugars may be coupled to the transport process.

Energy metabolism

The limited metabolic capacity of *B. burgdorferi* is similar to that found in *M. genitalium* (Fig. 3, Table 2). Genes encoding all of the enzymes of the glycolytic pathway were identified. Analysis of the metabolic pathway suggests that *B. burgdorferi* uses glucose as a primary energy source, although other carbohydrates, including glycerol, glucosamine, fructose and maltose, may be used in glycolysis. Pyruvate produced by glycolysis is converted to lactate, consistent with the microaerophilic nature of *B. burgdorferi*. Generation of reducing power occurs through the oxidative branch of the pentose pathway. None of the genes encoding proteins of the tricarboxylic acid cycle or oxidative phosphorylation were identified. The similarity in metabolic strategies of two distantly related, obligate parasites, *M. genitalium* and *B. burgdorferi*, suggests convergent evolutionary gene loss from more metabolically competent, distant progenitors.

Addition of *N*-acetylglucosamine (NAG) to culture medium is required for growth of *B. burgdorferi*⁶. NAG is incorporated into the cell wall, and may also serve as an energy source. The cp26 plasmid encodes a PTS cellobiose transporter homologue that could have specificity for the structurally similar compound chitobiose (di-*N*-acetyl-D-glucosamine). A gene product on the chromosome with sequence similarity to chitobiase (BB2) may convert chitobiose to NAG. *B. burgdorferi* can metabolize NAG to fructose-6-phosphate, which then can enter the glycolytic cycle through the action of *N*-acetylglucosamine-6-phosphate deacetylase and glucosamine-6-phosphate isomerase. NAG is the primary constituent of chitin, which makes up the tick cuticle⁶, and may be a source of carbohydrate for *B. burgdorferi* when it is associated with its tick host.

The parallels between *B. burgdorferi* and *M. genitalium* appear to extend to other aspects of their metabolism. Both organisms lack a respiratory electron transport chain, so ATP production must be accomplished by substrate-level phosphorylation. Consequently, membrane potential is established by the reverse reaction of the V_1V_0 -type ATP synthase, here functioning as an ATPase to expel protons from the cytoplasm (Fig. 3, Table 2). The ATP synthase genes in *B. burgdorferi* appear to be transcribed as part of a sevengene operon. They are not typical of those usually found in eubacteria, more closely resembling the eukaryotic vacuolar (V-type) and archaeal (A-type) H^+ -translocating ATPases⁴², both in size

and sequence similarity, than the bacterial F_1F_0 ATPases. Genome analysis of *Treponema pallidum*, the pathogenic spirochaete that causes syphilis, has also revealed the presence of a V_1V_0 -type ATP synthase (C. M. F. *et al.*, manuscript in preparation), suggesting that this may be a feature of spirochaetes.

Regulatory systems

Although the expression of *Borrelia* genes varies according to the current host species, temperature, host body location and other local factors, control of gene expression appears to differ from more well studied eubacteria. A typical set of homologues of heat-shock response genes is present (groES, groEL, grpE, dnaJ, hslU, hslV, dnaK and htpG), and B. burgdorferi is known to have such a response; however, it lacks the σ -32 that controls their transcription in E. coli. Only a few homologues to other eubacterial regulatory proteins are present, including only two response-regulator two-component systems.

Motility and chemotaxis

Like other spirochaetes, *B. burgdorferi* has periplasmic flagella that are inserted at each end of the cell and extend towards the middle of the cell body. The unique flagella allow the organism to move through viscous solutions, an ability that is presumed to be important in its migration to distant tissues following deposition in the skin layers⁴³. Proteins involved in motility and chemotaxis are encoded by 54 genes, more than 6% of the *B. burgdorferi* chromosome, most of which are arranged in eight operons containing between 2 and 25 genes.

B. burgdorferi contains several copies of the chemotaxis genes (cheR, cheW, cheA, cheY and cheB) downstream of the methylaccepting chemotaxis proteins. Other eubacteria also have duplications of some che genes, but those genes in B. burgdorferi are the most redundant set yet found. B. burgdorferi lacks recognizable virulence factors; thus, its ability to migrate to distant sites in the tick and mammalian host is probably dependent on a robust chemotaxis response. Multiple chemotaxis genes may provide redundancy in this system in order to meet such challenges or, alternatively, these genes may be differentially expressed under varied physiological conditions. Another speculative possibility is that the flagellar motors at the two ends of the B. burgdorferi cell are different and require different che systems. In support of this idea is the observation that one of the motor switch genes, fliG, is also present in two copies.

Membrane protein analysis

Much of the previous work on *B. burgdorferi* has focused on outer-surface membrane genes because of their potential importance in bacterial detection and vaccination. Nearly all *Borrelia* membrane proteins have been found to be typical bacterial lipoproteins. A search of *B. burgdorferi* ORFs for a consensus lipobox in the first 30 amino acids identified 105 putative lipoproteins, representing more than 8% of coding sequences. This contrasts with a total of only 20 putative lipoproteins in the 1.67-million base pair *H. pylori* genome (1.3% of coding sequences)²³. The periplasmic binding proteins involved in transport of amino acids/peptides and phosphate in *B. burgdorferi* are candidate lipoproteins, suggesting that they may be anchored to the outer surface of the cytoplasmic membrane as in Gram-positive bacteria, rather than localized in the periplasmic space

In better-characterized eubacteria, prolipoprotein diacylglycerol transferase (*lgt*), prolipoprotein signal peptidase (*lsp*), and apolipoprotein:phospholipid *N*-acyl transferase (*lnt*) are required for post-translational processing and addition of lipids to the aminoterminal cysteine. Genes for the first two of the enzymes (*lgt* and *lsp*) are present in the *B. burgdorferi* genome, but the gene for *lnt* was not identified, although biochemical evidence argues for all three activities in *B. burgdorferi*⁴⁴. The sequence similarity of an *lnt*

homologue in *B. burgdorferi* may be too low to be identified using our search methods, or its activity may be present in a new enzyme. In *E. coli* the Sec protein export system moves lipoproteins through the inner membrane, and *Borrelia* carries a complete set of these protein-secretion gene homologues (*secA/D/E/F/Y* and *tth*; only the non-essential *secB* is missing).

Analysis of telomeres

The two chromosomal telomeres of strain B31 have similar 26-bp inverted terminal sequences (Fig. 4). We found no other similarity between the two ends, and these 26-bp sequences are very similar to the previously characterized *Borrelia* telomeres. Terminal restriction fragments from both B31 chromosomal termini were shown to exhibit snapback kinetics (data not shown), strongly indicating that both terminate in covalently closed hairpins, like previously characterized *Borrelia* telomeres^{28,45,46}.

The left chromosomal telomere of strain B31 is identical to the previously characterized left telomere of strain Sh-2-82 (ref. 28), except for a 31 bp insertion in B31 26 bp from the end. The rightmost 7,454 bp contains surprisingly few ORFs, given the ORF density elsewhere on the chromosome. The function of this region is unknown, but it contains several unusual features. The right terminal 900 bp contains considerable homology to the left ends of lp17 and lp28-3. The region between 3,600 bp and 8,000 bp from the right end also contains several areas with similarity to plasmid sequences, including a portion of the transposase-like gene approximately 4,500 bp from the right end. The spacing between the two conserved motifs (ATATAAT and TAGTATA) in the right 26-bp terminal repeat is the same as most previously known plasmid telomeres but different from the previously known chromosomal telomeres. These findings support the idea that the right end of the Borrelia chromosome has historically exchanged telomeres with the linear plasmids²⁸.

Conclusions

The *B. burgdorferi* genome sequence will provide a new starting point for the study of the pathogenesis, prevention and treatment of Lyme disease. With the exception of a small number of putative virulence genes (haemolysins and drug-efflux proteins), this organism contains few, if any, recognizable genes involved in virulence or host–parasite interactions, suggesting that *B. burgdorferi* differs from better-studied eubacteria in this regard. It will be interesting to determine the role of the multi-copy plasmid-encoded genes, as previous work has implicated plasmid genes in infectivity and virulence. The completion of the genome sequence from a second spirochaete, *Treponema pallidum* (C.M.F. *et al.*, manuscript in preparation) will allow for the identification of genes specific to each species and to this bacterial phylum, and will provide further insight into prokaryotic diversity.

Methods

Cell lines. A portion of a low-passage subculture of the original Lyme-disease spirochaete tick isolate⁴ was obtained from A. Barbour. The type strain of *B. burgdorferi* (ATCC 35210)³, B31, was derived from this isolate by limiting dilution cloning⁵. Cells were grown in Barbour–Stoenner–Kelly medium II (BSKII)⁶, omitting the additions of antibiotics and gelatin, in tightly closed containers at 33–34 °C. Cells were subcultured three or fewer times *in vitro* between successive rounds of infection in C3H/HeJ mice to minimize loss of infectivity and plasmid content^{17,18}. After four successive transfers of infection in mice, a primary culture of B31, established from infected ear tissue, was expanded to 2.51 by four successive subcultures. All available evidence indicates that the B31 line used for preparation of genomic DNA was probably clonal, as genetic heterogeneity was undetectable by several criteria including macrorestriction analysis (S. Casjens, unpublished data) and plasmid analysis of clonal derivatives of the B31 line¹³.

Sequencing. The *B. burgdorferi* genome was sequenced by a whole-genome random sequencing method previously applied to other microbial genomes^{20–24}.

articles

An approximately 7.5-fold genome coverage was achieved by generating 19,078 sequences from a small insert plasmid library with an average edited length of 505 bases. The ends of 69 large insert lambda clones were sequenced to obtain a genome scaffold; 50% of the genome was covered by at least one lambda clone. Sequences were assembled using TIGR Assembler as described^{20–24}, resulting in a total of 524 assemblies containing at least two sequences, which were clustered into 85 groups based on linking information from forward and reverse sequence reads. All Borrelia sequences that had been mapped were searched against the assemblies in an attempt to delineate which were derived from the various elements of the B. burgdorferi genome. Some contigs were also located on the existing physical map by Southern analysis. Sequence and physical gaps for the chromosome were closed as described²⁰⁻²⁴. At the completion of the project, less than 3% of the chromosome had single-fold coverage. The linear chromosome of B. burgdorferi has covalently closed hairpin structures at its termini that are similar to those reported for linear plasmids in this organism¹¹. The telomeric sequences (106 and 72 bp, respectively, from the left and right ends) were obtained after nicking the terminal loop with S1 nuclease and amplifying terminal sequences by ligation-mediated polymerase chain reaction (PCR) as described²⁸. The unknown terminal sequence was determined in both directions on four independent plasmid clones of the amplified DNA from each telomere. A minimum amount of S1 nuclease was used and, because of their sequence similarity to other Borrelia telomeres, it is likely that few, if any, nucleotides were lost from the B31 chromosomal telomeres in this process.

Identification of ORFs. Coding regions (ORFs) were identified using compositional analysis using an interpolated Markov model based on variable-length oligomers⁴⁷. ORFs of >600 bp were used to train the Markov model, as well as B. burgdorferi ORFs from GenBank. Once trained, the model was applied to the complete B. burgdorferi genome sequence and identified 953 candidate ORfs. ORFs that overlapped were visually inspected, and in some cases removed. Non-overlapping ORFs that were found between predicted coding regions and >30 amino acids in length were retained and included in the final annotation. All putative ORFs were searched against a non-redundant amino-acid database as described²⁰⁻²⁴. ORFs were also analysed using 527 hidden Markov models constructed for several conserved protein families (PFAM v2.0) using HMMER⁴⁸. Families of paralogous genes were constructed by pairwise searches of proteins using FASTA. Matches that spanned at least 60% of the smaller of the protein pair were retained and visually inspected. A total of 94 paralogous gene families containing 293 genes were identified

Identification of membrane-spanning domains (MSDs). TopPred⁴⁹ was used to identify potential MSDs in proteins. A total of 526 proteins containing at least one putative MSD were identified, of which 183 were predicted to have more than one MSD. The presence of signal peptides and the probable position of a cleavage site in secreted proteins were detected using Signal-P as described²³; 189 proteins were predicted to have a signal peptide. Lipoproteins were identified by scanning for a lipobox in the first 30 amino acids of every protein. A consensus sequence relaxed from that used for H. pylori²³ was defined for the purpose of this search based on known or putative B. burgdorferi lipoprotein consensus sequences.

Received 3 November; accepted 18 November 1997.

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Acknowledgements. We thank A. G. Barbour for isolation of the Borrelia burgdorferi strain; A. Barbour. P. Rosa, K. Tilly, J. Riberio, B. Stevenson and D. Soll for discussions; N. K. Patel for technical assistance; M. Heaney, J. Scott and A. Saeed for software and database support; and V. Sapiro, B. Vincent and D. Maas for computer system support. This work was supported by a grant to J.C.V. and C.M.F. from the G. Harold and Leila Y. Mathers Charitable Foundation.

Correspondence and requests for materials should be sent to C.M.F. (e-mail: gbb@tigr.org). The annoted genome sequence and gene family alignments are available on the World-Wide Web at http://www.tigr.org/tdb/mdb/bbdb/bbdb.html. Sequences have been deposited with GenBank under the following accession numbers: AE00783 (chromosome); AE00784 (lp28-3); AE000785 (lp25); AE00786 (lp28-2); AE00787 (lp38); AE00788 (lp36); AE00789 (lp28-4); AE00790 (lp54); AE00791 (cp9); AE00792 (cp26); AE00793 (lp17); and AE00794 (lp28-1).

