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 genitalium*²¹. 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 Riley²³). 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 ames 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

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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	

lasmids	
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%)	
00	

Intergenic sequence (29%)
430 coding sequences
70 (16%) with identified database match
110 (26%) match hypothetical proteins
250 (58%) with no database match

Ribosomal RNA	Chromosome coordinates
16S	444581-446118
23\$	438590-441508
5S	438446-438557
23S	435334-438267
5S	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 stem—loop 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

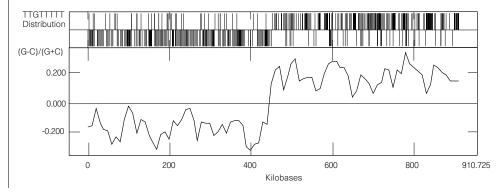


Figure 2 Distribution of TTGTTTTT and GC skew in the *B. burgdorferi* chromosome. Top, distribution of the octamer TTGTTTTT. The lines in the top panel represent the location of this octamer in the plus strand of the sequence, and those in the second panel represent the location of this oligomer in the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

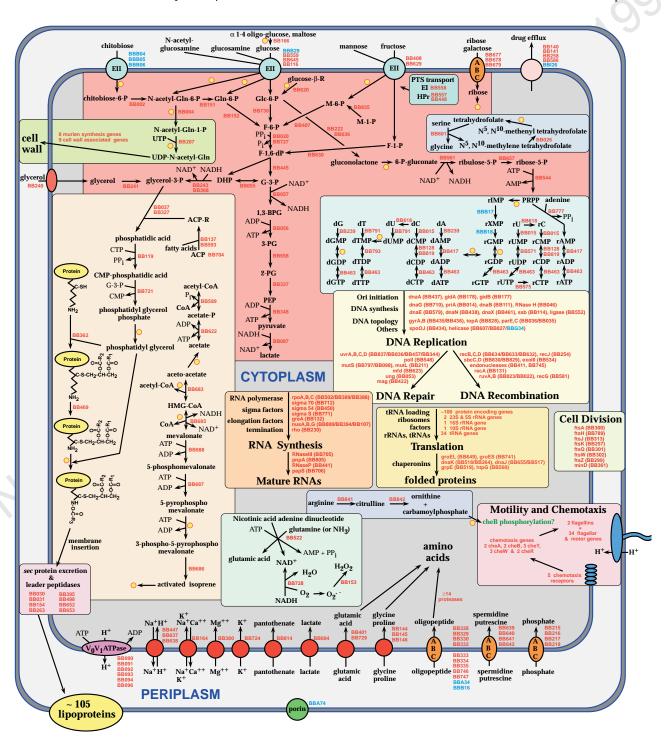


Figure 3 Solute transport and metabolic pathways in *B. burgdorferi*. A schematic diagram of a *B. burgdorferi* cell providing an integrated view of the transporters and the main components of the metabolism of this organism, as deduced from the genes identified in the genome. The ORF numbers correspond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

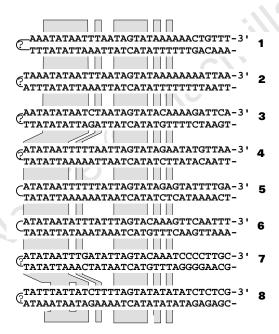


Figure 4 Telomere nucleotide sequences from *Borrelia* species. Nucleotide sequences are shown for known *Borrelia* telomeres as indicated: 1,*B. burgdorferi* Sh-2-82 chromosome left end; 2, *B. burgdorferi* B31 chromosome left end; 3, *B. afzelii* R-IP3 chromosome right end; 4, *B. burgdorferi* B31 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}.

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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.

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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).