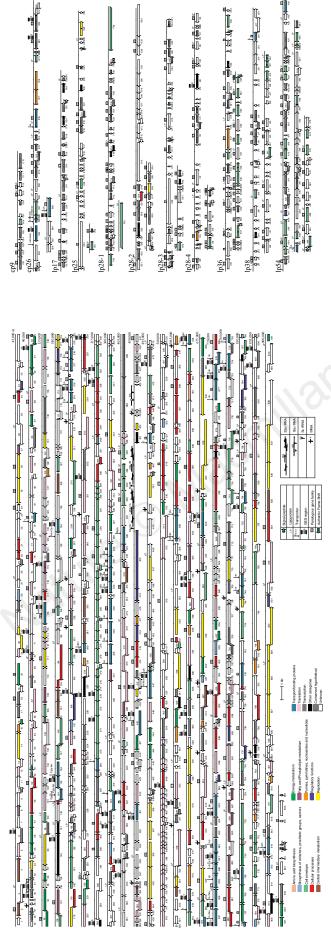


Table 2. Identification of 8. ba	<i>radorteri</i> genes
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B8#	Identification (Species) 9	¢Sm.	ID68-3			BB291		100
	فلنجر لنديدتنا الم		BBH20	outer membrene porin (orrecs),	74		nigr besel-body rod prt (figC) (Bb) nigr besel-body rod prt (figB) (Bb)	100
Serine			BBH21	put (Bb) outer membrene porin (orreca),	14	BB774	figr beed-body rod prt (figs) (80)	`₩
	orino OHMT to o (glyd.) (Ec)	73		prt (Bb)	74	BB271	flyr biceyn pr((lh.k.) (Bb)	100
						BB272	figr bloeyn prt (INB) (Bb)	100
	horio el asiectoro, praethetic		1025 BBE09	met mile //Dts	98	BB273 BB274	flýr biceýn prt (NR) (Bb) Mar biceus ant 6000 (Bb)	100
Foliate	eni seriet Sa		BEENS	prtp23 (Bb)	20	BB275	filgr biceyn prt (NC) (Bb) filgr biceyn prt (NP) (Bb)	100
	mathylian alatra hydrofolata		<u>op26</u>			BB276	flyr biceyn prt (12) (Bb)	100
	CHoos (fdC) (Bb)	61	BBB19	orter ourrece prt C (copC)(Bb)	100	B8147	figr filement 41 kDe core prt	
			BBB 07	orter ourte co-prt, prt (Bb)	46		(MeE) (Btb)	100
BB197	ma' pomphyminogen oxidese;		.002			55660	filgrifilement outer layer prt (fla.k) (Et)	99
20171	prt (Be)	58		exported grt A (eppA) (Bb)	100	BB284	figr hook essembly prt (figD) (Bb)	
B8 6 58	oxygen-in-dependent					BB283	figr hook prt (figE) (Bb)	100
	coproporphymogen III coldese,	_		secoulus end poeptidoglycen		BB181	figr hook-see coasted pit (figK) (Bb)	99
	prt (Ba)	ទា	BB160 BB582	danine recomese (ell) (Ec) CPD-se put (Be)	54 54	68149	figr hook-see-coiefied prt 2 (filib) (Bb)	99
			B8200	DebrineDelenine Igee		BB1 %2		~
	vinane enal ubiquinane	_		(8dk.) (Eo)	60		(figL) (Bb)	99
BB314	cotapreny Loss Sasse (laps) (Ec)	न्त	BB100	glutamate recemese (muri) (Ec)	58	887 <i>1</i> 5	flgr hook-beed body complex	
Pendoth	anata		88825	N.A. chromogli L. alarina amidesiq	53	88292	prt (NAO) (Ba) 11gr hook-basel body complex	58
BB812	pantithanata matabalam		88732	pot (En potición EP (pops) (Ng)	ž	DOCK	př. NE) (BB)	100
	1ev cprt (dfp) (Ed)	58	BB138	penidlin-BP (pbp-1) (Nm)	52	BB230	figr motor rotation grt B	• • • •
			88718	penidilin-SP (pope) (Hi)	52		(m̃o®) (Bb)	100
Pyridox			BB303	phospho-N-Acmuremoyl-		BB281		
BB768	pyridoxal kinese exten roa	47		pente poptidoFeee (mre/r) (Bb)	100	88277	(micht) (Bb) figr michorewhon pot (NN) (Bb)	100
	b and (80)		88715	red shape-determining		BB278		100
70/emi	₩		20113	pt (mre8-1) (Eo)	73	BB221		54
BB821	4mathyl6(b-OHathyl)#hiszola		88716	rod shape-determining prt		BB290	figr motor-avaltah prt (NiCs-2) (Bb)	100
	mond ^p	58	nome.	fnreC) (Be)	হা	BB772	flår P-ring prt (flat) (Ar)	<u>,</u>
	Boeyn prt (thil) (Eo)		BB719	rod ehepe-determining prt (mreB-2) (Hi)	61	BB279 BB282		100
Puktin	nodeotides		88805	demotype Dulla-Dulla CPDade	61	BB236	figr prt (fbC) (8b)	100
BB522	NH(3)dep NAD+ See (R0)	65		(deal) (Hi)	5 5	BB238	nigr prt (MbB) (Bb)	100
			BB472	UDPN/(0:1-certoxywinyffeee		BB287	ng prt (nox) (Bb)	100
Out on				(Murx) (Ed)	59	BB180	figr prt, put (Bb)	100
	mes, époprofeirs, endiparins - besiomembrene prt B (tmpB) (Bt	0100	B8698	UDP-NA conuremete CHese (murB) (Be)	5 5	88650 88270	filgr prt (ffs.f) (Vp) filgr-associated (KTP-BP (ffs.F) (Bb)	57 100
BB383	basiomembrane prt A (bmpA) (Bt		88817	UDP-N-Lamuremete-elenine ligese		B8288	figre pecific ATP Sees (fill) (Bb)	100
BB384	- basiomembrane prt C (bmpC) (Bt	oji oo		fourQ (H)	54		* * * * * * * * * * * * * * * * * * * *	
88395	besigmembrane prt D (bmpD) (Bt		886%	UDP-NA considerance D			PURCONOR	
BB1 08 BB319	besiomembrene prt (Tp) exported prt (tpn⊗b) (Tp)	50 50		glutamate (gese (murD) (Bs)	52	G976/9 BB567		
				share (main) (no)		DD0011		
BB:347	nitranedin Nibrinogen-BP, put (Sp):	-53	BB201	UDP-N-4 cmure model en ul-			(che/L41)(Bb)	99
B8 442	ittranedin filbrin ogen-BP, put (Sp) inner membrane prt (Hi)	53 63	BB201	UDP-N-A convire moytelenyt- Digitatemete-2,6-		88889	(chex.4.) (Bb) chanctesse histiane Kese	99
BB 442 BB 395	inner membrane prt (Hi) Spoprotein LA7 (Bb)			Diglutemete-2,6- deminopimelete (gese (murE) (Hi)	53		òhamatásishistidhe Keee (dhek-2) (Bti)	99 100
B8 442	inner membrene prt (H) Spoprotein LA7 (Bb) membrene-scoodsted prt	63 100	BB201 BB304	Diglutamete-2,6 deminopimelete ligese (murE) (Hi) UDP-N-4 amure moytelen yl-D-	53	BB8 69 BB0 40	chemotésis fiertaine Keel (chell-2) (Bb) chemotesis prit MTeel (chell-1)	100
B8442 B8395 B8603	inner membrene prt (H) Spoprotein LA7 (Bb) membrene-accodated prt p86 (Bb)	63 100 100		Digitamete-2,6- deminopimelate ligade (murE) (Hi) UDP-N-A anure moytelenyl Di- glutemyl-2,8-diemino-pimelate-	53	BB040	chancteise hetaine Kee (chall-2) (Bb) chancteise pri MTee (chall-1) (Re)	
88442 88396 88903 88753 88756	inner membrene prt (H) Spoprotein LA7 (Bb) membrene-scoodsted prt	68 100 100 49 48	BB304	Digitamete-2,6 deminopimete igase (muris) (Hi) UDP-N-4 churemoylelenyt D- gutemyt-2,6-diemino-pimete- Delanyt-D-denine igase (huri-) (Bb))53 100	B8040 B8414	chandsishistane Kwe (diel 2) (Bb) chandsish prt MTwe (diel-1) (Rs) chandsish prt MTwe (diel-2) (Rn)	100
B8 442 B8396 B8 603 B8 753 B8 796 B8167	inner membrene pit (H) ipoprotein LA7 (Bb) membrene-associated pit p86 (Bb) membrene-aspenning prt put (Se) outer membrene pit (Ng) outer membrene pit (tip(S)) (Tp)	63 100 100 49 48 48		Dightemate-2,6- deminopinelete ligese (mur E) (Hi) UDP-N-4 churencylelenyl-2- glutemyl-2-6-demino-pinelete- Delenyl-2-demine ligese (hur F) (Bb) UDP-N-4 cyluccemine-N-		BB040	ich an cháise faith an Rese (chall 2) (Bb) chan desis pri MTese (chall-1) (Re) chan desis pri MTese (chall-2) (Rm) (Rm)	100 61 57
88 442 88 396 88 603 88 753 88 796 88 197 88 736	inner membrane pit (H) ipoprotein LAT (Bb) ipoprotein LAT (Bb) membrane-associated pit pit (Bb) membrane-associated pit put (Se) outer membrane pit (Nig) outer membrane pit (pit (Se)) (Tp) rare ipopit A (ripA) (H)	68 100 100 49 48	BB304	Digittamete-2,6 deminopimeter ligese (muris) (Hi) UPP-N-1 amuremoulel enyl Digitamy (-2,6-demino-pimete- putamy (-2,6-demino-pimete- putamy (-2,6-demino-pimete- putamy (-1,6-demino-N- Admuramy (-1,6-demino-N- Admuramy (-1,6-demino-N- Admuramy (-1,6-demino-pimete)		B8040 B8494 B8651	chanctisis histaine Kee (dref2) (Bb) chanctisis pri MTee (dref1) (Re) chanctisis pri MTee (dref2) (Rm) chanctisis response regulator (oheY-1) (Tp)	100 61
B8 442 B8396 B8 603 B8 753 B8 796 B8167	inner membrane pit (H) ipoprobin LAT (Bb) membrane-accordated pit pis (Bb) membrane-accordated pit pis (Bb) membrane-accordated pit pis (Bb) membrane-accordated pit pis (Bb) cutar membrane-pit (Ng) cutar membrane-pit (pin50) (Tp) rare-ipopit A (rbb) (H) authore-icoated membrane	83 100 100 49 48 48 58	BB304	Dightemate-2,6- deminopinelete igeee (murE) (Hi) UPP-N-4 muremoyleleny(D- gluteny(-2,6-demino-pinid ete- Deleny(D-elenino ligeeo murf (ISD) UPP-N-4 glucceemine-N- Amuremy(-pertapept)dej pyrophoephory(-undeceprend	100	B8040 B8414	chandasia histaine Kee (diel. 2) (Bt) chandasia pri MTee (diel. 1) (Re) chandasia pri MTee (diel. 2) (Rm) chandasia reponse regulator (diel. 1) (Tp) chandasia reponse regulator	100 61 57 74
88 442 88 396 88 603 88 753 88 796 88 197 88 736	inner membrane pit (H) ipoprotein LAT (Bb) ipoprotein LAT (Bb) membrane-associated pit pit (Bb) membrane-associated pit put (Se) outer membrane pit (Nig) outer membrane pit (pit (Se)) (Tp) rare ipopit A (ripA) (H)	63 100 100 49 48 48	BB304	Digittamete-2,6 deminopimeter ligese (muris) (Hi) UPP-N-1 amuremoulel enyl Digitamy (-2,6-demino-pimete- putamy (-2,6-demino-pimete- putamy (-2,6-demino-pimete- putamy (-1,6-demino-N- Admuramy (-1,6-demino-N- Admuramy (-1,6-demino-N- Admuramy (-1,6-demino-pimete)		B8040 B8494 B8651	chandaise fiertaine Kee (dief. 2) (Bt) chandaise prit MTee (dief. 1) (Re) chandaise prit MTee (dief. 2) (Rm) chandaise reponse regulator (ohe Y-1) (Tp) chandaise response regulator (ohe Y-2) (Rm)	100 81 57 74 70
B8 442 B8 395 B8 603 B8 753 B8 795 B8 16 7 B8 736 B8 153 B8 153	inner membrene pit (H) ipoprotein L.47 (Bb) membrene-associated prt pis (Bb) membrene-associated prt pis (Bb) membrene-penning prt put (Se) outer membrene prt (Ng) outer membrene prt (tpris) (Tp) rere ipoprt A (tpA) (H) surface-located membrene prt 1 (tmp1) (Mh)	83 100 100 48 48 48 58	B8304 B8767	Dightemete-2,6- deminopinisher ligese (murit) (Hi) UPP-NA diminopinisher ligese guternyi-2,6-demino-pinishe- palanyi-D-alanine ligese fruit (IBN) UPP-NA dijiucceamine-N- Admuramyi-(pentapeptide) pyriphiceptoryi-undeceptend NAG Tees (murit) (Be) polysecchericies, (inopolyseccheric	100 58	BB040 BB414 BB651 BB670 BB872	chamatisis histatine Kese (disel. 2) (Bb) chamatisis prt MTese (disel. 1) (Rs) chamatisis prt MTese (disel. 1) (Rs) chamatisis prt MTese (disel. 2) (Rm) chamatisis response regulator (cheY-1) (Tp) chamatisis response regulator (cheY-2) (Rm) chamatisis response regulator (cheY-2) (Rm) chamatisis response regulator (cheY-2) (Bb)	100 81 57 74 70 98
B8 442 B8 395 B8 903 B8 753 B8 795 B8 16 7 B8 735 B8 10 B8 153	inner membrane pit (H) ipoprobia LAT (Bb) membrane-accordated prt pis (Bb) membrane-accordated prt pis (Bb) membrane-accordated prt put (Se) outer membrane prt (Ng) outer membrane prt (priss) (Tp) rare ipoprit A (rbb) (H) authocal coated membrane prt 1 (lmp1) (Mh) Sc prt (Bb)	88 100 100 48 48 48 58 48	BB304 BB767 Surfece end end	Dightemate-2,6- deminopinelette (gese (murE) (Hi) UDP-N-A amuremoyleleny(D- gutemy(-2,6-demino-pinid ete- Deleny(D-elenino (gese murf (Rb)) UDP-N-A gilucceemine-N- Aanuremy(-pertepeptide) pyraphoephory(-undeceprend NAG Tese (murd) (Be) pulys ecchericles, (populys eccheric gess)	100 58 Aar	BB040 BB414 BB651 BB670 BB872 BB860	chandaise histaine Kee (diel. 2) (Bts) chandaise prit MTee (diel. 2) (Re) chandaise prit MTee (diel. 2) (Rm) chandaise response regulator (ohe/3) (Tp) chandaise response regulator (ohe/3) (Rm) chandaise response regulator (ohe/3) (Bts) (CTP-BP (end) (Ed)	100 81 57 74 70 88
B8 442 B8 395 B8 603 B8 735 B8 735 B8 167 B8 735 B8 153 B8 153 B8 153 B8 153	inner membrene pit (H) ipoproble LA7 (Bb) membrene-sessisted pit p86 (Bb) membrene-spenning prt put (Se) outer membrene pit (Ng) outer membrene pit (tips50) (Tp) rese ipoprit A (tips5) (H) surface-loosted membrene prt 1 (imp1) (Mh) SC prt (Bb) decorin BP A (dtpA) (Bb)	80 100 100 48 48 48 58 48 58	BB304 BB767 Sulface and and BB744	Dightemate-2,6- deminopimelete igeee (murE) (Hi) UDP-N-I amuremoylelenyi D- ghtemyi 2,8-demino-pimidete- D-elenyi D-elenine igeee (murE) (Bb) UDP-N-I ajlucceemine-N- I amuremyi-(pentapopilde) (pyraphoephoryi-undeceprend N-I ar Teee (mura) (Be) (polycecateriales, shopelyseccheria (ges) entigen, pss/100 (Bb)	100 5% Mar 100	B8040 B8484 B8651 B8670 B8872 B8860 B8781	ohamotoise hietatine Keee (chell. 2) (Bts) ohamotoise prit MTeee (chell. 2) (Re) ohamotoise prit MTeee (chell. 2) (Rm) ohamotoise response regulator (oheY3) (Tp) ohamotoise response regulator (oheY4) (Rm) ohamotoise response regulator (oheY4) (Rm) ohamotoise response regulator (oheY4) (Bts) offn-88 (ohe) (Bd) (GTP-88 (ohe) (Bd) (GTP-88 (ohe) (Bd)	100 81 57 74 70 88 88
B8 442 B8 395 B8 903 B8 753 B8 795 B8 16 7 B8 735 B8 10 B8 153	inner membrene pit (H) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrene-accorded pit pit (Bb) membrene apanning prt put (Se) outer membrene pit (Ipi) outer membrene pit (Ipi) outer membrene pit (Ipi) (Ipi) rare ipopit A (IpiA) (H) authopal coated membrene pit 1 (Imp1) (Mh) St pit (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb)	88 100 100 48 48 48 58 48	BB3 04 BB7 67 Surface end end BB7 44 BB6 72	Dightemate-2,6- deminopinelette (gese (murE) (Hi) UDP-N-A amuremoyleleny(D- gutemy(-2,6-demino-pinid ete- Deleny(D-elenino (gese murf (Rb)) UDP-N-A gilucceemine-N- Aanuremy(-pertepeptide) pyraphoephory(-undeceprend NAG Tese (murd) (Be) pulys ecchericles, (populys eccheric gess)	100 58 Aar	BB040 BB414 BB651 BB670 BB872 BB860	chandaise histaine Kee (diel. 2) (Bts) chandaise prit MTee (diel. 2) (Re) chandaise prit MTee (diel. 2) (Rm) chandaise response regulator (ohe/3) (Tp) chandaise response regulator (ohe/3) (Rm) chandaise response regulator (ohe/3) (Bts) (CTP-BP (end) (Ed)	100 81 57 74 70 88 88
B8.442 B8.395 B8.603 B8.705 B8.705 B8.705 B8.105 B8.153 IDSA B8.124 B8.124 B8.125 B8.125 B8.125 B8.125	inner membrane pit (H) ipoprotein LAT (Bb) ipoprotein LAT (Bb) membrane-accordated prt pis (Bb) membrane-accordated prt pis (Bb) membrane-pre (Ng) outer membrane prt (Ng) outer membrane prt (Ng) outer membrane prt (Ng) outer membrane prt (Ng) (Tp) rare ipoprit A (NpA) (H) aurisoelcosted membrane prt 1 (Impl) (Nh) 32 prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb)	80 100 40 40 40 40 50 40 50 40 50 50 54 100 54 100	BB3 04 BB7 67 Sulfects end end BB7 44 BB6 72	Dightemete-2,6- deminopinelete igeee (murE) (Hi) UDP-N-A muremoyleleny/D- gluteny/L-elenine igeee murE) (Bb) UDP-N-A glucceemine-N- Amuremy-(pentapapilda) py-qchoephory/-undeceprend NAG Teee (murG) (Be) pulyseccherides, ibopulyseccherid geos entigen, ps3/100 (Bb) glycceyl Teee (grD) (Hi)	100 5% Aer 100 5%	B8040 B8444 B8651 B8670 B8872 B8880 B8781 B8658 B8658 B8658 B8658 B8658 B8658 B8658	chandaise histaine Kee (diel. 2) (Bb) (handaise prit MTee (diel. 2) (Re) (handaise prit MTee (diel. 2) (Re) (handaise prit MTee (diel. 2) (Re) (handaise response regulator (ohe/1) (Tp) (handaise response regulator (ohe/2) (Rin) (oher/2) (Rin)	100 81 87 74 70 88888158
B8442 B8395 B8395 B8795 B8795 B8195 B8153 B8153 JC54 B8125 B8125 B8135 B81435 B81435 B81435	inner membrene pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrene-accordated pit p86 (Bb) membrene-apenning prt put (Se) outer membrene pit (Inpl) outer membrene pit (Inpl) (Tip) rere ipoprit A (Inpl) (Hi) autrecel coeted membrene prt 1 (Impl) (Mh) S2 prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb)	80 100 100 48 48 58 48 59 48 50 94 100 54	B8304 B8767 Sulfection and articles B8764 B8672 Ip54 B8J.64	Digittemete-2,6 deminopimeter ligese (murit) (Hi) UPP-N-Lamuremortel ent/D- gittemyl-2,6-diemino-pimelete- Delenyl-D-elemino-ligese fhurf (Eb) UPP-N-Laglucceamine-N- Admuremyk(pertapeptide) pyrighosphoryl-undeceprend N-Lattere (murit) (Be) pulpseccheriales, (hopolyseccherial gest entigen, pss/100 (Bb) glycceyl Tesse (gtD) (Hi) entigen, RSS (Bb)	100 5% Aer 100 5%	B8040 B8444 B8670 B8670 B8731 B8676 B8761 B8676 B8697 B8697 B8697 B8697	ohamotoise hietatine Keel (dhell 2) (Bb) ohamotoise pet Millee (dhell 1) (Re) ohamotoise pet Millee (dhell 1) (Re) ohamotoise pet Millee (dhell 2) (Rm) ohamotoise response regulator (ohe Y 1) (Tp) ohamotoise response regulator (ohe Y 2) (Rm) ohamotoise response regulator (ohe Y 3) (Bb) (XTP-SP (end) (Bd) (XTP-SP (end) (Bd) (XTP-SP (obg) (3)n) MC pet (map-1) (Th) MC pet (map-2) (Td) MC pet (map-4) (Ed) MC pet (map-4) (Ed)	100 ខ ភ ក ខ និងនិង្សិស្ស
B8.442 B8.395 B8.603 B8.705 B8.705 B8.705 B8.105 B8.153 IDSA B8.124 B8.124 B8.125 B8.125 B8.125 B8.125	inner membrene pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrene-accordated pit pit (Bb) membrene apanning prt put (Se) outer membrene pit (Ipi20) (Tp) rere ipoprit A (IpiA) (Hi) authoeloosted membrene prt 1 (Imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrene porin	\$\\ 100\\ 48\\ 48\\ 58\\ 100\\ 100\\ 54\\ 100\\	58304 58767 Surface end end 58744 58644 1054 58164 58164	Dightemate-2,6 deminopimeter ligase (murit) (Hi) UPP-NA diminorpide anyl Dightemyl-2,6-diamino-pimeter- Dehryl Didemino-pimeter- Dehryl Didemino-pimeter- Dehryl (Bb) UPP-NA dijucceamine-N- Admuranyk (pertapoptide) pyrophosphory (undeseptend NA OTTES (muro) (Bs) polysischerioles, (hopolysischeriolises, pertagen, pss (100 (Bb) glycceyl Tesse (gfD) (Hi) entigen, RSS (Bb) entigen, RSS (Bb) entigen, RSS (Bb)	100 58 Aec 100 58 100 48	BB0 40 BB444 BB651 BB6570 BB872 BB6781 BB678 BB696 BB696 BB698 BB698 BB880 BB881	chandsiss histaine Kee (diel. 2) (Bb) (handsiss pit MTee (diel. 1) (Re) (handsiss pit MTee (diel. 2) (Rm) (handsiss reponse regulator (oheY-1) (Tp) (handsiss reponse regulator (oheY-2) (Rm) (handsiss reponse regulator (oheY-2) (Rm) (handsiss reponse regulator (oheY-2) (Rm) (oheY-2)	100 81 87 74 70 88888158
B8442 B8395 B8395 B8795 B8795 B8195 B8153 B8153 JC54 B8125 B8125 B8135 B81435 B81435 B81435	incor membrane pit (H) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrane-accordated pit pis (Bb) membrane-accordated pit pis (Bb) membrane-pit (Ng) outer membrane-pit (Ng) outer membrane-pit (Ng) (IP) rare ipoprit A (ItpA) (H) auriscelocated membrane pit 1 (Imp1) (Mh) 82 pit (Bb) decorin BP A (IttpA) (Bb) decorin BP B (IttpA) (Bb) ipoprotein (Bb)	80 100 40 40 40 40 50 40 50 40 50 50 54 100 54 100	B8304 B8767 Sulfection and articles B8764 B8672 Ip54 B8J.64	Digittemete-2,6 deminopimeter ligese (murit) (Hi) UPP-N-Lamuremortel ent/D- gittemyl-2,6-diemino-pimelete- Delenyl-D-elemino-ligese fhurf (Eb) UPP-N-Laglucceamine-N- Admuremyk(pertapeptide) pyrighosphoryl-undeceprend N-Lattere (murit) (Be) pulpseccheriales, (hopolyseccherial gest entigen, pss/100 (Bb) glycceyl Tesse (gtD) (Hi) entigen, RSS (Bb)	100 5% Aer 100 5%	B8040 B8444 B8670 B8670 B8731 B8676 B8761 B8676 B8697 B8697 B8697 B8697	chandaise histaine Kee (diel. 2) (Bb) (charl.	100 ខ ភ ក ខ និងនិង្សិស្ស
B8442 B8365 B805 B8753 B8765 B8167 B8156 B81436 B8425 B8436 B8436 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462 B8462	inner membrene pit (Hi) ipoprotein LA7 (Bb) membrene-accodiated pit pit (Bb) membrene-accodiated pit pit (Bb) membrene apenning pit put (Se) outer membrene pit (Ipp3) (Tip) rere ipoprit A (IrbA) (Hi) autrice-located membrene pit 1 (Imp1) (Mh) St pit (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (B	\$\\ 100\\ 4\\ 4\\ 5\\ 5\\ 100\\ 100\\ 54\\ 100\\ 100\\ 100\\ 100\\ 299\\ 299\\	58304 58767 Sulface 404 405 58744 58672 1054 584.64 584.64 584.63 1088	Dightemate-2,6 deminopimeter ligase (murit) (Hi) UPP-NA diminorpide anyl Dightemyl-2,6-diamino-pimeter- Dehryl Didemino-pimeter- Dehryl Didemino-pimeter- Dehryl (Bb) UPP-NA dijucceamine-N- Admuranyk (pertapoptide) pyrophosphory (undeseptend NA OTTES (muro) (Bs) polysischerioles, (hopolysischeriolises, pertagen, pss (100 (Bb) glycceyl Tesse (gfD) (Hi) entigen, RSS (Bb) entigen, RSS (Bb) entigen, RSS (Bb)	100 58 Aer 100 58 100 43 52	BB0 40 BB444 BB651 BB6570 BB872 BB6781 BB678 BB696 BB696 BB698 BB698 BB880 BB881	chandsiss histaine Kee (diel. 2) (Bb) (handsiss pit MTee (diel. 1) (Re) (handsiss pit MTee (diel. 2) (Rm) (handsiss reponse regulator (oheY-1) (Tp) (handsiss reponse regulator (oheY-2) (Rm) (handsiss reponse regulator (oheY-2) (Rm) (handsiss reponse regulator (oheY-2) (Rm) (oheY-2)	100 ខ ភ ។ ១ និងនិងស្រីងខង
B8442 B8365 B803 B8755 B8765 B8163 B8145	incor membrane pit (Hi) ipoprotein LA7 (Bb) membrane-associated prt pis (Bb) membrane-associated prt pis (Bb) membrane apanning prt put (Se) outer membrane prt (Ing) outer membrane prt (Ing) outer membrane prt (Ing) (Ing) (Ing) (Ing) (Ing) Sept (Bb) decoin BP A (dtpA) (Bb) decoin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer aumitical prt A (cepA) (Bb) outer aumitical prt A (cepA) (Bb) outer aumitical prt B (acpB) (Bb) outer aumitical prt (Bb) outer membrane prt (Bb)	\$\\ 100\\ 4\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	B8304 B8767 Surfece end end 88744 B8672 Ip54 B8166 B813	Dightemate-2,6 deminopimeter ligase (murit) (Hi) UPP-NA diminorpide anyl Dightemyl-2,6-diamino-pimeter- Dehryl Didemino-pimeter- Dehryl Didemino-pimeter- Dehryl (Bb) UPP-NA dijucceamine-N- Admuranyk (pertapoptide) pyrophosphory (undeseptend NA OTTES (muro) (Bs) polysischerioles, (hopolysischeriolises, pertagen, pss (100 (Bb) glycceyl Tesse (gfD) (Hi) entigen, RSS (Bb) entigen, RSS (Bb) entigen, RSS (Bb)	100 58 Aec 100 58 100 48	BB0 40 BB414 BB651 BB670 BB712 BB670 BB711 BB670 BB690 BB690 BB690 BB691 BB891 BB891 BB891 BB981 BB985 BB981 BB985 BB985 BB985	chandsish histaine Kee (diel. 2) (Bb) chandsish pit MTee (diel. 2) (Re) chandsish pit MTee (diel. 2) (Rm) chandsish reponse regulator (che)(1) (Tp) chandsish reponse regulator (che)(2) (Rm) chandsish reponse regulator (che)(2) (Rm) chandsish reponse regulator (che)(2) (Rm) chandsish reponse regulator (che)(3) (Bb) (3TP-8P (ere) (Ed) (3TP-8P (ere) (Ed) (3TP-8P (ere) (Ed) (3TP-8P (mp-2) (Td) MC pit (mp-2) (Td) MC pit (mp-2) (Td) MC pit (mp-2) (Td) MC pit (mp-2) (Ed) MC pit (mp-2) (Ed) pregulatemate mathyleaterese (che8-1) (8d) pregulatemate mathyleaterese (che8-2) (8d)	100 ខ ភ ។ ១ និងនិងស្រីងខង
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B8442 B8365 B8075 B8763 B8767 B8167 B8145 B8145 B8145 B8145 B8145 B8145 B8145 B8145 B816 B816 B816 B816 B816 B816 B816 B816	incor membrane pit (H) ipoprotein LA7 (Bb) membrane-accordated pit p86 (Bb) membrane-accordated pit p86 (Bb) membrane-accordated pit p86 (Bb) membrane-accordated pit p86 (Bb) cutar membrane-pit (Ng) cutar membrane-pit (Ng) prit (Ng) pri	\$\\ 100\\ 4\\ 4\\ 5\\ \\$\\ 100\\ 5\\ 100\\ 100\\ 5\\ 100\\ 1	58304 58767 Surfece end end 58744 58672 1054 583,64 583,64 583,63 583,73 1033 583,41	Digitamate-2,6 deminopimete igese (muris) (Hi) UDP-N-M ammemorial any (D- gitamy)-2,6-diemino-pimete- Delany (D-demino-pimete- Delany (D-demino-pimete- MUDP-N-M aglucceamine-N- Admurany (I) pertapopit del prophesphory (undecepted del N-M (Tese (muris) (Be) puly secthericles, (hopoly sectheric gest entigen, pss/100 (Bb) glycceyl Tese (IgtD) (Hi) entigen, RSS (Bb) entigen, RSS, prt (Bb) entigen, RSS, prt (Bb) entigen, RSS, prt (Bb)	100 58 66 100 58 100 48 52 47	B8040 B8414 B8651 B8670 B8872 B8800 B8781 B8678 B8697 B8800 B8801 B8645 B8645 B8645	chandaise histaine Kee (diek.2) (Bb) chandaise pit MTee (diek.2) (Ro) chandaise pit MTee (diek.2) (Ro) chandaise pit MTee (diek.2) (Ro) chandaise reponse regulator (cheY.1) (Tp) chandaise reponse regulator (cheY.2) (Ron) MC prt (mqp-2) (Td) MC prt (mqp-2) (Td) MC prt (mqp-4) (Ed) prt glutamate mathylecterese (cheE-1) (Ro) prt glutamate mathylecterese (cheE-2) (Ro) prt glutamate mathylecterese (cheE-2) (Ro) putine-E chemotaxis prt (cheM-1) (Bb)	10 ត ភ ក ខ នងខង្សាល់ងនង ន
B8442 B8395 B8935 B8755 B8755 B8162 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163 B8163	incor membrane pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrane-accorded pit pit (Bb) membrane apanning prt put (Se) outer membrane pit (Ipi) outer membrane pit (Ipi) outer membrane pit (Ipi) (Ipi) rare ipopit A (IpiA) (Hi) surface-loosted membrane prt 1 (Imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrane potin (mass) (Bb) outer auriface pit A (cepA) (Bb) outer auriface pit B (acpB) (Bb) outer membrane pit (Bb) outer membrane pit (Bb) St prt (Bb) St prt (Bb)	\$\\ 100\\ 4\\ 4\\ 5\\ 100\\ 10	58304 58767 Sulface 404 405 58744 58672 1054 584.64 584.64 584.63 1088	Digittemete-2.6. deminopmeter ligase (murE) (Hi) UPP-N-1 ammemoral einst Digitement (Ligase) glutemyt-2.6-diemino-pimalete- Desinyt-Dielemino-ligase fmurF (Eb) UPP-N-1 aglucceamine-N- Admuremyt-(pentapoptide) pyraphosphoryt-undeceprend N-1 ammemoral (Be) pulps-catheriales, (hopodyse-coherial gless entigen, pss/100 (Bb) glycceyt Teese (lgtD) (Hi) entigen, RSS (Bb) entigen, RSS (Bb) entigen, RSS (ptr (Bb) entigen, RSS (ptr (Bb) entigen, RSS (ptr (Bb))	100 58 Aer 100 58 100 43 52	BB0 40 BB414 BB651 BB670 BB712 BB670 BB711 BB670 BB690 BB690 BB690 BB691 BB891 BB891 BB891 BB981 BB985 BB981 BB985 BB985 BB985	chandaise histaine Kee (diel. 2) (Bb) ohandaise prt MTee (diel. 2) (Re) ohandaise prt MTee (diel. 2) (Rm) ohandaise reponse regulator (ohe)(1) (Tp) ohandaise reponse regulator (ohe)(2) (Rm) ohandaise reponse regulator (ohe)(2) (Rm) ohandaise reponse regulator (ohe)(3) (Bb) (XTP-8P (ore) (Ed) (XTP-	100 S 57 74 70 % % % % % 575 % S 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
B8442 B8365 B8075 B8775 B8776 B8167 B8145 B8145 B8145 B8145 B8145 B8145 B8165	incor membrane pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrane-accorded pit pit (Bb) membrane apanning prt put (Se) outer membrane pit (Ipi) outer membrane pit (Ipi) outer membrane pit (Ipi) (Ipi) rare ipopit A (IpiA) (Hi) surface-loosted membrane prt 1 (Imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrane potin (mass) (Bb) outer auriface pit A (cepA) (Bb) outer auriface pit B (acpB) (Bb) outer membrane pit (Bb) outer membrane pit (Bb) St prt (Bb) St prt (Bb)	\$\\ 100\\ 4\\ 4\\ 5\\ \\$\\ 100\\ 54\\ 100\\ 54\\ 100\\	B8304 B8767 SUMMAN B8767 SUMMAN B8764 B8672 ID54 B8488 B8473 ID58 B8473 ID58 B8471 B8475 B8475 B8475	Digitamate-2,6 deminopmente igese (muris) (Hi) USP-N-M ammemorial any IS- glutamy I-2,6-dismino-pimilate- Delany IS-dismino-pimilate- Delany IS-dismino-pimilate- Delany IS-dismino-pimilate- Mary I (Bb) USP-N-M agluccesmine-N- Admuramy II (Denta popilate) prophosphory - undeceptend NAG Tese (muris) (Be) Adjuse advariate, illipopily se coherior gents antigen, pss-7100 (Bb) glycooy I Tese (IgtD) (Hi) antigen, pss-7100 (Bb)	100 5% Auc 100 5% 100 4% 52 47 50 99	B8040 B8414 B8651 B8670 B8872 B8800 B8781 B8678 B8697 B8800 B8801 B8645 B8645 B8645	chandaise histaine Kee (diel. 2) (Bb) chandaise prt MTee (diel. 2) (Re) chandaise prt MTee (diel. 2) (Re) chandaise prt MTee (diel. 2) (Re) chandaise reponse regulator (cheix1) (Tp) chandaise reponse regulator (cheix1) (Rm) chandaise reponse regulator (cheix2) (Rm) chandaise reponse regulator (cheix3) (Bb) (CTP-8P (chej) (Bd) (Chej) (C	100 8 57 74 70 %%%%%%%%%% % % % % % % % % % % % % %
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B8442 B8365 B803 B8765 B8167 B8156 B8153 B8153 B8153 B8163 B	incor membrane pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrane-accorded pit pit (Bb) membrane apanning prt put (Se) outer membrane pit (Ipi) outer membrane pit (Ipi) outer membrane pit (Ipi) (Ipi) rare ipopit A (IpiA) (Hi) surface-loosted membrane prt 1 (Imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrane porin (mass) (Bb) outer surface pit A (cepA) (Bb) outer aurface pit B (acpB) (Bb) surface membrane pit (Bb) st prt (Bb) st prt (Bb) surface ipopit P27 (Bb) outer surface pit D (cepD) (Bb)	\$\\ 100\\ 4\\ 4\\ 5\\ \\$\\ 100\\ 54\\ 100\\ 54\\ 100\\	58304 58767 30/7400 40/247 5874 58672 1054 58043 1038 58041 1038 58041 58675 58685 586	Dightemate-2,6 deminopmenter igese (murE) (Hi) UPP-N-M ammemorial ent/D- gutemyl-2,6-diemino-pinidete- Dehnyl-D-alenine igese (murE) (Bb) UPP-N-M aglucceamine-N- Admuremyl-(pentapopilde) pyrighosphoryl-undeceptend NACT-tee (mura) (Be) pulys-ecchericles, (hopelys-ecchericles) gess entigen, pss/100 (Bb) glycceyl-Tee-e (gfD) (Hi) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) immunogenio-pxt RSS, pxt (Bb)	100 58 Aer 100 58 100 48 52 47 50 99 97 71	BB0 40 BB414 BB651 BB670 BB72 BB680 BB718 BB650 BB691 BB691 BB691 BB691 BB811 BB45 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB681 BB687 BB687	chandsise histaine Kee (diel. 2) (Bb) ohandsise pit MTee (diel. 2) (Re) ohandsise pit MTee (diel. 2) (Rm) ohandsise pit MTee (diel. 2) (Rm) ohandsise reponse regulator (oheY-1) (Tp) ohandsise reponse regulator (oheY-2) (Rm) OHO-BP (ohe) (Ed) OTP-BP (ohe) (Ed) MC pit (map-2) (Td) MC pit (map-2) (Td) MC pit (map-2) (Td) MC pit (map-2) (Td) MC pit (map-2) (Ed) prightmate mathylesterese (oheB-1) (80) putine-Biohandsise pit (oheW-1) (Bb) putine-Biohandsise pit (dheW-2) (Bb) putine-Biohandsise pit (dheW-2) (Bb)	100 8 57 74 70 %%%%%%%%%% % % % % % % % % % % % % %
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B8442 B8365 B8365 B8763 B8765 B8167 B8145 B8124 B8125 B8135 B8135 B8145 B8146	incer membrane pit (Hi) ipoprotein LA7 (Bb) imembrane-accordated pit p86 (Bb) imembrane-accordated pit p86 (Bb) imembrane-accordated pit p86 (Bb) imembrane-accordated pit p86 (Bb) imembrane-accordated pit p87 (Bb) imembrane-pit (Ng) imembrane-pit (Ng) imembrane-pit (Ng) imembrane-pit (Ng) imembrane-pit (Ng) imembrane-pit (Bb) impoprotein (Bb) i	\$\\ 100\\ 4\\ \\$\\ \$\\ \\$\\ \\$\\ \\$\\ \\$\\ \\$	B8304 B8767 Sulface 40/4/40 B8764 B8672 IP54 B8A64 B8A73 IP63 B8A73 IP63 B8A75 B8A75 B8A75 B8A75 B8A76	Dejlutemete-2,6 deminopmeter ligese (murE) (Hi) UDP-N-M ammemoryleilen/(D- glutemy/-2,6-diemino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-N- Admuremy/(Demterpe)) (deg prophosphoryl-undeceprend NAGTæe (murd) (8e) pulpsecaherides, (hopolysecoherid gless entigen, pss/100 (8b) glycosyl Tese (grD) (Hi) entigen, RSE (8b) entigen, RSE (8b) entigen, RSE, pxt (8b) entigen, RSE, pxt (8b) entigen, RSE, pxt (8b) immunogenio-pxt RSE, pxt (8b)	100 58 Asc 100 58 100 48 52 47 50 99 97 71 49 68	BB0 40 BB414 BB671 BB670 BB880 BB72 BB678 BB678 BB678 BB680 BB881 BB445 BB680 BB812 BB680 BB812 BB696 BB810	chands is histaine Kee (diel. 2) (Bb) chands is pit MTee (diel. 2) (Re) chands is pit MTee (diel. 2) (Re) chands is pit MTee (diel. 2) (Rm) chands is reponse regulator (chel/1) (Tp) chands is reponse regulator (chel/2) (Rm) chands is repons	100 8 57 74 70 88 88 82 57 52 88 88 89 88 88 100 48 44 4
B8442 B8365 B803 B8765 B8167 B8153 B8153 B8153 B8163 B	incer membrene pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrene-accodeded pit p86 (Bb) membrene-accodeded pit p86 (Bb) membrene-accodeded pit p86 (Bb) membrene-accodeded pit p86 (Bb) cutar membrene-pit (Ng) cutar membrene-pit (Ng) pre-e ipoprit A (hbA) (Hi) surface-looded membrene- pit 1 (mp1) (Mh) s2 pri (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein	\$\\ 100\\ 4\\ 5\\ \$\\ 5\\ 100\\ 100\\ 5\\ 100\\	58304 58767 30/7400 40/247 5874 58672 1058 58/47 58/47 58/47 58/47 58/47 58/46 5	Dejlutemate-2,6 deminopmenter ligese (murE) (Hi) UPP-NA drawnemortel ent/C- glutemyl-2,6-diemino-pinidete- Delanyl-Delanine ligese (murE) (Bb) UPP-NA dglucceamine-N- Admuremyl-(pentapoptide) pyrighosphoryl-undeceptend NACT-tee (murc) (Be) polysectherioles, (hopolysectheriol jest entigen, pss/100 (Bb) glycceyl Teee (grD) (Hi) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) immunogenio-pxt RST, pxt (Bb)	100 58 Aer 100 58 100 48 52 47 50 99 97 77 49 88 49	BB0 40 BB414 BB651 BB670 BB872 BB880 BB7818 BB698 BB698 BB881 BB455 BB688 BB812 BB688 BB870 C4// 4/6 BB088 BB1968 BB1968 BB1968 BB1968 BB1968 BB1968 BB1968	chanchisis histaine Kee (diel. 2) (Bb) ohanchisis pit MTee (diel. 1) (Re) ohanchisis pit MTee (diel. 2) (Rm) ohanchisis reponse regulator (ohe)-1) (Tp) ohanchisis reponse regulator (ohe)-2) (Rm) ohanchisis reponse regulator (ohe)-2) (Rm) ohanchisis reponse regulator (ohe)-2) (Rm) ohanchisis reponse regulator (ohe)-3) (Bb) (CTP-SP (ohe) (Ed) (CTP-SP (ohe) (Ed) (CTP-SP (ohe) (Ed) MC pit (map-2) (Td) MC pit (map-2) (Td) MC pit (map-3) (Td) MC pit (map-3) (Ed) pit (map-4) (Ed) pit (map-4) (Ed) pit (map-8) (Ed) pit	100 8 57 74 70 88882552882 88 89 88 88 100 484548
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B8442 B8365 B8365 B8767 B8767 B8767 B81424 B81425 B81436 B	incer membrane pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrane-accorded pit pit (Bb) membrane apanning prt put (Se) outer membrane pit (Inp.) (Tip) rare ipoprit A (Inp.A) (Hi) authopoloosted membrane prt 1 (Imp1) (Mh) St prt (Bb) decorin BP A (dtp.A) (Bb) decorin BP B (dtp.B) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrane potin (maxS) (Bb) outer authoce prt A (cap.A) (Bb) outer authoce prt B (acp.B) (Bb) st prt (Bb) st prt (Bb) st prt (Bb) surface ipoprit P27 (Bb) outer membrane prt (Bb) outer membrane prt (Bb) outer membrane prt (Bb) surface ipoprit P27 (Bb) outer membrane prt (Bb) prt pit (Bb)	80 100 49 48 59 46 80 94 100 100 100 100 100 100 100 100 100 10	B8304 B8767 SUMMANA B8767 SUMMANA B8764 B8064 B8065 B8075 B80675	Dejlutemate-2,6 deminopmente ligese (murE) (Hi) UPP-N-M ammemorial ent/D- glutemyl-2,6-diemino-pimilete- Delanyl-D-alemine ligese (murE) (Bb) UPP-N-M aglucceamine-N- Aamuremyk (pentapopilde) pyraphosphoryl-undeceprend N-M-Tree (mura) (Be) polysectheriales, (hopolysectherial gles) glycceyl Tree (grD) (Hi) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) immunogenio-pxt RSS, pxt (Bb) entigen, RSS, pxt (Bb)	100 58 46 100 58 100 48 52 47 50 99 97 77 49 68 49	BB0 40 BB414 BB651 BB670 BB872 BB880 BB7818 BB698 BB698 BB881 BB45 BB688 BB812 BB688 BB812 BB688 BB812 BB688 BB812 BB688 BB816 BB870 BB196	chandshis histaine Kee (disk.2) (Bb) chandshis pit MTee (disk.1) (Re) chandshis pit MTee (disk.2) (Rm) chandshis reponse regulator (cheY.1) (Tp) chandshis reponse regulator (cheY.2) (Rm) MC pit (mqp.1) (Tit) MC pit (mqp.2) (Tid) MC pit (mqp.2) (Tid) MC pit (mqp.2) (Tid) MC pit (mqp.4) (Ed) pit (mqp.4) (Ed) prightmate mathylesterese (cheB.2) (80) purine-Bichenotaris pit (cheW.1) (Bb) purine-Bichenotaris pit (cheW.2) (Bb) (Bb) Sion cell division control pit 27, pit (M) cell division control pit 27, pit (M) cell division control pit 27, pit (M) cell division pit (theY) (Bb)	100 8 57 74 70 88 88 82 57 52 88 88 89 58 88 100 48 45 57 77 77 100 100 100 100 100 100 100 100
B8442 B8395 B8395 B8795 B8795 B8197 B8143	incer membrane pit (Hi) ipoprotein LA7 (Bb) imembrane-associated pit p86 (Bb) membrane-associated pit p86 (Bb) membrane-aspanning prt put (Se) outer membrane pit (Ng) outer membrane pit (IppSI) (Tip) rare ipoprit A (IrbA) (Hi) surface-looated membrane prt 1 (Imp1) (IvAh) S2 prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb)	\$\\ 100 100 4\\\ 4\\\ 5\\\ 6\\\ 6\\\ 0 100 54 100 100 100 100 100 100 81 100 81 82 55 99 53	B8304 B8767 S0/74-02 8074-04 B8767 B8674 B8680 B8473 IDS3 B86815 B8680	Dejlutemete-2,6 deminopmeter ligese (murE) (Hi) UDP-N-M ammemoryleilen/(D- glutemy/-2,6-diemino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-pimilete- Delen/(D-demino-pimilete- Martinen/(Demino-pimilete- Amuremy/(Demino-N- Amur	100 58 46 100 58 100 48 52 47 50 99 97 77 49 68 49 55	B80 40 B8414 B8611 B8670 B8872 B8800 B8781 B8678 B8696 B8697 B8800 B8781 B8445 B8696 B8700 C4// 4// B8083 B8196 B8290 B8700 B8700 B8700 B8006 B8290 B8006 B8290 B8006	chandaise histaine Kee (dhall 2) (Bb) (chandaise prt MTee (dhall) (Re) (chandaise prt MTee (dhall) (Re) (chandaise prt MTee (dhall) (Re) (chandaise reponse regulator (chard) (TD) (chandaise reponse regulator (chard) (TD) (chandaise reponse regulator (chard) (Em) (chardaise reponse regulator (chardaise (Ed) (CTP-8P (cha) (Ed) (CTP-8P (cha) (Ed) (CTP-8P (cha) (Ed) (CTP-8P (cha) (Ed) (MC prt (map-4) (Ed) (MC prt (m	100 日 57 14 70 88 88 88 55 55 55 88 88 88 88 75 77 77 77 77 100 100
B8442 B8365 B8365 B8767 B8767 B8767 B81424 B81425 B81436 B	incer membrane pit (Hi) ipoprotein LA7 (Bb) ipoprotein LA7 (Bb) membrane-accorded pit pit (Bb) membrane apanning prt put (Se) outer membrane pit (Inp.) (Tip) rare ipoprit A (Inp.A) (Hi) authopoloosted membrane prt 1 (Imp1) (Mh) St prt (Bb) decorin BP A (dtp.A) (Bb) decorin BP B (dtp.B) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrane potin (maxS) (Bb) outer authoce prt A (cap.A) (Bb) outer authoce prt B (acp.B) (Bb) st prt (Bb) st prt (Bb) st prt (Bb) surface ipoprit P27 (Bb) outer membrane prt (Bb) outer membrane prt (Bb) outer membrane prt (Bb) surface ipoprit P27 (Bb) outer membrane prt (Bb) prt pit (Bb)	\$\\ 100 100 40 40 50 100 100 100 100 100 100 100	B8304 B8767 SUMMAN AND AND AND AND AND AND AND AND AND A	Dejlutemete-2,6 deminopmeter ligese (murE) (Hi) UPP-N-M ammemorial ent/D- glutemyl-2,6-diemino-pimilete- Delenyl-D-elemino-pimilete- Delenyl-D-elemino-pimilete- Delenyl-D-elemino-pimilete- Delenyl-D-elemino-pimilete- prophosphoryl-undeceprend N-M ammemyl-(pentapopilete) prophosphoryl-undeceprend N-M ammemyl-(pentapopilete) prophosphoryl-undeceprend N-M ammemyl-(pentapopilete) glycodyl-Tese (tyrU) (Hi) entigen, pss/100 (Bb) glycodyl-Tese (tyrU) (Hi) entigen, pss/100 (Bb) entigen, pss/100 (Bb) entigen, pss/ ppt (Bb) entigen, pss/ ppt (Bb) entigen, pss/ ppt (Bb) immunogenio-ppt pss/ (Bb) immunogenio-ppt pss/ (Bb) immunogenio-ppt pss/ ppt (Bb) entigen, pss/ ppt (Bb) entigen, pss/ ppt (Bb)	100 58 46 100 58 100 48 52 47 50 99 97 77 49 68 49 55	BB0 40 BB414 BB651 BB670 BB872 BB880 BB7818 BB698 BB698 BB881 BB45 BB688 BB812 BB688 BB812 BB688 BB812 BB688 BB812 BB688 BB816 BB870 BB196	chandsiss histaine Kee (dhall 2) (Bb) (chandsis pt MTee (dhall 1) (Re) (chandsis pt MTee (dhall 2) (Re) (chandsis pt MTee (dhall 2) (Re) (chandsis pt MTee (dhall 2) (Re) (chandsis reponse regulator (chall 3) (Re) (chall 3) (Re) (chandsis reponse regulator (chall 3) (Re) (chall 4) (Re) (chall 4) (Re) (chall 6) (Re) (chall 6) (Re) (chall 7) (Re) (chall 7) (Re) (chall 8) (chall 8) (chall 9) (chal	100 8 57 74 70 88 88 82 57 52 88 88 89 58 88 100 48 45 57 77 77 100 100 100 100 100 100 100 100