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B8319 B8347 B8442 B8395 B8603 B8753	exported prt (tps%b) (Tp) **tbranedin (tbrin ogen BP, put (Sp) inner membrane prt (Hi) ipoprotein LA7 (Bb) membrane-associated prt ps% (Bb) membrane-associated prt put (Se)	50 53 63 100 100 40		igese (murD) (Be) UDP-N-X cruremoylelenyt- D-glutamete-2,6: deminopimelete igese (murE) (Hi) UDP-N-X cruremoylelenyt-0- gutamyt-2,6-demino-pimelete- D-elenyt-0-elenine igese	153	BB567 BB869	chamotosse histoline Keee (chext.1) (Bb) chamotosse histoline Keee (chext.2) (Bb) chamotosse prt MTeee (chext.1) (Re) chamotosse prt MTeee (chext.2)	100 61
B8319 B8347 B8442 B8395 B8603 B8753 B8753 B8755	exported prt (tps%b) (Tp) thraneoth (tbnfogen-SP, put (Sp) inner membrane prt (H) ipoprotein L.47 (Sb) membrane-accordated prt ps% (Sb) membrane-accordated prt put (Se) outer membrane-prt (Ng)	50 53 63 100 100 40 48	BB304	igese (murD) (Bo) UDP-N-A cruremoylelenyl- Deglatemate-2,8- deminopimelete igese (murE) (Hi) UDP-N-A cruremoylelenyl-D- glutemyl-2,8-dismino-pimelete- Delenyl-D-elenine igese (murE) (Bb)		88667 88869 88040 88414	chamotosis histoline Keele (chell 1) (Bb) chamotosis histoline Keele (chell 2) (Bb) chamotosis prt MTeele (chell-1) (Bo) chamotosis prt MTeele (chell-2) (Bm)	100
B8319 B8347 B8442 B8395 B8603 B8753	exported prt (tps%b) (Tp) thraneoth (tbrinogen-SP, put (Sp) inner membrene prt (H) lipoprotein LA7 (Bb) membrene-secodiated prt p8 (Bb) membrene-secodiated prt (Se) membrene-seconing prt put (Se) outer membrene prt (Ng) outer membrene prt (tps%) (Tp)	50 53 63 100 100 40		igese (murD) (Bs) UDP-N-A criuremoylelenyl- Deylutemate-2,8- deminopimelete igese (murE) (Hi) UDP-N-A criuremoylelenyl-D- glutemyl-2,8-dismino-pimelete- D-slenyl-D-elenine igese frunf (Bb) UDP-N-A cgluccesmine-N-	153	BB567 BB869 BB040	ohemotasse histoline Keee (ohek 1) (Bb) ohemotasse histoline Keee (cheel 2) (Bb) ohemotasse prt MTeee (cheR-1) (Re) ohemotasse prt MTeee (cheR-2) (Rm) ohemotasse preponee reguletor	100 61
BB319 BB347 BB342 BB395 BB395 BB753 BB753 BB755 BB167	exported prt (tps%b) (Tp) thraneoth (tbnfogen-SP, put (Sp) inner membrane prt (H) ipoprotein L.47 (Sb) membrane-accordated prt ps% (Sb) membrane-accordated prt put (Se) outer membrane-prt (Ng)	50 50 100 100 40 40 40 50	BB304	igese (murD) (Bo) UDP-N-A cruremoylelenyl- Deglatemate-2,8- deminopimelete igese (murE) (Hi) UDP-N-A cruremoylelenyl-D- glutemyl-2,8-dismino-pimelete- Delenyl-D-elenine igese (murE) (Bb)) 53 100	88667 88869 88040 88414	chamotosis histoline Keele (chell 1) (Bb) chamotosis histoline Keele (chell 2) (Bb) chamotosis prt MTeele (chell-1) (Bo) chamotosis prt MTeele (chell-2) (Bm)	100 61 57 74