<u>lp28-2</u>				ton motive force interconversion		BB575	CTP Sase (pyrG) {Mj}	71
BBG08	stage 0 sporulation prt J (spoOJ) {Bb}	66	BB094 BB093	V-type ATPase, sub A (atpA) {Mb} V-type ATPase, sub B (atpB) {Mb}	64 62	Salvage	of nucleosides and nucleotides	
Cell killii	na		BB092 BB096	V-type ATPase, sub D (atpD) {Mj} V-type ATPase, sub E (atpE) {Mj}	51 54	BB777	adenine phosphoribosylTase (apt) {Ta}	63
BB143	-hemolysin (hlyA) {Ah}	62	BB091	V-type ATPase, sub I (atpl) {Eh}	53	BB618	cytidine deaminase (cdd) {Mp}	61
BB117 BB506	hemolysin III (ypIQ) {Bs} hemolysin (tlyA) {Sh}	61 59	BB090	V-type ATPase, sub K (atpK) {Mj}	54	BB239	deoxyguanosine/deoxyadenosine kinase(I) sub 2 (dck) {La}	59
BB059 BB202	hemolysin (tlyC) (Sh)	65 54	Electror BB061	transport thioredoxin (trxA) {Ec}	59	BB375 BB588	pfs prt (pfs-1) {Ec} pfs prt (pfs-2) {Hi}	64 59
	hemolysin, put {Syn}	04	BB515	thioredoxin RDase (trxB) {Bb}	99	BB791	thymidine kinase (tdk) {Bs}	47
Chapero BB741	ones chaperonin (groES) {Pg}	77	Fermen	tation		BB015	uridine kinase (udk) {Bb}	100
BB602 BB519	chaperonin, put {Cb} grpE prt (grpE) {Bb}	72 100	BB622 BB589	acetate kinase (ackA) {Ec} P AcTase (pta) {Tt}	63 65	<u>lp36</u> BBK17	adenine deaminase (adeC) {Bs}	57
BB295	heat shock prt (hslU) {Bb}	100		. , , , ,	00			37
BB296 BB649	heat shock prt (hslV) {Bb} heat shock prt (groEL) {Bb}	100 100	Glycolys BB337	enolase (eno) {Bs}	79	General	ory functions	
BB517 BB655	heat shock prt (dnaJ-1) {Bb} heat shock prt (dnaJ-2) {Ca}	100 59	BB445 BB730	fructose-bisP aldolase (fba) {Ec} glucose-6-P isomerase (pgi) {Pf}	80 62	BB184	carbon storage regulator (csrA) {Hi}	63
BB264	heat shock prt 70 (dnaK-1) {Bb}	61	BB057	glyceraldehyde 3-P DHase		BB647	ferric uptake regulation prt	
BB518 BB560	heat shock prt 70 (dnaK-2) {Bb} heat shock prt 90 (htpG) {Bb}	100 100	BB630	(gap) {Bb} 1-phosphofructoKase (fruK) {Hi}	99 52	BB198	(fur) {Sp} guanosine-3',5'-bis(diP) 3'-	48
Detoxific	cation		BB056 BB658	phosphoglycerate Kase (pgk) {Bb} phosphoglycerate mutase (gpmA)	99	BB737	pyrophosphohydrolase (spoT) {Ec} histidine phosphoKase/PPase,	61
BB153	superoxide dismutase (sodA) {Hi}	68	BB348	{Ec} pyruvate Kase (pyk) {Bs}	79 62	BB176	put {MI} methanol DHase regulator	49
BB690	neutrophil activating prt (napA) {Hi}		BB727	pyroP-fructose 6-P 1-PPTase			(moxR) {Bb}	99
BB179	thiophene and furan oxidation prt (thdF) {Bb}	100	BB020	(pfk) {Eh} pyroP-fructose 6-P 1-PPTase,	65	BB416	pheromone shutdown prt (traB) {Ef}	61
Protein .	and peptide secretion		BB055	sub (pfpB) {Bb} trioseP isomerase {Bb}	100 100	BB042	P transport system regulatory prt (phoU) {Pa}	57
BB154	preprt translocase sub (secA) {Bb}				.00	BB379	prt Kase C1 inhibitor (pkcl) {Bb}	100
BB395 BB498	preprt translocase sub (secE) {BI} preprt translocase sub (secY) {Sc}	62 64	BB222	phosphate pathway glucose-6-P 1-DHase, put {As}	48	BB419	response regulatory prt (rrp-1) {Syn}	57
BB362	prolipoprt diacylglyceryl Tase (lgt) {Ec}	56	BB636 BB561	glucose-6-P 1-DHase (zwf) {Hi} phosphogluconate DHase	64	BB763	response regulatory prt (rrp-2) {Ec}	67
BB652	prt-export membrane prt	63	BB657	(gnd) {Sd}	71 61	BB764	sensory transduction histidine	60
BB653	(secD) {Ec} prt-export membrane prt			ribose 5-P isomerase (rpi) {Mj}	01	BB420	Kase, put {Bs} sensory transduction	
BB030	(secF) {Hi} signal peptidase I	63	Sugars BB407	mannose-6-P isomerase		BB693	histidine Kase, put {Syn} xylose operon regulatory prt	61
BB031	(lepB-1) {Bs} signal peptidase I (lepB-2) {Syn}	51 57	BB444	(manA) {Ec} nucleotide sugar epimerase {Vc}	54 69	BB831	(xyIR-1) {Th.} xylose operon regulatory	48
	orginal population i (lopb 2) (oyii)					DDOOT	Aylodo oporon rogulatory	
BB263	signal peptidase I (lepB-3) {St}	57	BB676	phosphoglycolate PPase (gph) {Hi}	50		prt (xyIR-2) {Syn}	51
BB263 BB469 BB694	signal peptidase II (Isp) {Sc} signal recognition particle	60	BB207	UTP-glucose-1-P uridylylTase (gtaB) {Bs}	63	<u>lp54</u>		
BB469 BB694	signal peptidase II (lsp) (\$c) signal recognition particle prt (ffh) {Bs}			UTP-glucose-1-P uridylylTase			prt (xyIR-2) {Syn} chpAl prt, put {Ec}	55
BB469 BB694 BB610	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi}	60 70	BB207 BB545 Fatty ac	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism	63	BBA07 Replicati	chpAl prt, put {Ec}	
BB469 BB694 BB610 Transfor BB591	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffth) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs}	60 70 50	BB207 BB545	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase	63 43	BBA07 Replicati Degrada	chpAl prt, put {Ec} ion ation of DNA endonuclease precursor	55
BB469 BB694 BB610 Transfor	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffth) {Bs} trigger factor (tig) {Hi}	70 50	BB207 BB545 Fatty ac General	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism	63	BBA07 Replicati Degrada	chpAl prt, put {Ec} ion ation of DNA	
BB469 BB694 BB610 <i>Transfor</i> BB591 BB798 Central	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism	60 70 50	BB207 BB545 Fatty ac General BB037 BB685	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm}	63 43	Replicati Degrada BB411 DNA rep	chpAl prt, put {Ec} ion ation of DNA endonuclease precursor (nucA) {As} blication, restriction, modification,	55
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec}	60 70 50	BB207 BB545 Fatty ac General BB037 BB685 BB683	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At}	63 43 100 52 53	Replicati Degrada BB411 DNA reprecombin	chpAl prt, put {Ec} ion ation of DNA endonuclease precursor (nucA) {As} polication, restriction, modification, ination, and repair 3-methyladenine DNA	55 53
BB469 BB694 BB610 Transfor BB591 BB798 Central BB241 BB243	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi}	60 70 50 54 52 74	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (ftadA) {Hi} acyl carrier prt {Syn}	63 43 100 52	Replicati Degrada BB411 DNA rep recombin BB422 BB827	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} clication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec}	55
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic	60 70 50 54 52	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P	63 43 100 52 53 67 65	Replicati Degrada BB411 DNA rep recombin BB422 BB827	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} blication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication	55 53 56 61
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars	60 70 50 54 52 74	BB207 BB545 Fatty ac General BB037 BB685 BB685 BB683 BB109 BB704 BB721 BB327	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So}	63 43 100 52 53 67 65 55 50	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435	chpAl prt, put {Ec} chpAl prt, put {Ec} chaition of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs}	55 53 56 61 100 67
BB469 BB694 BB610 Transfol BB591 BB798 Central i General BB241 BB243 BB376 Amino s BB152	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi}	60 70 50 54 52 74	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA{Bs})	63 43 100 52 53 67 65 55 50	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344	chpAl prt, put {Ec} ion ation of DNA endonuclease precursor (nucA) {As} blication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec}	55 53 56 61 100 67 99 55
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase	60 70 50 54 52 74 52 72	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mwaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn}	63 43 100 52 53 67 65 55 50	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) (Bb) DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt	55 53 56 61 100 67 99 55 56
BB469 BB694 BB610 <i>Transfor</i> BB591 BB798 Central i <i>General</i> BB241 BB243 BB376 <i>Amino</i> s BB152	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi}	60 70 50 54 52 74 52 72	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA{Bs}) long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase	63 43 100 52 53 67 65 55 50 8) 54	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} olication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi}	55 53 56 61 100 67 99 55
BB469 BB694 BB610 <i>Transfor</i> BB591 BB798 Central BB241 BB243 BB376 <i>Amino</i> s BB152 BB151	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn}	60 70 50 54 52 74 52 79 54	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs} long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj}	63 43 100 52 53 67 65 55 50 8) 54 54 56 51	BBA07 Replicati Degradda BB411 DNA reprecombia BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) (Bb) DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) (Hi]	55 53 56 61 100 67 99 55 56
BB469 BB694 BB610 <i>Transfor</i> BB591 BB798 Central i General BB241 BB243 BB376 <i>Amino</i> s BB152 BB151 <i>Degrada</i> BB620 BB002	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As}	60 70 50 54 52 74 52 72 79 54	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA{Bs}) long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj} mevalonate pyroP DCase {Sc} phosphatidate cytidylylTase (cdsA),	63 43 100 52 53 67 65 50 0) 54 54 56 51 52	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} olication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA mismatch repair prt, put {Syn}	555 533 566 61 1000 67 99 55 566 55 57 51
BB469 BB694 BB610 <i>Transfor</i> BB591 BB798 Central i General BB241 BB243 BB376 <i>Amino</i> s BB152 BB151 <i>Degrada</i> BB620 BB002	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn}	60 70 50 54 52 74 52 79 54	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB327 BB368 BB137 BB593 BB688 BB119	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} melvalonate pyroP DCase {Sc} phosphatidate cytidylylTase (cdsA), AFS{Ec}	63 43 100 52 53 67 65 55 50 8) 54 54 56 51	BBA07 Replicati Degradda BB411 DNA reprecombia BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797	chpAl prt, put {Ec} ion ation of DNA endonuclease precursor (nucA) {As} bilication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA mismatch repair prt, put {Syn} DNA polymerase I (polA) {Hi}	55 53 56 61 100 67 99 55 56 55 57
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB620 BB620 Phosphe BB533	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec}	60 70 50 54 52 74 52 72 79 54	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA{Bs}) long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj} mevalonate pyroP DCase {Sc} phosphatidate cytidylylTase (cdsA),	63 43 100 52 53 67 65 50 8) 54 54 56 51 52 61 52	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} olication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase II, sub (dnaE) {Ec}	555 533 566 61 1000 67 99 55 566 55 57 51
BB469 BB694 BB610 Transfor BB591 BB798 Central if General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospho BB533 Polysaca BB166	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) (Bs) trigger factor (tig) (Hi) rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) (Hi) SAM Sase (metK) (Bs) sugars glucosamine-6-P isomerase (nagB) (Hi) N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} brus compounds phnP prt (phnP) (Ec) charides - (cytoplasmic) 4glucanoTase (maiQ) {Syn}	60 70 50 54 52 74 52 72 79 54 58 54 48 55	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines,	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj} mevalonate pyroP DCase {Sc} phosphatidate cytidylylTase (cdsA), AFS{Ec} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotides	63 43 100 52 53 67 65 55 50 87 65 54 54 54 56 51 52 61 52 53	BBA07 Replicati Degradda BB411 DNA reprecombia BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) (Bb) DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaN) {Bb}	555 533 566 61 1000 67 99 55 56 55 57 51 61
BB469 BB694 BB610 Transfor BB591 BB798 Central if General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosphe BB533 Polysace	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic)	60 70 50 54 52 74 52 72 79 54 58 54 48	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB249 BB687 Purines, Nucleot BB417	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA{Bs}) long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj} mevalonate Kase {Mj} mevalonate pyroP DCase {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase {adk} {Bs}	63 43 100 52 53 67 65 55 50 8 54 54 54 56 51 52 53 61 52 53	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} olication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutL) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaE) {Bb} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaX) {Bs}	555 533 566 61 1000 677 999 555 566 557 511 611 622 1000 611
BB469 BB694 BB610 Transfor BB591 BB798 Central if General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospho BB533 Polysaci BB166 BB004 BB835	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic) 4glucanoTase (malQ) {Syn} phosphoglucomutase (femD) {Mj} phosphognomerican particles in glad production particles signal recognition particles signal recognition particles signal recognition particle signal recognition par	60 70 50 54 52 74 52 72 79 54 58 54 48	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB327 BB368 BB137 BB593 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P D-Hase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} mevalonate Kase {Mj} mevalonate Kase {Mj} mevalonate pyroP DCase {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (cmk-1) {Bs}	63 43 100 52 53 67 65 55 50 0) 54 54 56 51 52 61 52 53 88 64 58	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA ligase (luyD) {Ec} DNA ligase (liya) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bs} DNA primase (dnaG) {Bs}	555 533 566 611 1000 677 99 555 566 557 511 611 622 1000 611 566
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysaca BB166	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic) 4glucanoTase (malQ) {Syn} phosphoglucomutase (femD) {Mi} phosphomannomutase (cpsG) {Hi} metabolism	60 70 50 54 52 74 52 72 79 54 58 54 48	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB819 BB463	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj} mevalonate Kase {Mj} mevalonate Kase {Mj} mevalonate cytidylylTase (cdsA), AFS{Ec} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj} nucleoside-diP kinase (mkB) {Bs}	63 43 100 52 53 67 65 50 0) 54 54 56 51 52 61 52 53 64 58 64 58 67 70	BBA07 Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB828	chpAl prt, put {Ec} chpAl prt, put {Ec} chion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA ligase (luyrD) {Ec} DNA ligase (luyrD) {Ec} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase (dnaG) {Bs} DNA recombinase (recG) {Syn} DNA topoisomerase I (topA) {Syn}	55 53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 64
BB469 BB694 BB610 Transfor BB591 BB798 Central if General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysaca BB166 BB004 BB835 Energy if	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic) 4glucanoTase (malQ) {Syn} phosphoglucomutase (femD) {Mj} phosphomannomutase (cpsG) {Hi} metabolism	60 70 50 54 52 74 52 72 79 54 58 54 48	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB819	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (ftadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} plosphatidate cytidylylTase {Syn} melvalonate Kase {Mj} mevalonate Kase {Mj} mevalonate Kase, put {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj}	63 43 100 52 53 67 65 55 50 8 54 54 56 51 52 53 88 64 58 57	BBA07 Replicati Degrada BB411 DNA reprecemble BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB799 BB438 BB461 BB710 BB581 BB828 BB035 BB036	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) (Bb) DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaX) {Bs} DNA primase (dnaG) {Bs} DNA topoisomerase I (topA) {Syn} DNA topoisomerase I (topA) {Syn} DNA topoisomerase IV (parC) {Bb}	55 53 56 61 100 67 99 55 56 57 51 61 62 100 64 58 56
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB002 Phospha BB533 Polysaca BB166 BB004 BB835 Energy i Aerobic BB728	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic) 4glucanoTase (maiQ) {Syn} phosphoglucomutase (femD) {Mj} phosphomannomutase (cpsG) {Hi} metabolism NADH oxidase, water-forming	60 70 50 54 52 74 52 72 79 54 58 54 48 55 52 57	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB819 BB463 BB793 BB571	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mi} mevalonate Kase {Mi} mevalonate kase {Syn} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, nucleotidide and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} thymidylate kinase (tmk) {Mj}	63 43 100 52 53 67 65 55 50 8 54 54 54 56 51 52 53 88 64 58 57 70 59	BBA07 Replicati Degrada B8411 DNA reprecombin B8422 BB827 B8437 B8435 B8436 B8344 B8552 B8211 B8797 B8098 B8548 B8579 B8488 B8579 B8488 B8579 B8488 B8570	chpAl prt, put {Ec} chpAl prt, put {Ec} chion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaA) {Bb} DNA polymerase III, sub (dnaX) {Bs} DNA primase (dnaG) {Bs} DNA recombinase (recG) {Syn} DNA topoisomerase I (topA) {Syn} DNA topoisomerase I (folC) {Bb}	55 53 56 61 100 67 99 55 56 57 51 61 62 100 61 56 60 64 58
BB469 BB694 BB610 Transfor BB591 BB798 Central if General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosphe BB533 Polysace BB166 BB004 BB805 BB166 BB004 BB835 Energy if Aerobic BB728 Amino a BB841	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic) 4glucanoTase (malQ) {Syn} phosphoglucomutase (femD) {Mj} phosphomannomutase (cpsG) {Hi} metabolism NADH oxidase, water-forming (nox) {Sh} acids and amines arginine deiminase (arcA) {Cp}	60 70 50 54 52 74 52 72 79 54 58 54 48 55 52 57	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB819 BB463 BB793 BB571	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P D-Hase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mi} mevalonate Kase {Mi} mevalonate pyroP DCase {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-2) {Mi} uridylate kinase (mk-1) {Bs} cytidylate kinase (mk-1) {Bs} thymidylate kinase (mk-1) {Mi} uridylate kinase (smbA) {Mj} ibonucleotide biosynthesis phosphoribosyl pyroP Sase	63 43 100 52 53 67 65 55 50 8 54 54 56 51 52 61 52 53 68 64 58 57 70 70 59 54	BBA07 Replicati Degrada BB411 DNA reprecombine BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB448 BB579 BB438 BB461 BB710 BB581 BB828 BB035 BB036 BB745 BB036 BB745 BB037	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bs} DNA recombinase (recG) {Syn} DNA topoisomerase IV (parE) {Bb} endonuclease III (nth) {Syn} excinuclease ABC, sub A (uurA) {Ec}	55 53 56 61 100 67 99 55 56 57 51 61 62 100 64 58 56
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB602 BB002 Phospha BB633 Polysaca BB164 BB804 BB835 Energy i Aerobic BB728	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagB) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As} orus compounds phnP prt (phnP) {Ec} charides - (cytoplasmic) 4- glucanoTase (malQ) {Syn} phosphoglucomutase (femD) {Mi} phosphognucomutase (femD) {Mi} phosphomannomutase (cpsG) {Hi} metabolism NADH oxidase, water-forming (nox) {Sh} acids and amines	60 70 50 54 52 74 52 72 79 54 58 54 48 55 52 57	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB819 BB463 BB793 BB571 Purine (BB544)	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P O-acylTase, put {So} glycerol-3-P O-acylTase, put {So} glycerol-3-P O-acylTase, put {So} plycerol-3-P O-acylTase, put {So} plosphatidate cytidylylTase (cdsA), AFS{Ec} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Mj} nucleoside-diP kinase (tmk) {Mj} uridylate kinase (smbA) {Mj}	63 43 100 52 53 67 65 55 50 8 54 54 54 56 51 52 53 88 64 58 57 70 59	BBA07 Replicati Degrada BB411 DNA reprecombine BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB641 BB710 BB581 BB828 BB035 BB348 BB035 BB348 BB035 BB035 BB348 BB035 BB348 BB035 BB348 BB035 BB348 BB035 BB348 BB378 BB8888	chpAl prt, put {Ec} chpAl prt, put {Ec} chion attion of DNA endonuclease precursor (nucA) {As} chication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bs} DNA rimase (dnaG) {Bs} DNA ropoisomerase I/ (parC) {Syn} DNA topoisomerase I/ (parC) {Syn} DNA topoisomerase I/ (parC) {Bb} DNA topoisomerase I/ (parC) {Bb} DNA topoisomerase III (nth) {Syn} excinuclease ABC, sub B (uvrB) {Ec}	55 53 56 61 100 67 99 55 56 57 51 61 62 100 61 56 60 64 58 59
BB469 BB694 BB694 BB610 Transfor BB591 BB798 Central if General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysaca BB166 BB004 BB835 Energy if Aerobic BB728 Amino a BB841 BB842 Anaerob	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) (Bs) trigger factor (tig) (Hi) remation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec} glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase (nagA) {Hi} N-Acglucosamine-6-P deAcase (nagA) {Hi} ation of polysaccharides -glucosidase, put {Syn} -N-Achexosaminidase, put {As}	60 70 50 54 52 74 52 72 79 54 48 56 52 57 59 75 74	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB819 BB463 BB793 BB793 BB793 Cp26 BBB18	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mwaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (ftadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} glycerol-3-P O-acylTase, put {So} glycerol-3-P DHase, NAD(P)+ (gpsA {Bs}) long-chain-fatty-acid CoA ligase {Syn} long-chain-fatty-acid CoA ligase {Syn} melvalonate Kase {Mj} mevalonate Kase {Mj} mevalonate cytidylylTase (cdsA), AFS{Ec} phosphatidate cytidylylTase (cdsA), AFS{Ec} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj} nucleoside-diP kinase (ndk) {Bs} thymidylate kinase (smbA) {Mj} ibbonucleotide biosynthesis phosphoribosyl pyroP Sase (prs) {Mp}	63 43 100 52 53 67 65 55 50 8 54 54 56 51 52 53 64 58 57 70 59 54	BBA07 Replicati Degrada BB411 DNA reprecemble BB422 BB827 BB437 BB435 BB436 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB828 BB035 BB036 BB745 BB837 BB837 BB836 BB457	chpAl prt, put {Ec} ion attion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bs} DNA recombinase (recG) {Syn} DNA topoisomerase I (topA) {Syn} DNA topoisomerase IV (parC) {Bb} DNA topoisomerase IV (parC) {Bb} endonuclease III (nth) {Syn} excinuclease ABC, sub B (uvrA) {Ec} excinuclease ABC, sub C (uvrC) {Syn}	55 53 56 61 100 67 99 55 56 55 57 51 61 62 100 64 56 60 64 56 56 56 56 4
BB469 BB694 BB610 Transfor BB591 BB798 Central i General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospho BB633 Polysaca BB166 BB004 BB835 Energy I Aerobic BB728 Amino a BB841 BB842	signal peptidase II (Isp) (Sc) signal recognition particle prt (ffh) (Bs) trigger factor (tig) (Hi) rmation competence locus E, put (Bs) competence prt F, put (Hi) intermediary metabolism glycerol kinase (glpK) (Ec) glycerol-3-P DHase, anaerobic (glpA) (Hi) SAM Sase (metK) (Bs) sugars glucosamine-6-P isomerase (nagB) (Hi) N-Acglucosamine-6-P deAcase (nagA) (Hi) ation of polysaccharides -glucosidase, put (Syn) -N-Achexosaminidase, put (As) orus compounds phnP prt (phnP) (Ec) charides - (cytoplasmic) 4- glucanoTase (maiQ) (Syn) phosphoglucomutase (femD) (Mj) phosphomannomutase (cpsG) (Hi) metabolism NADH oxidase, water-forming (nox) (Sh) acids and amines arginine deiminase (arcA) (Cp) ornithine carbamoylTase (arcB) (Ng)	60 70 50 54 52 74 52 72 79 54 48 55 52 57 59 75	BB207 BB545 Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleot BB417 BB128 BB371 BB128 BB193 BB447 BB128 BB191 BB447 BB128 BB191 BB447 BB128 BB191	UTP-glucose-1-P uridylylTase (gtaB) {Bs} xylulokinase (xylB) {Bs} xylulokinase (xylB) {Bs} id and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm} 3-OH-3-methylglutaryl-CoA Sase {At} Ac-CoA C-AcTase (fadA) {Hi} acyl carrier prt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs} glycerol-3-P O-acylTase, put {So} plycerol-3-P O-acylTase, put {So} phosphatidate cytidylylTase (cdsA), AFS{Ec} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotidide and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} tytidylate kinase (cmk-1) {Mj} uridylate kinase (smbA) {Mj} uridylate kinase (smbA) {Mj} uridylate kinase (smbA) {Mj} ibonucleotide biosynthesis phosphoribosyl pyroP Sase (prs) {Mp}	63 43 100 52 53 67 65 55 50 8 54 54 54 56 51 52 53 64 58 57 70 59 54	BBA07 Replicati Degrada BB411 DNA reprecombine BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB641 BB710 BB581 BB828 BB035 BB348 BB035 BB348 BB035 BB035 BB348 BB035 BB348 BB035 BB348 BB035 BB348 BB035 BB348 BB378 BB8888	chpAl prt, put {Ec} chpAl prt, put {Ec} chaiton of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb} DNA helicase (uvrD) {Ec} DNA ligase (lig) {Ta} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutL) {Hi} DNA polymerase I (polA) {Hi} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaE) {Ec} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub (dnaN) {Bs} DNA recombinase (recG) {Syn} DNA topoisomerase I (topA) {Syn} DNA topoisomerase II (topA) {Syn} Endonuclease III (topA) {Syn} Endonuclease III (topA) {Syn} Endonuclease ABC, sub B (uvrB) {Ec} excinuclease ABC, sub B (uvrB) {Ec} excinuclease ABC, sub C	555 533 566 61 1000 67 99 55 56 55 57 51 61 62 1000 61 56 60 64 58 56 59 4 71

ColpC) (Pp) 67 1 kRNA modification enzyme 1 kRNA modification enzy	ribosomal prt L33 (rpmG) (Bs) 76 ribosomal prt L34 (rpmH) (Bb) 100 ribosomal prt L35 (rpmI) (Bs) 74 ribosomal prt L36 (rpmI) (Bs) 89 ribosomal prt L36 (rpmI) (Bs) 89 ribosomal prt S1 (rpsA) (Ec) 55 ribosomal prt S2 (rpsB) (Pa) 79 ribosomal prt S3 (rpsC) (Hi] 71 ribosomal prt S4 (rpsD) (Hi] 63 ribosomal prt S5 (rpsE) (Bs) 77 ribosomal prt S6 (rpsF) (Os) 50 ribosomal prt S7 (rpsG) (Sc) 75 ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S10 (rpsI) (Bb) 100 ribosomal prt S10 (rpsI) (Bb) 100 ribosomal prt S11 (rpsK) (Hi) 77 ribosomal prt S12 (rpsL) (An) 89 ribosomal prt S14 (rpsK) (Bs) 72 ribosomal prt S15 (rpsC) (Tt) 77 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S17 (rpsC) (Mc) 76 ribosomal prt S18 (rpsR) (Bs) 99 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 rodification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) glu-tRNA amidoTase, sub C (gatC) (Bs) glu-tRNA amidoTase, sub B (gatB) (Bs) methionyl-tRNA formylTase
Page	ribosomal prt L34 (rpmH) (Bb) 100 ribosomal prt L35 (rpml) (Ba) 74 ribosomal prt L36 (rpml) (Bs) 74 ribosomal prt S1 (rpsA) (Ec) 55 ribosomal prt S2 (rpsB) (Pa) 79 ribosomal prt S2 (rpsB) (Pa) 79 ribosomal prt S3 (rpsC) (Hi) 63 ribosomal prt S4 (rpsD) (Hi) 63 ribosomal prt S5 (rpsE) (Bs) 77 ribosomal prt S6 (rpsF) (Os) 50 ribosomal prt S7 (rpsG) (Sc) 75 ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S10 (rpsI) (Bb) 100 ribosomal prt S10 (rpsI) (Bb) 77 ribosomal prt S10 (rpsI) (Bb) 77 ribosomal prt S10 (rpsI) (Bb) 77 ribosomal prt S11 (rpsK) (Hi) 77 ribosomal prt S15 (rpsD) (Tt) 77 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mc) 68 rRNA methylase (yacO) (Mc) 66 rodification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 63 glu-tRNA amidoTase, sub C (gatC) (Bs) 63 glu-tRNA amidoTase, sub B (gatB) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB644 ex-decoxyribonuclease V, chain (recC) (Hi) 51 55 65 65 65 65 65 65	ribosomal prt L35 (rpml) (Ba) 74 ribosomal prt L36 (rpml) (Bs) 89 ribosomal prt S1 (rpsA) (Ec) 55 ribosomal prt S2 (rpsB) {Pa} 79 ribosomal prt S3 (rpsC) {Hi} 71 ribosomal prt S3 (rpsC) {Hi} 71 ribosomal prt S4 (rpsD) {Hi} 63 ribosomal prt S5 (rpsE) {Bs} 77 ribosomal prt S5 (rpsE) {Bs} 77 ribosomal prt S6 (rpsF) {Os} 50 ribosomal prt S6 (rpsF) {Os} 75 ribosomal prt S8 (rpsH) {Syn} 66 ribosomal prt S9 (rpsI) {Hi} 71 ribosomal prt S9 (rpsI) {Hi} 71 ribosomal prt S10 (rpsJ) {Bb} 100 ribosomal prt S11 (rpsK) {Hi} 77 ribosomal prt S12 (rpsL) {An} 89 ribosomal prt S13 (rpsM) {Cp} 76 ribosomal prt S16 (rpsP) {Bs} 72 ribosomal prt S16 (rpsP) {Bs} 72 ribosomal prt S16 (rpsP) {Bs} 72 ribosomal prt S16 (rpsP) {Bs} 70 ribosomal prt S17 (rpsO) {Mc} 76 ribosomal prt S18 (rpsR) {Bs} 78 ribosomal prt S19 (rpsS) {Bb} 99 ribosomal prt S19 (rpsS) {Bb} 99 ribosomal prt S20 (rpsT) {Bb} 100 ribosomal prt S21 (rpsU) {Mx} 68 rRNA methylase (yacO) {Mc} 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) {Ec} 53 AT (nifS) {Syn} 61 glu-tRNA amidoTase, sub C (gatC) (Bs) glu-tRNA amidoTase, sub B (gatB) (Bs) glu-tRNA amidoTase, sub A (gatA) (Bs) 63 glu-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
Chain (recC) (Hi)	ribosomal prt L36 (rpmJ) (Bs) 89 ribosomal prt S1 (rpsA) (Ec) 55 ribosomal prt S2 (rpsB) (Pa) 79 ribosomal prt S3 (rpsC) (Hi) 71 ribosomal prt S4 (rpsD) (Hi) 63 ribosomal prt S4 (rpsD) (Hi) 63 ribosomal prt S5 (rpsE) (Bs) 77 ribosomal prt S6 (rpsF) (Os) 50 ribosomal prt S7 (rpsG) (Sc) 75 ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S10 (rpsI) (Bb) 100 ribosomal prt S11 (rpsK) (Hi) 77 ribosomal prt S13 (rpsK) (Cp) 76 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S17 (rpsQ) (Mc) 76 ribosomal prt S17 (rpsQ) (Mc) 76 ribosomal prt S19 (rpsP) (Bs) 78 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 64 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
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BB830	ribosomal prt S2 (rpsB) (Paj 79 ribosomal prt S3 (rpsC) [HI] 71 ribosomal prt S4 (rpsD) [HI] 63 ribosomal prt S5 (rpsE) [Bs] 77 ribosomal prt S6 (rpsE) [Os] 50 ribosomal prt S6 (rpsF) [Os] 50 ribosomal prt S8 (rpsH) [Syn] 66 ribosomal prt S8 (rpsH) [Syn] 66 ribosomal prt S9 (rpsI) [Hi] 71 ribosomal prt S10 (rpsI) [Bb] 100 ribosomal prt S11 (rpsK) [Hi] 77 ribosomal prt S12 (rpsL) [An] 89 ribosomal prt S13 (rpsM) [Co] 76 ribosomal prt S13 (rpsM) [Co] 76 ribosomal prt S15 (rpsD) [Tt] 77 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S17 (rpsQ) [Mc] 76 ribosomal prt S19 (rpsR) [Bs] 78 ribosomal prt S19 (rpsR) [Bs] 78 ribosomal prt S19 (rpsR) [Bs] 68 ribosomal prt S20 (rpsT) [Bb] 100 ribosomal prt S21 (rpsU) [Mx] 68 rRNA methylase (yacO) [Mc] 66 ribosomal prt S21 (rpsU) [Mx] 68 rRNA methylase (yacO) [Mc] 66 glu-tRNA amidoTase, sub C (gatC) [Bs] glu-tRNA amidoTase, sub B (gatB) [Bs] glu-tRNA amidoTase, sub A (gatA) [Bs] methionyl-tRNA formylTase (fmt) [Ec] 56 peptidyl-tRNA hydrolase (pth) [Bb] 100
BB177 glucose-inhibited div prt A (gldB) BB022 prolyl-tRNA Sase (proS) (Sc) 65 BB492 ribosomal prt S3 (rpsC) (Hs) Fibosomal prt S4 (rpsD) (Hs) Fibosomal prt S5 (rpsE) (Bs) Fibosomal prt S6 (rpsE) (PsE) (Bs) Fibosomal prt S6 (rpsE) (PsE) Fibosomal prt S6 (rpsE) (PsE) Fibosomal prt S6 (rpsE) (PsE) Fibosomal prt S6 (rpsE) Fi	ribosomal prt S3 (rpsC) [Hi] 71 ribosomal prt S4 (rpsP) [Hi] 63 ribosomal prt S5 (rpsF) [Ss] 77 ribosomal prt S5 (rpsF) {Os} 75 ribosomal prt S6 (rpsF) {Os} 75 ribosomal prt S7 (rpsG) [Sc] 75 ribosomal prt S8 (rpsH) {Syn} 66 ribosomal prt S9 (rpsI) [Hi] 71 ribosomal prt S9 (rpsI) [Hi] 71 ribosomal prt S10 (rpsI) (Bb) 100 ribosomal prt S11 (rpsK) [Hi] 77 ribosomal prt S11 (rpsK) [Hi] 77 ribosomal prt S13 (rpsM) {Op} 76 ribosomal prt S16 (rpsF) [Bs] 70 ribosomal prt S16 (rpsP) [Bs] 72 ribosomal prt S16 (rpsP) [Bs] 72 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S17 (rpsO) [Mc] 76 ribosomal prt S17 (rpsO) [Mc] 76 ribosomal prt S18 (rpsR) [Bs] 78 ribosomal prt S17 (rpsO) [Mc] 76 ribosomal prt S17 (rpsO) [Mc] 76 ribosomal prt S17 (rpsO) [Mc] 76 ribosomal prt S18 (rpsR) [Bs] 99 ribosomal prt S20 (rpsT) [Bb] 100 ribosomal prt S21 (rpsU) [Mx] 68 rRNA methylase (yacO) [Mc] 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) [Ec) 53 AT (nifS) [Syn] 91 glu-tRNA amidoTase, sub C (gatC) (Bs) 10-tRNA amidoTase, sub B (gatB) (Bs) 10-tRNA amidoTase, sub A (gatA) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 64 peptidyl-tRNA hydrolase (pth) [Bb] 100
BB178 glucose-inhibited div prt A gidA (Bb) glucose-inhibited div prt A gidA (Bb) 100 BB720 threonyl-tRNA Sase (serS) (Bs) 62 BB495 ribosomal prt S6 (rpsE) (Bs) 63 BB161 ribosomal prt S6 (rpsE) (Bs) 64 BB162 ribosomal prt S6 (rpsE) (Bs) 65 BB163 ribosomal prt S6 (rpsE) (Bs) 67 BB163 ribosomal prt S6 (rpsE) (Bs) 67 BB163 ribosomal prt S6 (rpsE) (Bs) 68 BB363 ribosomal prt S6 (rpsE) (Bs) 67 BB163 ribosomal prt S6 (rpsE) (Bs) 68 BB363 ribosomal prt S6 (rpsE) (Bs) 67 BB163 ribosomal prt S6 (rpsE) (Bs) 67 BB164 ribosomal prt S6 (rpsE) (Bs) 68 BB364 ribosomal prt S6 (rpsE) (Bs) 67 BB164 ribosomal prt S6 (rpsE) (Bs) 67 BB165 ribosomal prt S6 (rpsE) (Bs) 68 BB164 ribosomal prt S6 (rpsE) (Bs) 67 BB165 ribosomal prt S6 (rpsE) (Bs) 68 BB164 ribosomal prt S6 (rpsE) (Bs) 67 BB165 ribosomal prt S1 (rpsE) (Bs) 68 BB165	ribosomal prt S4 (rpsD) (Hi) 63 ribosomal prt S5 (rpsE) [Bs] 77 ribosomal prt S5 (rpsE) [Bs] 77 ribosomal prt S6 (rpsF) [Os] 50 ribosomal prt S7 (rpsG) [Sc] 75 ribosomal prt S8 (rpsH) [Syn] 66 ribosomal prt S8 (rpsH) [Syn] 66 ribosomal prt S10 (rpsI) [Bb] 100 ribosomal prt S11 (rpsK) [Hi] 77 ribosomal prt S11 (rpsK) [Hi] 77 ribosomal prt S12 (rpsL) [An] 89 ribosomal prt S13 (rpsM) [Cp] 76 ribosomal prt S14 (rpsK) [Bs] 72 ribosomal prt S15 (rpsC) [Tt] 77 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S17 (rpsQ) [Mc] 76 ribosomal prt S18 (rpsR) [Bs] 78 ribosomal prt S19 (rpsC) [Mc] 68 ribosomal prt S20 (rpsT) [Bb] 100 ribosomal prt S21 (rpsU) [Mx] 68 rRNA methylase (yacO) [Mc] 66 rodification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) [Ec] 53 AT (nifS) [Syn] 61 glu-tRNA amidoTase, sub B (gatB) (Bs) 63 glu-tRNA amidoTase, sub B (gatB) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) [Ec] 56 peptidyl-tRNA hydrolase (pth) [Bb] 100
BB178 glucose-inhibited div prt A (gidA) (Bb) BB224 (gidA) (Bb) BB225 BB225 BB226 Holliday junction DNA helicase (ruvB) (Bb) BB227 Holliday junction DNA helicase (ruvB) (Bb) BB228 BB229	ribosomal prt S5 (rpsE) (Bs) 77 ribosomal prt S6 (rpsF) (Os) 50 ribosomal prt S6 (rpsF) (Os) 50 ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S10 (rpsI) (Bs) 100 ribosomal prt S11 (rpsK) (Hi) 77 ribosomal prt S12 (rpsL) (An) 89 ribosomal prt S13 (rpsM) (Cp) 76 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 72 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S19 (rpsS) (Bb) 68 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mc) 66 rodification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 63 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB022 Holliday junction DNA helicase (ruyB) (Bb) 100 BB370 tryptophanyl-tRNA Sase (trxA) (Cl) 65 BB386 ribosomal prt S7 (rpsG) (Sc) tryptophanyl-tRNA Sase (trxA) (Cl) 65 BB386 ribosomal prt S7 (rpsG) (Sc) tryptophanyl-tRNA Sase (trxA) (Cl) 65 BB386 ribosomal prt S7 (rpsG) (Sc) tryptophanyl-tRNA Sase (trxA) (Cl) 65 BB386 ribosomal prt S7 (rpsG) (Sc) tryptophanyl-tRNA Sase (trxA) (Cl) 65 BB386 ribosomal prt S7 (rpsG) (Sc) tryptophanyl-tRNA Sase (trxA) (Cl) 65 BB386 ribosomal prt S8 (rpsH) (Syn) S8 S0 S0 S0 S0 S0 S0 S0	ribosomal prt S6 (rpsF) (Os) ribosomal prt S7 (rpsG) (Sc) ribosomal prt S8 (rpsH) (Syn) ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S10 (rpsI) (Bb) ribosomal prt S11 (rpsK) (Hi) ribosomal prt S11 (rpsK) (Hi) ribosomal prt S12 (rpsL) (An) 89 ribosomal prt S13 (rpsM) (Cp) ribosomal prt S16 (rpsP) (Bs) ribosomal prt S17 (rpsQ) (Mc) ribosomal prt S18 (rpsR) (Bs) ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) AT (nifS) (Syn) glu-tRNA amidoTase, sub C (gatC) (Bs) glu-tRNA amidoTase, sub B (gatB) (Bs) glu-tRNA amidoTase, sub A (gatA) (Bs) methionyl-tRNA formylTase (fmt) (Ec) peptidyl-tRNA hydrolase (pth) (Bb)
BB022 Holliday junction DNA helicase (ruVB) (Bb) 100 BB370 tryptophanyl-tRNA Sase (trsA) (Cl) 65 BB386 ribosomal prt S8 (rpsH) (Syn) S8 BB386 ribosomal prt S8 (rpsH) (Syn) S8 BB386 ribosomal prt S8 (rpsH) (Syn) S8 S8 S8 S8 S8 S8 S8 S	ribosomal prt S7 (rpsG) (Sc) ribosomal prt S8 (rpsH) (Syn) ribosomal prt S8 (rpsH) (Syn) ribosomal prt S9 (rpsI) (Hi) ribosomal prt S10 (rpsI) (Bb) 100 ribosomal prt S11 (rpsK) (Hi) ribosomal prt S11 (rpsK) (Hi) ribosomal prt S12 (rpsL) (An) ribosomal prt S13 (rpsM) (Cp) ribosomal prt S13 (rpsM) (Cp) ribosomal prt S16 (rpsP) (Bs) ribosomal prt S16 (rpsP) (Bs) ribosomal prt S16 (rpsP) (Bs) ribosomal prt S17 (rpsC) (Mc) ribosomal prt S18 (rpsR) (Bs) ribosomal prt S19 (rpsC) (Bb) ribosomal prt S20 (rpsT) (Bb) ribosomal prt S20 (rpsT) (Bb) ribosomal prt S21 (rpsU) (Mx) ribosomal prt S21 (rpsU) (Mx) ribosomal prt S20 (rpsT) (Bb) ribo
Record R	ribosomal prt S8 (rpsH) (Syn) 66 ribosomal prt S9 (rpsI) (Hi) 71 ribosomal prt S10 (rpsJ) (Bb) 100 ribosomal prt S110 (rpsJ) (Bb) 100 ribosomal prt S110 (rpsL) (An) 89 ribosomal prt S112 (rpsL) (An) 89 ribosomal prt S13 (rpsM) (Cp) 76 ribosomal prt S15 (rpsC) (Tt) 77 ribosomal prt S15 (rpsC) (Tt) 77 ribosomal prt S15 (rpsC) (Rc) 76 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S17 (rpsQ) (Mc) 76 ribosomal prt S18 (rpsR) (Bs) 78 ribosomal prt S19 (rpsC) (Mc) 76 ribosomal prt S19 (rpsC) (Mc) 68 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 **Codification** 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 63 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB023 Hollida'y junction DNA helicase (ruvA) (Bb) 100	ribosomal prt S9 (rpsl) (Hii) 71 ribosomal prt S10 (rpsl) (Bb) 100 ribosomal prt S11 (rpsk) (Hi) 77 ribosomal prt S11 (rpsk) (Hi) 77 ribosomal prt S12 (rpsl.) (An) 89 ribosomal prt S13 (rpsM) (Cp) 76 ribosomal prt S14 (rpsN) (Bs) 72 ribosomal prt S15 (rpsO) (Tt) 77 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsR) (Bs) 76 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S20 (rpsT) (Bb) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) glu-tRNA amidoTase, sub C (gatC) (Bs) glu-tRNA amidoTase, sub B (gatB) (Bs) glu-tRNA amidoTase, sub A (gatA) (Bs) methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
(ruvA) (Bb) 100	ribosomal prt S10 (rps.) (Bb) 100 ribosomal prt S11 (rpsK) (Hi) 77 ribosomal prt S12 (rpsL) (An) 89 ribosomal prt S13 (rpsM) (Op) 76 ribosomal prt S13 (rpsM) (Op) 76 ribosomal prt S14 (rpsN) (Bs) 72 ribosomal prt S16 (rpsO) (Tt) 77 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S17 (rpsO) (Mc) 76 ribosomal prt S17 (rpsO) (Mc) 76 ribosomal prt S19 (rpsR) (Bs) 99 ribosomal prt S20 (rpsT) (Bb) 99 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 91 glu-tRNA amidoTase, sub C (gatC) (Bs) 63 glu-tRNA amidoTase, sub B (gatB) (Bs) 64 glu-tRNA amidoTase, sub A (gatA) (Bs) 65 petidyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB014	ribosomal prt S11 (rpsK) (Hi) 77 ribosomal prt S12 (rpsL) (An) 89 ribosomal prt S13 (rpsM) (Cp) 76 ribosomal prt S13 (rpsM) (Cp) 76 ribosomal prt S14 (rpsM) (Bs) 72 ribosomal prt S15 (rpsO) (Tt) 77 ribosomal prt S16 (rpsP) (Bs) 70 ribosomal prt S17 (rpsQ) (Mc) 76 ribosomal prt S18 (rpsR) (Bs) 78 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 lodification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 76 glu-tRNA amidoTase, sub B (gatB) (Bs) glu-tRNA amidoTase, sub A (gatA) (Bs) methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB131 recA prt (recA) (Bb) 100 copeptides BB608 aminoacyl-histidine dipeptidase (pepD) (Hi) 55 BB401 ribosomal prt S13 (rpsM) (Cp) (PepD) (Hi) 55 BB401 ribosomal prt S14 (rpsM) (Es) BB401 ribosomal prt S16 (rpsP) (Bs) BB402 ribosomal prt S16 (rpsP) (Bs) BB403 ribosomal prt S16 (rpsP) (Bs) BB404 ribosomal prt S16 (rps	ribosomal prt \$12 (rpsL) (An) 89 ribosomal prt \$13 (rpsM) (Cp) 76 ribosomal prt \$14 (rpsN) (Bs) 72 ribosomal prt \$14 (rpsN) (Bs) 72 ribosomal prt \$15 (rpsO) (Tt) 77 ribosomal prt \$16 (rpsP) (Bs) 70 ribosomal prt \$16 (rpsP) (Bs) 70 ribosomal prt \$17 (rpsQ) (Mc) 76 ribosomal prt \$19 (rpsR) (Bs) 88 ribosomal prt \$20 (rpsT) (Bb) 100 ribosomal prt \$20 (rpsT) (Bb) 100 ribosomal prt \$21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 rodification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) (Bs) (Bs) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB607 rep helicase, ss DNA-dep ATPase (rep) (Hi) 61 61 61 61 61 61 61 6	ribosomal prt \$13 (rpsM) (Cp) 76 ribosomal prt \$14 (rpsN) {Bs} 72 ribosomal prt \$15 (rpsO) {Tt} 77 ribosomal prt \$15 (rpsO) {Tt} 77 ribosomal prt \$16 (rpsP) {Bs} 70 ribosomal prt \$16 (rpsP) {Bs} 70 ribosomal prt \$17 (rpsO) {Mc} 76 ribosomal prt \$18 (rpsR) {Bs} 78 ribosomal prt \$19 (rpsS) {Bb} 99 ribosomal prt \$20 (rpsT) {Bb} 100 ribosomal prt \$21 (rpsU) {Mx} 68 rRNA methylase (yacO) {Mc} 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) {Ec} 53 AT (nifS) {Syn} 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 76 glu-tRNA amidoTase, sub B (gatB) (Bs) 76 glu-tRNA amidoTase, sub A (gatA) (Bs) 76 methionyl-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
ATPase (rep) (Hi) 61 61 62 63866 64 64 64 64 64 65 65	ribosomal prt S14 (rpsN) (Bs) 72 ribosomal prt S15 (rpsO) [Tt] 77 ribosomal prt S16 (rpsP) [Bs] 70 ribosomal prt S17 (rpsQ) [Mc] 76 ribosomal prt S18 (rpsR) [Bs] 78 ribosomal prt S18 (rpsR) [Bs] 99 ribosomal prt S20 (rpsT) [Bb] 100 ribosomal prt S21 (rpsU) [Mx] 68 rRNA methylase (yacO) [Mc] 66 odification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) [Ec] 53 AT (nifS) [Syn] 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 56 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) [Ec] 56 peptidyl-tRNA hydrolase (pth) [Bb] 100