BB319 BB347 BB346 BB396 BB396 BB753 BB755 BB167 BB167 BB167	exported prt (tps@b) (Tp) thraneoth (tbringen-Br, put (Sp) inner membrene prt (H) ipoprotein LA7 (Bb) membrene-excodeted prt p8 (Bb) membrene-excodeted prt p8 (Bb) membrene-expending prt put (Se) outer membrene prt (Ng) outer membrene prt (tps@) (Tp) men (poprt A (tps.) (H) put 1 (tps.) (Mb) prt 1 (tps.) (Mb)	50 50 100 100 48 48 53 48	BB304	igese (murb) (Bs) UDP-N-A criver moylelen yl- Dejistemete-2,6 deminopmete igese (mur E) (Hi) UDP-N-A criver moylelen yl-D- glutamyl-2,6-dismino-pimelete- Delanyl-D-alanine igese (murf) (Bb) UDP-N-A cglucceamine-N- Acmuramyl-(pentapeptide)	153	BB667 BB669 BB040 BB414 BB651 BB670	chamictorio histoline Keele (chall 1) (Bb) chamictorio histoline Keele (chall 2) (Bb) chamictorio pri Millere (chall 1) (Be) chamictorio pri Millere (chall 2) (Bm) chamictorio response regulator (chall (Bb) chamictorio (chall (Bb) chamictorio (chall (Bb)	100 61 57
B8319 B8347 B8442 B8395 B8603 B8703 B8705 B8167 B8735	exported prt (tpnStb) (Tp) throu edin fibrin ogenEP, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane essociated prt pst (Bb) membrane expansing prt put (Se) outer membrane prt (Ng) outer membrane prt (tpnSt) (Tp) are ipoprt A (fpA) (H) surfacel coated membrane	50 50 100 100 40 40 40 50	BB304 BB767	igase (murD) (Bs) UDP-N-A criuremoylelenyl- Deylutemate-2,8- deminopimelete igase (murE) (Hi) UDP-N-A criuremoylelenyl-D- glutemyl-2,8-dismino-pimelete- glutemyl-2,8-dismino-pimelete- D-alenyl-D-alenine igase frunf (Bb) UDP-N-A cgluccesmine-N- Acmuremyl-(pertapeptide) pyr cphosphoryl-undesprend NAG Tase (murG) (Bs)	153 100 58	BB667 BB669 BB040 BB414 BB651 BB670	ohemotasse histoline Keele (oheAL) (Bb) ohemotasse histoline Keele (dheR-2) (Bb) ohemotasse prt MTeele (dheR-2) (Fin) ohemotasse prt MTeele (dheR-2) (Fin) ohemotasse preparee regulator (oheY-1) (Tip) ohemotasse response regulator (oheY-2) (Fin)	100 61 57 74 70
B8319 B8347 B8346 B8395 B803 B8753 B8795 B8167 B8167 B8167 B8167	exported prt (tps@b) (Tp) thraneoth (tbringen-Br, put (Sp) inner membrene prt (H) ipoprotein LA7 (Bb) membrene-excodeted prt p8 (Bb) membrene-excodeted prt p8 (Bb) membrene-expending prt put (Se) outer membrene prt (Ng) outer membrene prt (tps@) (Tp) men (poprt A (tps.) (H) put 1 (tps.) (Mb) prt 1 (tps.) (Mb)	50 50 100 100 48 48 53 48	BB304 BB767 Surfece	igese (murb) (Be) UDP-N-A criuremoylelenyl- Dejistemete-2,8- deminopmetete igese (mur E) (Hi) UDP-N-A criuremoylelenyl-D- glutemyl-2,8-dismino-pimelete- Delenyl-D-elenino-ligese (murf) (Bb) UDP-N-A criuremoylelenyl- Acmuremyl-(pertapeptide) pyriphosphoryl-undeceprend NACT-tee (murc) (Be) polysecchericles, ilipopolyseccheric	153 100 58	BB667 BB869 BB040 BB414 BB651 BB670 BB872	chemichasis histoline Keele (chell-1) (Bb) chemichasis histoline Keele (chell-2) (Bb) chemichasis prt Millere (chell-1) (Re) chemichasis response regulator (chell-1) (Tip) chemichasis response regulator (chell-1) (Tip) chemichasis response regulator (chell-1) (Tip) chemichasis response regulator (chell-1) (Bb)	100 61 57 74 70 98