BB111 replicative DNA helicase (dnaB) {Ec} (dnaB) {Ec} 58 BB069 (dnaB) {	ribosomal prt \$15 (rpsO) (Tt) 77 ribosomal prt \$16 (rpsP) (Bs) 70 ribosomal prt \$17 (rpsQ) (Mc) 76 ribosomal prt \$17 (rpsQ) (Mc) 76 ribosomal prt \$18 (rpsR) (Bs) 78 ribosomal prt \$19 (rpsS) (Bb) 99 ribosomal prt \$20 (rpsT) (Bb) 100 ribosomal prt \$21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 **Codification** 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 63 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
Characteristics Characteri	ribosomal prt \$16 (rpsP) (Bs) 70 ribosomal prt \$17 (rpsQ) (Mc) 76 ribosomal prt \$18 (rpsR) (Bs) 78 ribosomal prt \$18 (rpsR) (Bs) 99 ribosomal prt \$20 (rpsT) (Bb) 99 ribosomal prt \$20 (rpsT) (Bb) 100 ribosomal prt \$21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) glu-tRNA amidoTase, sub C (gatC) (Bs) (Bs) (Bs) (Bs) (Bs) (Bs) (Bs) (Bs
BB114 ss DNA-BP (ssb) (Syn) 62 BB611 ATP-dep Clp protease proteolytic component (clpP-1) (Hil) 79 BB113 ribosomal prt S17 (rpsQ) (Mc) ss-DNA-specific exonuclease (recJ) (Hil) 52 BB757 ATP-dep Clp protease proteolytic component (clpP-2) (Hil) 67 BB133 ribosomal prt S18 (rpsR) (Bs) component (clpP-2) (Hil) 67 BB233 ribosomal prt S20 (rpsT) (Bb) BB053 uracil DNA glycosylase (ung) (Hil) 68 (clpA) {Ec} 56 BB516 rRNA methylase (yacO) {Mc} BB053 uracil DNA helicase, put {Bs} 59 BB834 ATP-dep Clp protease, sub X (clpA) {Ec} 56 BB516 rRNA modification BB8052 replicative DNA helicase, put {Bs} 59 BB834 ATP-dep Clp protease, sub C (clpC) {Pp} 67 tRNA modification BB605 adenine specific DNA MTase, put {Hp} 57 BB359 carboxyl-terminal protease (LA (lon-1) {Bb} 100 ATP-dep protease (LA (lon-2) {Hil} 65 BB234 Tibosomal prt S17 (rpsQ) (Mc) BB205 polyribonucleotide nucleotidylTase 68 BB611 ATP-dep Clp protease proteolytic component (clpP-1) (Hil) 79 BB113 ribosomal prt S17 (rpsQ) (Mc) BB113 ribosomal prt S17 (rpsQ) (Mc) BB113 ribosomal prt S17 (rpsQ) (Mc) BB113 ribosomal prt S18 (rpsR) (Bs) BB113 ribosomal prt S18 (rpsR) (Bs) BB113 ribosomal prt S19 (rpsS) (Bb) Component (clpP-2) (Hil) 67 BB233 ribosomal prt S21 (rpsU) (Mx) BB206 ribosomal prt S21 (rps	ribosomal prt S17 (rpsQ) (Mc) 76 ribosomal prt S18 (rpsR) (Bs) 78 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 56 glu-tRNA amidoTase, sub B (gatB) (Bs) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB254 ss-DNA-specific exonuclease (recl) (Hi) 52 BB757 ATP-dep Clp protease proteolytic component (clpP-1) (Hi) 79 BB482 ribosomal prt S18 (rpsR) (Bs) ATP-dep Clp protease proteolytic component (clpP-2) (Hi) 67 BB233 ribosomal prt S20 (rpsT) (Bb) ATP-dep Clp protease, sub A (clpA) (Ec) BB653 uracil DNA glycosylase (ung) (Hi) 68 (clpA) (Ec) BB632 replicative DNA helicase, put (Bs) 59 BB834 ATP-dep Clp protease, sub X (clpA) (Ec) 75 tRNA modification BB825 ATP-dep Clp protease, sub C (clpC) (Pp) (Ec) 75 tRNA modification BB826 ribosomal prt S20 (rpsT) (Bb) (Ms) (ClpA) (Ec) 8B516 rRNA methylase (yacO) (Mc) BB613 ribosomal prt S20 (rpsT) (Bb) (Ms) BB256 ribosomal prt S21 (rpsD) (Ms) BB256 ribosomal prt S21 (rpsD) (Ms) BB256 ribosomal prt S20 (rpsT) (Bb) BB256 ribosomal prt S21 (rpsT) (Bb) BB256 ribosomal prt S20 (rpsT) (Bb) BB256 ribosomal prt S20 (rpsT) (Bb) BB256 ribosomal prt S20 (rpsT) (Bb) BB256 ribosomal prt S21 (rpsT) (Bb) BB256 ribosomal prt S20 (rpsT) (Bb) BB256 ribosomal prt S20 (rpsT) (Bb BB256 ribosomal prt S20 (rpsT) (Bb) BB256 ribosomal prt S20 (rp	ribosomal prt S18 (rpsR) (Bs) 78 ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 odification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 56 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
(recJ) (Hi) 52 BB757 ATP-dep Clp protease proteolytic component (clpP-2) (Hi) 67 BB233 ribosomal prt S19 (rpsS) (Bb) BB263 uracil DNA glycosylase (ung) (Hi) 68 BB653 uracil DNA glycosylase (ung) (Hi) 68 BB653 uracil DNA plycosylase (ung) (Hi) 68 BB653 uracil DNA plycosylase (ung) (Hi) 68 BB654 uracil DNA helicase, put (Bs) 59 BB652 replicative DNA helicase, put (Bs) 59 BB253 ATP-dep Clp protease, sub X (clpX) (Ec) 75 BB254 ATP-dep Clp protease, sub C (clpC) (Pp) 67 (clpC) (Pp) 67 (clpC) (Pp) 67 (p	ribosomal prt S19 (rpsS) (Bb) 99 ribosomal prt S20 (rpsT) (Bb) 100 ribosomal prt S21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 756 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB623 transcription-repair coupling factor (mfd) (Hi) 60 BB369 ATP-dep Clp protease, sub A (clpA) {Ec} BB653 uracil DNA glycosylase (ung) {Hi} 68 BB663 uracil DNA plicase, put {Bs} 59 BB6632 replicative DNA helicase, put {Bs} 59 BB824 ATP-dep Clp protease, sub C (clpX) {Ec} Transcription BB625 adenine specific DNA MTase, put {Hp} 57 BB359 after a BB205 spoU prt (spoU) {Ec} 54 BB204 BB805 polyribonucleotide nucleotidylTase 68 BB8067 peptidase, put {Sc} Component (clpP-2) {Hi} 60 BB369 ATP-dep Clp protease, sub C (clpX) {Ec} Transcription Component (clpP-2) {Hi} 67 BB203 ribosomal prt S20 (rpsT) {Bb} BB205 ribosomal prt S20 (rpsT) {Bb} BB206 protease, sub A ATP-dep Clp protease, sub X (clpX) {Ec} Transcription Component (clpP-2) {Hi} 68 BB206 protease, sub C (clpX) {Ec} Transcription BB203 ATP-dep protease LA (lon-1) {Bb} 100 (miaA) {Ec} BB204 ATP-dep protease LA (lon-2) {Hi} 65 BB341 glu-tRNA amidoTase, sub C (grading prt (hflK) {Ec} BB341 glu-tRNA amidoTase, sub B (grading prt (hflK) {Ec} BB341 glu-tRNA amidoTase, sub B (grading prt (hflK) {Ec} BB342 glu-tRNA amidoTase, sub A (grading prt (hflC) {Ec} BB343 polyribonucleotide nucleotidylTase 68 BB067 poptidase, put {Sc} BB344 BB067 poptidase, put {Sc} BB345 protease, sub A (si ClpA) {Ec} Transcription BB343 pribosomal prt S20 (rpsT) {Bb} BB256 ribosomal prt S20 (rpsT) {Bb} ATP-dep Clp protease, sub A (si ClpA) {Ec} BB341 glu-tRNA amidoTase, sub B (grading prt (hflK) {Ec} BB341 glu-tRNA amidoTase, sub A (grading prt (hflK) {Ec} BB342 glu-tRNA amidoTase, sub A (grading prt (hflK) {Ec} BB343 protease, sub A (grading prt (hflK) {Ec} BB344 protease, su	ribosomal prt \$20 (rpsT) (Bb) 100 ribosomal prt \$21 (rpsU) (Mx) 68 rRNA methylase (yacO) (Mc) 66 codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nif5) (Syn) glu-tRNA amidoTase, sub C (gatC) (Bs) 101 (Bs) 102 (Bs) 103 (Bs) 104 (Bs) 105 (Bs) 105 (Bs) 105 (Bs) 106 (Bs) 107 (Bs) 107 (Bs) 107 (Bs) 108 (Bs) 109 (Bs) 100 (Bs
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BB053 uracil DNA glycosylase (ung) (Hi) 68 D28-2 BBG32 replicative DNA helicase, put (Bs) 59 BB834 ATP-dep Clp protease, sub C (clpC) (Pp) 67 BB253 ATP-dep Drotease ATP-dep Clp protease, sub C (clpC) (Pp) 67 BB254 ATP-dep Drotease ATP-dep	rRNA methylase (yacO) {Mc} 66 odification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) {Ec} 53 AT (nifS) {Syn} 61 glu-tRNA amidoTase, sub C (gatC) {Bs} 56 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) {Bs} 63 glu-tRNA amidoTase, sub A (gatA) {Bs} 65 petidyl-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
Page 2 BBG32 replicative DNA helicase, put {Bs} 59 BB834 ATP-dep Clp protease, sub X (c pX) {Ec} 75 tRNA modification BB832 2-methylthio-N6-isopentyladency (c pC) {Pp} 67 tRNA modification ERNA modification ERNA modification ERNA modification ERNA modification ERNA modification ERNA modification enzyme (miaA) {Ec} BB25 ATP-dep protease LA (lon-1) {Bb} 100 (miaA) {Ec} BB829 ATP-dep protease LA (lon-2) {Hi} 65 BB084 AT (nifS) {Syn} BB829 Carboxyl-terminal protease (ctp) BB343 glu-tRNA amidoTase, sub C (group ERNA BB204 Cll stability-governing BB343 glu-tRNA amidoTase, sub B (group ERNA BB344 BB344 Glu-tRNA amidoTase, sub B (group ERNA BB344 Glu-tRNA amidoTase, sub B (group ERNA BB344 Glu-tRNA amidoTase, sub B (group ERNA Glu-tRNA Glu-tRNA Glu-tRNA Gli-tRNA Gli-tRN	codification 2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) {Ec} 53 AT (nifS) {Syn} glu-tRNA amidoTase, sub C (gatC) {Bs} 56 glu-tRNA amidoTase, sub B (gatB) {Bs} (Bs) 63 glu-tRNA amidoTase, sub A (gatA) {Bs} 61 methionyl-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
D28-2 BBG32 replicative DNA helicase, put {Bs} 59 BB834 ATP-dep Clp protease, sub C (clpC) {Pp} ATP-dep protease LA (lon-1) {Bb} 100 (miaA) {Ec}	2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nif5) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 56 glu-tRNA amidoTase, sub B (gatB) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BBG32 replicative DNA helicase, put {Bs} 59 BB834 ATP-dep Clp protease, sub C (clpC) {Pp} 67 BBE29 adenine specific DNA MTase, put {Bs} 57 BBE29 adenine specific DNA MTase, put {Hp} 57 BBS29 adenine specific DNA MTase, put {Bs} 67 BBS20 adenine specific DNA MTase, put {Bs} 100 ATP-dep protease, sub C (second protease) {Bs} 100 ATP-dep protease, sub C (second protease) {Bs} 100 ATP-dep protease, sub C (second protease) {Bs} 100 BBS20 adenine specific DNA MTase, put {Bs} 100 BBS20 adenine specific	2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA) (Ec) 53 AT (nif5) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 56 glu-tRNA amidoTase, sub B (gatB) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
Colp Color Pp 67 RNA modification enzyme RNA modification en	tRNA modification enzyme (miaA) {Ec} 53 AT (nifS) {Syn} 61 glu-tRNA amidoTase, sub C (gatC) {Bs} glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) 63 glu-tRNA amidoTase, sub A (gatA) 61 methionyl-tRNA formylTase 61 fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
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Page	(miaA) (Ec) 53 AT (nifS) (Syn) 61 glu-tRNA amidoTase, sub C (gatC) 56 glu-tRNA amidoTase, sub B (gatB) 63 glu-tRNA amidoTase, sub A (gatA) 63 glu-tRNA amidoTase, sub A (gatA) 61 methionyl-tRNA formylTase 61 fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BBE29 adenine specific DNA MTase, put {Hp} 57 BB359 RB359 RB	AT (nifS) (Śyn) 61 glu-tRNA amidoTase, sub C (gatC) (Bs) 56 glu-tRNA amidoTase, sub B (gatB) (Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
Hp 57 BB359 carboxyl-terminal protease (cip) 65 8B343 glu-tRNA amidoTase, sub C (gr. Flash) Flash	glu-tRNA amidoTase, sub C (gatC) (Bs) 56 (Bs) 63 (Bs) 63 (Bs) 61 (Bs) 61 (Bs) (Bs) 61 (Ec) 56 (peptidyl-tRNA hydrolase (pth) (Bb) 100 (Bs) (Bs
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Transcription General BB052 spoU prt (spoU) {Ec} BB052 spoU prt (spoU) {Ec} BB204 Lambda Cll stability-governing prt (hflK) {Ec} 56 Lambda Cll stability-governing prt (hflK) {Ec} 56 Lambda Cll stability-governing prt (hflC) {Ec} Lambda Cll stability-governing prt (hflC) {Ec} S6 Degradation of RNA BB204 BB204 Lambda Cll stability-governing prt (hflC) {Ec} S6 BB342 glu-tRNA amidoTase, sub A (gright (spoul) {Bs}) BB343 glu-tRNA amidoTase, sub A (gright (spoul) {Bs}) BB344 BB342 BB342 BB342 BB342 BB342 BB342 Glu-tRNA amidoTase, sub A (gright (spoul) {Bs}) BB345 polyribonucleotide nucleotidylTase 68 BB067 peptidase, put {Sc} BB346 BB347 BB348 BB348 BB348 BB349 BB	glu-tRNA amidoTase, sub B (gatB) (Bs) 63 (glu-tRNA amidoTase, sub A (gatA) (Bs) 61 (fmt) (Ec) 56 (peptidyl-tRNA hydrolase (pth) (Bb) 100 (fmt) (Bb) 100 (fmt) (Bb) (fmt) (Bb) (Bb) (Bb) (Bb) (fmt) (Bb) (Bb) (Bb) (Bb) (Bb) (Bb) (Bb) (Bb
General BB052 spoU prt (spoU) {Ec} 54 BB204 Lambda CII stability-governing prt (hflC) {Ec} 56 BB342 glu-tRNA amidoTase, sub A (gi (hflC) {Ec} 56 BB342 glu-tRNA amidoTase, sub A (gi (hslC) {Ec} 56 BB342 glu-tRNA amidoTase, sub A (gi (bs) 56 BB342 glu-tRNA amidoTase, sub A (gi (bs) 56 BB342 glu-tRNA formylTase (bs) 56 BB342 glu-tRNA formylTase (bs) 56 BB342 glu-tRNA formylTase (bs) 56 (fmt) {Ec} (fmt) {Ec}	(Bs) 63 glu-tRNA amidoTase, sub A (gatA) (Bs) 61 methionyl-tRNA formylTase (fmt) (Ec) 56 peptidyl-tRNA hydrolase (pth) (Bb) 100
BB052 spoU prt (spoU) {Ec} 54 BB204 Lambda ČII stability-governing prt (hflC) {Ec} 56 BB052 polyribonucleotide nucleotidylTase 68 BB067 peptidase, put {Sc} 56 BB064 glu-tRNA amidoTase, sub A (gradation of RNA BB248 oligoendopeptidase F (pepF) {LI} 58 BB064 methionyl-tRNA formylTase (fmt) {Ec}	glu-tRNA amidoTase, sub A (gatA) {Bs} 61 methionyl-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
Degradation of RNA BB805 polyribonucleotide nucleotidylTase 68 BB067 peptidase, put {Sc} (hflC) {Ec} BB248 oligoendopeptidase F (pepF) {Ll} 58 BB064 methionyl-tRNA formylTase (ffmt) {Ec}	{Bs} 61 methionyl-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
Degradation of RNA BB805 polyribonucleotide nucleotidylTase 68 BB067 peptidase, put {Sc} BB064 methionyl-tRNA formylTase BB064 methionyl-tRNA formylTase (fmt) {Ec}	methionyl-tRNA formylTase (fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
BB805 polyribonucleotide nucleotidylTase 68 BB067 peptidase, put {Sc} 56 (fmt) {Ec}	(fmt) {Ec} 56 peptidyl-tRNA hydrolase (pth) {Bb} 100
	peptidyl-tRNA hydrolase (pth) {Bb} 100
	osellootilloviale sase i mis ii tent iiiii
	SAM: tRNA ribosylTase-isomerase
BB441 ribonuclease P prt component BB769 sialoglycoprotease (gcp) {Hi} 60 {Bb}	,
	tRNA-guanine transglycosylase
aminopeptidase (tgt) {Zm}	
	tRNA (guanine-N1)-MTase (trmD)
	{Mg} 68
BB389 DNA-directed RNA polymerase BB536 zinc protease, put {Hi} 52 (truB) {Ec}	{Mg} 68 tRNA pseudouridine 55 Sase
(rpoB) {Bb} 97	tRNA pseudouridine 55 Sase
BB388 DNA-directed RNA polymerase Nucleoproteins Translation factors	tRNA pseudouridine 55 Sase
(rpoC) {Ec} 71 BB232 hbbU prt {Bb} 100 BB088 GTP-B membrane prt (lepA) {H	tRNA pseudouridine 55 Sase (truB) {Ec} 57
	tRNA pseudouridine 55 Sase (truB) {Ec} 57
(rpoS) {Pa} 61 Protein modification Hi}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA)
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB)
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68
	tRNA pseudouridine 55 Sase (truB) (Ec) 57 tion factors GTP-B membrane prt (lepA) (Hi) 76 peptide chain release factor 1 (prfA) Hi) 73 peptide chain release factor 2 (prfB) {Sc) 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA)
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB)
(1.) (1.)	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC)
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72
	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G
BB394 transcription antitermination BB479 ribosomal prt L4 (rplD) (Bb) 100 (fus-2) {Tm}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67
BB394 transcription antitermination BB479 ribosomal prt L4 (rpID) (Bb) 100 (fus-2) {Tm} factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) (Hi) 80 BB214 translation elongation factor P	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {PV} 72 translation elongation factor G {fus-2) [Tm} 67 translation elongation factor P
BB394 transcription antitermination BB479 ribosomal prt L4 (rpID) (Bb) 100 (fus-2) {Tm} factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P BB132 transcription elongation factor BB493 ribosomal prt L6 (rpIF) {Sc} 72 (efp) {Ec}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {PV} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56
BB394 transcription antitermination BB479 ribosomal prt L4 (rpID) (Bb) 100 (fus-2) (Tm) factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P BB132 transcription elongation factor BB493 ribosomal prt L6 (rpIF) (Sc) 72 (efp) {Ec} (efp) {Ec} (greA) {Ec} (greA) {Ec} 56 BB390 ribosomal prt L7/L12 (rpIL) {Sc} 75 BB476 translation elongation factor	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor
BB394 transcription antitermination BB479 ribosomal prt L4 (rpID) (Bb) 100 (fus-2) {Tm} factor (rusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P BB32 transcription elongation factor BB493 ribosomal prt L6 (rpIE) {Ec} 72 (efp) {Ec} (efp)	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) (Bb) 100 (fus-2) {Tm} factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (greA) {Ec} 56 BB390 ribosomal prt L6 (rpIF) {Sc} 72 (efp) {Ec} transcription factor, put {Mx} 47 BB112 ribosomal prt L9 (rpII) {Ec} 57 TU (tuf) {Bb} BB230 transcription termination factor BB355 transcription termination factor BB391 ribosomal prt L10 (rpIJ) {Bs} 61 BB122 translation elongation factor	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) [Tm] 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) {Bb} 100 (fus-2) {Tm} 8B132 transcription elongation factor BB493 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (efp) {Ec} (efp) {Ec} transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rpIL) {Sc} 75 BB476 translation elongation factor BB230 transcription termination factor BB391 ribosomal prt L10 (rpII) {Bs} 61 BB122 translation elongation factor Rho (rho) {Bb} 100 BB393 ribosomal prt L11 (rpIK) {Tm} 73 TS (tsf) {Hi}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) {Bb} 100 (fus-2) {Tm} factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P BB320 transcription elongation factor P BB390 ribosomal prt L6 (rpIE) {Sc} 72 (efp) {Ec} (efp) {E	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 (fus-2) {Tm} factor (nusG) {Ec} 8B490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (greA) {Ec} 56 BB390 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec} 75 BB476 translation elongation factor P {Ec} 45 BB476 translation elongation factor P {Ec} 45 BB476 translation elongation factor P {Ec} 45 BB476 translation elong	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 (fus-2) {Tm} 4 translation elongation factor P (preA) {Ec} 64 BB490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P (preA) {Ec} 72 (preA) {Ec} 8B395 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P (preA) {Ec} 8B390 transcription termination factor BB391 ribosomal prt L9 (rplI) {Ec} 57 TU (tuf) {Bb} 8B391 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (preA) {Ec} 8B391 ribosomal prt L10 (rplI) {Ec} 75 BB476 translation elongation factor P (preA) {Ec} 8B391 ribosomal prt L10 (rplI) {Ec} 75 BB476 translation elongation factor P (preA) {Ec} 8B391 ribosomal prt L11 (rplK) {Tm} 73 TS (tsf) {Hi} 75 TS (tsf) {Hi} 75 TS (tsf) {Hi} 75 TS (tsf) {Hi} 75 TS (tsf) {Tm}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 (fus-2) {Tm} 100 (fu	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 port and binding proteins
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 BB214 translation elongation factor P BB132 transcription elongation factor P BB355 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 {rplL} {Sc} 75 BB476 translation elongation factor P BB230 transcription termination factor BB391 ribosomal prt L9 {rpl} {Ec} 57 BB476 translation elongation factor P BB230 transcription termination factor BB391 ribosomal prt L9 {rpl} {Ec} 57 TU {tuf} {Bb} BB122 translation elongation factor P BB230 transcription termination factor BB391 ribosomal prt L10 {rpl} {Bs} 61 BB122 translation elongation factor P BB393 ribosomal prt L11 {rpl} {Tm} 73 TS {tsf} {Hi} TS {tsf} {translation elongation factor P BB496 ribosomal prt L16 {trplP} {Syn} BB497 ribosomal prt L17 {trplQ} {Ec} G3 BB503 BB50	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53
BB394 transcription antitermination BB479 ribosomal prt L4 (rpID) (Bb) 100 (fus-2) (Tm) 100	tRIVA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {PV} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 port and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Syn} 57
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 Factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (efp)	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 2 (infB) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TG (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Syn} 74 ABC transporter, ATP-BP {Hi} 74
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 Factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P BB322 transcription elongation factor P BB335 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P BB230 transcription termination factor BB391 ribosomal prt L9 (rplI) {Ec} 57 BB122 translation elongation factor P BB230 transcription termination factor BB391 ribosomal prt L10 (rplJ) {Bs} 61 BB122 translation elongation factor P BB330 ribosomal prt L11 (rplK) {Tm} 73 TS (tsf) {Hi} 74 75 75 75 75 75 75 75	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G {fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {BB} 100 translation elongation factor TU (tuf) {BB} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G G (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {BI} 60
BB394 transcription antitermination factor (nusG) {Ec} 64 B8490 ribosomal prt L4 (rplD) {Bb} 100 BB214 translation elongation factor P BB492 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P BB492 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P BB492 ribosomal prt L7 (rplE) {Sc} 72 (efp) {Ec} 72 (efp) {Ec} 72 (efp) {Ec} 73 (efp) {Ec} 74 (efp) {Ec} 74 (efp) {Ec} 74 (efp) {Ec} 74 (efp) {Ec} 75 (ef	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G {fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 port and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Hi} 74 ABC transporter, ATP-BP {Bi} 60 ABC transporter, ATP-BP {Mj} 63
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 BB214 translation elongation factor P (efp) {Ec}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 Ort and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ylxH-1) {Bb} 100
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P BB322 transcription elongation factor P BB332 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P BB355 transcription factor, put {Mx} 47 BB112 ribosomal prt L9 (rplI) {Ec} 57 BB476 translation elongation factor P BB391 ribosomal prt L9 (rplI) {Ec} 57 BB476 translation elongation factor P BB391 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P BB391 ribosomal prt L11 (rplK) {Tm} 73 TS (tsf) {Hi} 72 BB706 polynucleotide adenylylTase (papS) {Bs} 57 B8485 ribosomal prt L14 (rplN) {Tm} 79 BB706 polynucleotide adenylylTase (papS) {Bs} 57 B8485 ribosomal prt L16 (rplP) {Syn} 81 Transport and binding proteins General BB494 ribosomal prt L18 (rplS) {Ec} 74 BB742 ABC transporter, ATP-BP {Bs} (ksgA) {Bs} 61 BB78 ribosomal prt L21 (rplU) {Ec} 58 BB754 ABC transporter, ATP-BP {Bl} (syn) BB802 ribosome-B factor A (rbfA) {Bs} 62 BB483 ribosomal prt L22 (rplV) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L22 (rplV) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L23 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B8400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC transporter, ATP-BP {Mi} B4400 ribosomal prt L24 (rplW) {Bb} 100 BB000 ABC	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 Ort and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ylxH-1) {Bb} 100
BB394 transcription antitermination factor (nusG) {Ec} 64 B8490 ribosomal prt L4 (rplD) {Bb} 100 factor (nusG) {Ec} 64 B8490 ribosomal prt L5 (rplE) {Hi} 80 B8214 translation elongation factor P BB322 transcription elongation factor P BB332 transcription elongation factor P BB355 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rplL) {Sc} 75 B8476 translation elongation factor P BB355 transcription termination factor BB391 ribosomal prt L9 (rplI) {Ec} 57 B8476 translation elongation factor P BB230 transcription termination factor BB391 ribosomal prt L10 (rplD) {Bs} 61 B8122 translation elongation factor P BB330 ribosomal prt L11 (rplK) {Tm} 73 TS (tsf) {Hi} 72 TS (tsf) {Hi} 73 TS (tsf) {Hi} 74 TS (tsf) {Hi} 75 TS (tsf)	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {Pv} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 Ort and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ylxH-1) {Bb} 100
BB394 transcription antitermination factor (nusG) [Ec] 64 BB490 ribosomal prt L4 (rplD) [Bb] 100 factor (nusG) [Ec] 64 BB490 ribosomal prt L5 (rplE) [Hi] 80 BB214 translation elongation factor P (efp) [Ec] 100 BB393 ribosomal prt L7/L12 (rplL) [Sc] 75 BB465 transcription factor, put [Mx] 47 BB112 ribosomal prt L9 (rplI) [Ec] 57 BB355 transcription termination factor 8B391 ribosomal prt L9 (rplI) [Ec] 57 TU (tuf) [Bb] 100 BB393 ribosomal prt L10 (rplI) [Bs] 61 BB122 translation elongation factor TU (tuf) [Bb] 100 BB393 ribosomal prt L11 (rplN) [Tm] 73 ribosomal prt L11 (rplN) [Tm] 73 ribosomal prt L14 (rplN) [Tm] 73 BB460 polynucleotide adenylylTase (papS) [Bs] 57 BB485 ribosomal prt L16 (rplP) [Syn] 68 (papS) [Bs] 57 BB485 ribosomal prt L16 (rplP) [Syn] 68 (papS) [Bs] 68 (papS) [Bs] 69 BB573 ABC transporter, ATP-BP [Bs] 69 BB573 ABC transporter, ATP-BP [Bs] 69 BB573 ABC transporter, ATP-BP [Syn] 61 BB784 ABC transporter, ATP-BP [Bs] 61 BB785 ribosomal prt L20 (rplT) [Ec] 70 BB466 ABC transporter, ATP-BP [Bs] 61 BB778 ribosomal prt L22 (rplV) [Bs] 100 BB269 ATP-BP (yiXH-1) [Bs] 62 BB489 ribosomal prt L22 (rplV) [Bs] 100 BB269 ATP-BP (yiXH-2) [Bs] 64 BB594 arginyl-tRNA Sase (alaS) [Ec] 62 (rplX) [Ec] 64 BB594 arginyl-tRNA Sase (args) [Mi] 55 BB780 ribosomal prt L27 (rplX) [Ec] 64 BB594 arginyl-tRNA Sase (args) [Mi] 55 BB780 ribosomal prt L27 64 BB780 ribosomal prt L27 64 BB780 ribosomal prt L29 (rplX) [Bs] 64 BB780 ribosomal prt L29 (rplX) [Bs] 100 BB269 ATP-BP (yiXH-2) [Bs]	tRIVA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {PV} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G G (fus-1) {Tm} 68 Ort and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Hi} 74 ABC transporter, ATP-BP {Hi} 74 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ylxH-1) {Bb} 100 ATP-BP (ylxH-2) {Bb} 54
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 factor (nusG) {Ec} 65 BB490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (greA) {Ec} 56 BB390 ribosomal prt L7/L12 (rplL) {Sc} 75 BB456 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (efp) {Ec} 61 BB196 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB192 ribosomal prt L10 (rplI) {Bs} 61 BB192 ribosomal prt L115 (rplO) {Bs} 68 ribosomal prt L16 (rplO) {Bs} 68 ribosomal prt L17 (rplO) {Ec} 63 BB590 dimethyladenosine Tase BB699 ribosomal prt L19 (rplS) {Ec} 74 BB792 ABC transporter, ATP-BP {Bs} 69 BB990 dimethyladenosine Tase BB188 ribosomal prt L19 (rplS) {Ec} 70 B8466 ABC transporter, ATP-BP {BI} 69 BB490 ribosomal prt L21 (rplU) {Ec} 58 BB754 ABC transporter, ATP-BP {BI} 69 BB490 ribosomal prt L22 (rplV) {Bb} 60 BB269 ATP-BP {VykH-1) {Bb} BB490 ribosomal prt L23 (rplW) {Bb} 60 BB269 ATP-BP {VykH-1) {Bb} BB490 ribosomal prt L24 (rplX) {Ec} 64 BB490 ribosomal prt L24 (rplX) {Ec} 64 BB490 ribosomal prt L24 (rplX) {Ec} 64 BB490 ribosomal prt L27 (rplX) {Ec} 64 BB490 ribosomal prt L27 (rplX) {Ec} 64 BB260 ABC transporter, ATP-BP {Mj} BB490 ribosomal prt L27 (rplX) {Ec} 64 BB260 ABC transporter, ATP-BP {Mj} BB490 ribosomal prt L27 (rplX) {Ec} 64 BB490 ribosomal prt L27 (rplX) {Ec} 64 BB260 ABC tra	tRIVA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 3 (infC) {PV} 72 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G G (fus-1) {Tm} 68 Ort and binding proteins ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Hi} 74 ABC transporter, ATP-BP {Hi} 74 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ylxH-1) {Bb} 100 ATP-BP (ylxH-2) {Bb} 54
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) {Bb} 100 BB214 translation elongation factor P (greA) {Ec} 56 BB390 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (greA) {Ec} 56 BB390 ribosomal prt L7/L12 (rpIL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G {Fv} 70 translation elongation factor B (fus-2) {Tm} 67 translation elongation factor G translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (yixH-1) {Bb} 100 ATP-BP (yixH-2) {Bb} 54 ABC transporter, ATP-BP {Mj} 63 ATP-BP (yixH-2) {Bb} 54
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rplD) {Bb} 100 factor (nusG) {Ec} 65 BB490 ribosomal prt L5 (rplE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} (greA) {Ec} 56 BB390 ribosomal prt L7/L12 (rplL) {Sc} 75 BB456 transcription factor, put {Mx} 47 BB112 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L7/L12 (rplL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (efp) {Ec} 57 BB496 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB122 translation elongation factor P (efp) {Ec} 61 BB196 ribosomal prt L9 (rplI) {Ec} 57 BB496 ribosomal prt L10 (rplI) {Bs} 61 BB192 ribosomal prt L10 (rplI) {Bs} 61 BB192 ribosomal prt L115 (rplO) {Bs} 68 ribosomal prt L16 (rplO) {Bs} 68 ribosomal prt L17 (rplO) {Ec} 63 BB590 dimethyladenosine Tase BB699 ribosomal prt L19 (rplS) {Ec} 74 BB792 ABC transporter, ATP-BP {Bs} 69 BB990 dimethyladenosine Tase BB188 ribosomal prt L19 (rplS) {Ec} 70 B8466 ABC transporter, ATP-BP {BI} 69 BB490 ribosomal prt L21 (rplU) {Ec} 58 BB754 ABC transporter, ATP-BP {BI} 69 BB490 ribosomal prt L22 (rplV) {Bb} 60 BB269 ATP-BP {VykH-1) {Bb} BB490 ribosomal prt L23 (rplW) {Bb} 60 BB269 ATP-BP {VykH-1) {Bb} BB490 ribosomal prt L24 (rplX) {Ec} 64 BB490 ribosomal prt L24 (rplX) {Ec} 64 BB490 ribosomal prt L24 (rplX) {Ec} 64 BB490 ribosomal prt L27 (rplX) {Ec} 64 BB490 ribosomal prt L27 (rplX) {Ec} 64 BB260 ABC transporter, ATP-BP {Mj} BB490 ribosomal prt L27 (rplX) {Ec} 64 BB260 ABC transporter, ATP-BP {Mj} BB490 ribosomal prt L27 (rplX) {Ec} 64 BB490 ribosomal prt L27 (rplX) {Ec} 64 BB260 ABC tra	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G {Fv} 70 translation elongation factor B (fus-2) {Tm} 67 translation elongation factor G translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (yixH-1) {Bb} 100 ATP-BP (yixH-2) {Bb} 54 ABC transporter, ATP-BP {Mj} 63 ATP-BP (yixH-2) {Bb} 54
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) {Bb} 100 BB214 translation elongation factor P (greA) {Ec} 56 BB390 ribosomal prt L5 (rpIE) {HI} 80 BB214 translation elongation factor P (efp) {Ec}	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G {Fv} 70 translation elongation factor B (fus-2) {Tm} 67 translation elongation factor G translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {Syn} 57 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (yixH-1) {Bb} 100 ATP-BP (yixH-2) {Bb} 54 ABC transporter, ATP-BP {Mj} 63 ATP-BP (yixH-2) {Bb} 54
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) {Bb} 100 BB214 translation elongation factor P (greA) {Ec} 56 BB390 ribosomal prt L5 (rpIE) {HI} 80 BB214 translation elongation factor P (efp) {Ec}	tRIVA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 1 (infA) {Ec} 87 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G (fus-2) {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor TS (tsf) {Hi} 75 translation elongation factor TS (tsf
BB394 transcription antitermination factor (nusG) {Ec} 64 BB490 ribosomal prt L4 (rpID) {Bb} 100 factor (nusG) {Ec} 64 BB490 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} Ec} BB392 ribosomal prt L5 (rpIE) {Hi} 80 BB214 translation elongation factor P (efp) {Ec} Ec} BB393 ribosomal prt L7/L12 (rpIL) {Sc} 75 BB476 translation elongation factor P (efp) {Ec} Ec} BB390 ribosomal prt L9 (rpII) {Ec} 57 BB476 translation elongation factor TU (tuf) {Bb} BB391 ribosomal prt L10 (rpII) {Bs} 61 BB122 translation elongation factor TU (tuf) {Bb} BB393 ribosomal prt L11 (rpIK) {Tm} 73 BB486 ribosomal prt L14 (rpIN) {Tm} 79 Factor (papS) {BS} Factor	tRNA pseudouridine 55 Sase (truB) {Ec} 57 tion factors GTP-B membrane prt (lepA) {Hi} 76 peptide chain release factor 1 (prfA) Hi} 73 peptide chain release factor 2 (prfB) {Sc} 70 ribosome releasing factor (frr) {Mt} 68 translation initiation factor 2 (infB) {Bs} 73 translation initiation factor 2 (infB) {Bs} 73 translation elongation factor G {fus-2} {Tm} 67 translation elongation factor P (efp) {Ec} 56 translation elongation factor TU (tuf) {Bb} 100 translation elongation factor TS (tsf) {Hi} 57 translation elongation factor G G (fus-1) {Tm} 68 ABC transporter, ATP-BP {Bs} 53 ABC transporter, ATP-BP {Bl} 60 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ykH-1) {Bb} 100 ATP-BP (ykH-1) {Bb} 100 ATP-BP (ykH-1) {Bb} 54 ABC transporter, ATP-BP {Mj} 63 ATP-BP (ykH-1) {Bb} 100 ATP-BP (ykH-1) {Bb} 100 ATP-BP (ykH-1) {Bb} 55 glutamate transporter (gltP) {Bs} 55 glutamate transporter, put {Bs} 55

	(proV) {Sc}	71		{Mg}	56	BB586	femA prt (femA) {Se}	47
BB145	GBP ABC transporter, permease		BB557	phosphocarrier prt HPr		BB141	membrane fusion prt (mtrC) {Hi}	47
	prt (proW) {Ec}	66		(ptsH-2) {Hi}	69	<u>lp28-4</u>		
BB144	GBP ABC transporter, BP		BB558	phosphoenolpyruvate-prt PPase		BBI26	multidrug-efflux transporter {Hp}	55
	(proX) {Ec}	43		(ptsl) {Sc}	65			
BB334	OP ABC transporter,		BB408	PTS system, fru-specific IIABC		<u>lp25</u>		
	ATP-BP (oppD) {Bs}	75		(fruA-1) {Ec}	65	BBE22	pyrazinamidase/nicotinamidase	
BB335	OP ABC transporter, ATP-BP		BB629	PTS system, fru-specific IIABC			(pncA) {Mt}	56
	(oppF) {Bs}	80		(fruA-2) {Ec}	68			
BB332	OP ABC transporter, permease prt		BB559	PTS system, glu-specific IIA		Transpo	oson-related functions	
	(oppB-1){Ec}	68		(crr) {Bb}	100			
BB747	OP ABC transporter, permease prt		BB645	PTS system, glu-specific IIBC		<u>lp38</u>		-//
DDooo	(oppB-2){Bs}	54	DD440	(ptsG) {Sc}	67	BBJ05	transposase-like prt, put {Bb}	89
BB333	OP ABC transporter, permease		BB116	PTS system, mal/glu-specific				
DD740	prt (oppC-1){Hi}	64	DD077	IIABC (malX) {Ec}	56	<u>lp36</u>	to a constant (DI)	00
BB746	OP ABC transporter, permease	F0	BB677	RG ABC transporter, ATP-BP	00	BBK25	transposase-like prt, put {Bb}	80
DDOOO	prt (oppC-2){Bs}	52	DDC70	(mglA) {Mg}	68	I=-00 1		
BB328	OP ABC transporter, periplasmic BP		BB678	RG ABC transporter,	F4	<u>lp28-1</u> BBF18	transposase-like prt, put {Bb}	96
		74	BB679	permease prt (rbsC-1) {Mg}	51	BBF19	transposase-like prt, put {Bb}	96
BB329	(oppA-1) {Bb} OP ABC transporter,	/4	DD0/9	RG ABC transporter, permease prt (rbsC-2) {Mp}	52	DDF19	transposase-like prt, put {bb}	90
DDSZS	periplasmic BP (oppA-2) {Bb}	94		permease pit (rbso-z) (wp)	52	lp28-2		
BB330	OP ABC transporter,	34	<u>cp26</u>				transposase-like prt {Bb}	99
DDSSU	periplasmic BP (oppA-3) {Bb}	81	BBB04	PTS system, cello-specific		DDG00	transposase-like pit (bb)	33
BB642	SP ABC transporter, ATP-BP	01	DDD04	IIC (celB) {Bs}	62	lp28-3		
DDOTE	(potA) {Ec}	69	BBB05	PTS system, cello-specific	02	BBH40	transposase-like prt, put {Bb}	57
BB641	SP ABC transporter, permease prt	00	DDDOO	IIA (celC) {Bs}	61	טרו ושם	transposase like prt, put (bb)	07
ББОТІ	(potB) {Ec}	65	BBB06	PTS system, cello-specific		lp17		
BB640	SP ABC transporter, permease prt	00	55500	IIB (celA) {Bs}	73		transposase-like prt, put {Bb}	99
550.0	(potC) {Ec}	63	BBB29	PTS system, glu-specific			transposase-like prt, put {Bb}	88
BB639	SP ABC transporter, periplasmic			IIBC, put {Ec}	70			
				.,,,,				
	BP (potD) {Ec}	53				Unknow	/n	
	BP (potD) {Ec}	53	Cations			Unknow BB528		57
<u>lp54</u>	BP (potD) {Ec}	53	Cations BB724	K+ transport prt (ntpJ) {Eh}	60		In aldose RDase, put (Bs) carotenoid biosyn prt, put (Ss)	57 58
<u>lp54</u> BBA34	. , , ,	53		K+ transport prt (ntpJ) {Eh} Mg2+ transport prt (mgtE) {Bb}	60 100	BB528	aldose RDase, put {Bs}	58
<u>lp54</u> BBA34	BP (potD) {Ec} OP ABC transporter, periplasmic BP (oppA-4) {Bc}	53 66	BB724			BB528 BB684	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss}	58 99 54
<u>lp54</u> BBA34	OP ABC transporter,		BB724 BB380	Mg2+ transport prt (mgtE) {Bb}	100	BB528 BB684 BB671	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb}	58 99 54 53
BBA34 cp26	OP ABC transporter, periplasmic BP (oppA-4) {Bc}		BB724 BB380 BB164 BB447 BB637	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf}	100 59	BB528 BB684 BB671 BB250 BB168 BB508	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp}	58 99 54 53 59
BBA34	OP ABC transporter,	66	BB724 BB380 BB164 BB447	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh}	100 59 57	BB528 BB684 BB671 BB250 BB168 BB508 BB219	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx}	58 99 54 53 59 54
BBA34 cp26	OP ABC transporter, periplasmic BP (oppA-4) {Bc}		BB724 BB380 BB164 BB447 BB637 BB638	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf}	100 59 57 48	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi}	58 99 54 53 59 54 58
BBA34 <u>cp26</u> BBB16	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter,	66	BB724 BB380 BB164 BB447 BB637 BB638	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi}	100 59 57 48 50	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP (Tp) gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs}	58 99 54 53 59 54
BBA34 cp26 BBB16 Anions	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb}	66	BB724 BB380 BB164 BB447 BB637 BB638	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf}	100 59 57 48	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP (Tp) gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide	58 99 54 53 59 54 58 47
BBA34 <u>cp26</u> BBB16	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter,	66 78	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi} chromate transport prt, put {Mj}	100 59 57 48 50	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj}	58 99 54 53 59 54 58
Cp26 BBB16 Anions BB218	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa)	66	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi} chromate transport prt, put {Mj} ategories	100 59 57 48 50	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide	58 99 54 53 59 54 58 47
BBA34 cp26 BBB16 Anions	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt	66 78 74	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other ca <i>Adaptati</i>	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi} chromate transport prt, put {Mj} ategories ions and atypical conditions	100 59 57 48 50	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi}	58 99 54 53 59 54 58 47 49
Cp26 BBB16 Anions BB218 BB216	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt (pstC) {Ec}	66 78	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other ca <i>Adaptat</i> BB237	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm)	100 59 57 48 50 58	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh}	58 99 54 53 59 54 58 47 49 62 53
Cp26 BBB16 Anions BB218	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease	66 78 74 58	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other ca Adaptata BB237 BB786	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs)	100 59 57 48 50 58	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb}	58 99 54 53 59 54 58 47 49 62 53 100
Cp26 BBB16 Anions BB218 BB216 BB217	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt (pstC) {Ec} P ABC transporter, permease prt (pstA) {Syn}	66 78 74	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other C <i>Adapta</i> BB237 BB786 BB785	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi} chromate transport prt, put {Mj} ategories ions and atypical conditions acid-inducible prt (act206) {Rm} general stress prt (ctc) {Bs} stage V sporulation prt G {Bm}	100 59 57 48 50 58	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB363	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb}	58 99 54 53 59 54 58 47 49 62 53 100 100
Cp26 BBB16 Anions BB218 BB216	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt (pstC) {Ec} P ABC transporter, permease prt (pstA) {Syn} P ABC transporter, periplasmic	66 78 74 58 63	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other ca Adaptata BB237 BB786	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi} chromate transport prt, put {Mj} ategories ions and atypical conditions acid-inducible prt (act206) {Rm} general stress prt (ctc) {Bs} stage V sporulation prt G {Bm} virulence factor mviN prt	100 59 57 48 50 58 45 51 74	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB035 BB336 BB336 BB333 BB033	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} pr15 prt {Mh} p26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp}	58 99 54 53 59 54 58 47 49 62 53 100 100 70
Cp26 BBB16 Anions BB218 BB216 BB217	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt (pstC) {Ec} P ABC transporter, permease prt (pstA) {Syn}	66 78 74 58	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other C <i>Adapta</i> BB237 BB786 BB785	Mg2+ transport prt (mgtE) {Bb} Na+/Ca+ exchange prt, put {Mj} Na+/H+ antiporter (napA) {Eh} Na+/H+ antiporter (nhaC-1) {Bf} Na+/H+ antiporter (nhaC-2) {Hi} chromate transport prt, put {Mj} ategories ions and atypical conditions acid-inducible prt (act206) {Rm} general stress prt (ctc) {Bs} stage V sporulation prt G {Bm}	100 59 57 48 50 58	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB333 BB033 BB033 BB297	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100
Cp26 BBB16 Anions BB218 BB216 BB217 BB215	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn)	66 78 74 58 63	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other Ct Adaptat. BB237 BB786 BB785 BB810	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi)	100 59 57 48 50 58 45 51 74	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB035 BB336 BB336 BB333 BB033	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} pr15 prt {Mh} p26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp}	58 99 54 53 59 54 58 47 49 62 53 100 100 70
EBA34 CD26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn)	66 78 74 58 63	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other Ct <i>Adaptat</i> BB237 BB785 BB785 BB810	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi)	100 59 57 48 50 58 45 51 74	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB363 BB363 BB033 BB297 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100
Cp26 BBB16 Anions BB218 BB216 BB217 BB215	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt (pstC) {Ec} P ABC transporter, permease prt (pstA) {Syn} P ABC transporter, periplasmic P-BP (pstS) {Syn}	78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other ca <i>Adaptat</i> BB237 BB786 BB786 BB786 BB786	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put [Mj] Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put [Mj] ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put [Hi]	100 59 57 48 50 58 45 51 74	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB336 BB336 BB336 BB336 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
BBA34 Cp26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) **Contact Contact C	66 78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other Ct <i>Adaptat</i> BB237 BB785 BB785 BB810	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put (Hi) outer membrane integrity prt	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB363 BB363 BB033 BB297 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100
Cp26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240 BB604	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) varates, organic alcohols, and acids glycerol uptake facilitator (glpF) (Bs) L-lactate permease (lctP) (Ec)	78 74 58 63 48	BB724 BB380 BB164 BB4647 BB637 BB638 Other BB451 Other ca Adaptat BB237 BB786 BB786 BB786 BB786	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put [Mj] Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put [Mj] ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put [Hi]	100 59 57 48 50 58 45 51 74	BB528 BB684 BB671 BB250 BB 168 BB508 BB219 BB421 BB524 BB702 BB045 BB336 BB363 BB033 BB033 BB033 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
BBA34 Cp26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) **Cransporter*, periplasmic P-BP	66 78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other Ct <i>Adaptat</i> BB237 BB785 BB785 BB810 <i>Colicin-t</i> BB766 BB546	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) stegories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put (Hi) outer membrane integrity prt (tolA) (Hi)	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB333 BB297 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mi} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs} thy1 prt (thy1) {Dd}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
Cp26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240 BB604	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) varates, organic alcohols, and acids glycerol uptake facilitator (glpF) (Bs) L-lactate permease (lctP) (Ec)	66 78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other Ct <i>Adaptat</i> BB237 BB785 BB785 BB810 <i>Colicin-t</i> BB766 BB546	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put (Hi) outer membrane integrity prt	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB 168 BB508 BB219 BB421 BB524 BB702 BB045 BB336 BB363 BB033 BB033 BB033 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
Cp26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240 BB604	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) ordrates, organic alcohols, and acids glycerol uptake facilitator (glpF) (Bs) L-lactate permease (lctP) (Ec) methylgalactoside ABC transporter, ATP-BP	78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other ca <i>Adaptat</i> BB237 BB786 BB785 BB810 <i>Colicin-t</i> BB766 BB546	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) Chromate transport prt, put (Mj) Ategories Ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) Telated functions colicin V production prt, put (Hi) outer membrane integrity prt (tolA) (Hi)	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB333 BB033 BB033 BB033 BB297 BB443	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mi} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs} thy1 prt (thy1) {Dd}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
CD26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240 BB604 BB318	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) (drates, organic alcohols, and acids glycerol uptake facilitator (glpF) (Bs) L-lactate permease (lctP) (Ec) methylgalactoside ABC transporter, ATP-BP (mglA) (Hi)	78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other ca <i>Adaptat</i> BB237 BB786 BB785 BB810 <i>Colicin-t</i> BB766 BB546	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put (Hi) outer membrane integrity prt (tolA) (Hi) rd analog sensitivity acriflavine resistance prt	100 59 57 48 50 58 45 51 74 51 52 44	BB528 BB684 BB671 BB250 BB 168 BB508 BB219 BB421 BB524 BB702 BB045 BB336 BB363 BB033 BB297 BB443 Ip54 BBA76	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mi} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs} thy1 prt (thy1) {Dd}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
CD26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240 BB604 BB318	OP ABC transporter, periplasmic BP (oppA-4) (Bc) OP ABC transporter, periplasmic BP (oppA) (Bb) P ABC transporter, ATP-BP (pstB) (Pa) P ABC transporter, permease prt (pstC) (Ec) P ABC transporter, permease prt (pstA) (Syn) P ABC transporter, periplasmic P-BP (pstS) (Syn) varates, organic alcohols, and acids glycerol uptake facilitator (glpF) (Bs) L-lactate permease (lctP) (Ec) methylgalactoside ABC transporter, ATP-BP (mglA) (Hi) pantothenate permease (panF)	78 74 58 63 48 57 57 54	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other Ct Adaptat. BB237 BB786 BB785 BB810 Colicin-1 BB766 BB546 Drug an BB140	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put (Mj) Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mj) ategories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put (Hi) outer membrane integrity prt (tolA) (Hi) d analog sensitivity acriflavine resistance prt (acrB) (Hi)	100 59 57 48 50 58 45 51 74 51 52 44	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB336 BB336 BB336 BB443 Ip54 BBA76 Ip28-4 BB106	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPPase {Hs} lipopolysaccharide biosyn-related prt {Mi} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs} thy1 prt (thy1) {Dd}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56
BBA34 Cp26 BBB16 Anions BB218 BB216 BB217 BB215 Carbohy BB240 BB604 BB318 BB814	OP ABC transporter, periplasmic BP (oppA-4) {Bc} OP ABC transporter, periplasmic BP (oppA) {Bb} P ABC transporter, ATP-BP (pstB) {Pa} P ABC transporter, permease prt (pstC) {Ec} P ABC transporter, permease prt (pstA) {Syn} P ABC transporter, periplasmic P-BP (pstB) {Syn} vortates, organic alcohols, and acids glycerol uptake facilitator (glpF) {Bs} L-lactate permease (lctP) {Ec} methylgalactoside ABC transporter, ATP-BP (mglA) {Hi} pantothenate permease (panF) {Ec}	78 74 58 63 48 57 57 54	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other Ct Adaptat. BB237 BB786 BB785 BB810 Colicin-1 BB766 BB546 Drug an BB140	Mg2+ transport prt (mgtE) (Bb) Na+/Ca+ exchange prt, put [Mi] Na+/H+ antiporter (napA) (Eh) Na+/H+ antiporter (nhaC-1) (Bf) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put [Mi] stegories ions and atypical conditions acid-inducible prt (act206) (Rm) general stress prt (ctc) (Bs) stage V sporulation prt G (Bm) virulence factor mviN prt (mviN) (Hi) related functions colicin V production prt, put (Hi) outer membrane integrity prt (tolA) (Hi) rd analog sensitivity acriflavine resistance prt (acrB) (Hi) bacitracin resistance prt	100 59 57 48 50 58 45 51 74 51 52 44	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB336 BB336 BB336 BB443 Ip54 BBA76 Ip28-4 BB106	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss} chemotaxis operon prt (cheX) {Bb} dedA prt (dedA) {Ec} dnaK suppressor, put {Ec} GTP-BP {Tp} gufA prt {Mx} hydrolase {Hi} inositol monoPase {Hs} lipopolysaccharide biosyn-related prt {Mj} lipopolysaccharide biosyn-related prt {Hi} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb} small prt (smpB) {Rp} smg prt {Bb} spollIJ-associated prt (jag) {Bs} thy1 prt (thy1) {Dd} pfs prt (pfs) {Ec} rev prt (rev) {Bb}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100 56 68