BB319 BB347 BB346 BB396 BB396 BB753 BB755 BB167 BB167 BB167	exported prt (trnStb) (Trp) fitr an eath inthin agen EP, put (Sp) inner membrane prt (H) ipopratein LA7 (Bb) membrane associated prt pst (Bb) membrane apanning prt put (Se) outer membrane prt (Ng) outer membrane prt (trpSt) (Trp) arre-ipoprt A (trpA) (H) surface located membrane prt 1 (imp1) (Mh) St prt (Bb)	50 50 100 100 48 48 53 48	BB304 BB767	igase (murb) (Bs) UDF-HA couremoylelenyl- Deglatemostes-2,6- deminopimelete igase (murb) (Hi) UDF-HA couremoylelenyl-D- glatemyl-2,6-dismino-pimelate- Destryl-1,8-dismino-pimelate- Destryl-Dedenine igase (murf) (Bb) UDF-HA cylucosemine-N- Acmuremyl-(pertapeptide) pyr-chosphoryl-undeceprend NA Crase (murc) (Bs) polysecchericles, ilpopolyseccheric igens	153 100 58	BB667 BB669 BB040 BB414 BB651 BB670	chemichasis histoline Keele (chell-1) (Bb) chemichasis histoline Keele (chell-2) (Bb) chemichasis pot Millere (chell-1) (Be) chemichasis pot Millere (chell-2) (Bm) chemichasis pot Millere (chell-2) (Bm) chemichasis response regulator (chell-1) (Tb) chemichasis response regulator (chell-2) (Bm) chemichasis response regulator (chell-2) (Bm) chemichasis response regulator (chell-2) (Bb) (CTP-BP) (ere) (Bc)	100 61 57 74 70 88 88
B8319 B8347 B8345 B8365 B8365 B8705 B8706 B8167 B8706 B8153 B8153 B8153	exported prt (tps%b) (Tp) throseotin fibrinogen-BP, put (Sp) inner membrene prt (H) ilipoprotein LAT (Bb) membrene-associated prt p8 (Bb) urter membrene-prt (Ng) outer membrene-prt (Ng) outer membrene-prt (Ng) (IP) mere (popt A (NgA) (H) surface-located membrene- prt (Impl) (Mh) SC prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb)	50 50 100 100 48 48 55 48 50 94 100	BB3 04 BB7 67 Surfece	igese (murb) (Be) UDP-N-A criuremoylelenyl- Dejistemete-2,8- deminopmetete igese (mur E) (Hi) UDP-N-A criuremoylelenyl-D- glutemyl-2,8-dismino-pimelete- Delenyl-D-elenino-ligese (murf) (Bb) UDP-N-A criuremoylelenyl- Acmuremyl-(pertapeptide) pyriphosphoryl-undeceprend NACT-tee (murc) (Be) polysecchericles, ilipopolyseccheric	100 58 465	BB667 BB040 BB040 BB444 BB651 BB670 BB872 BB860 BB781 BB678	ohemotasse histoline Keele (oheAL) (Bb) ohemotasse histoline Keele (dheAL) (Bb) ohemotasse pit MTeele (dheAL) (Bb) ohemotasse pit MTeele (dheAL) (Bm) ohemotasse pit MTeele (dheAL) (Bm) ohemotasse response regulator (oheYL) (Tp) ohemotasse response regulator (oheYL) (Bm) ohemotasse response regulator (oheYL) (Bm) ohemotasse response regulator (oheYL) (Bm) (BC) (CTP-BP (end) (Bc) (CTP-BP (obe)) (Bd) (MC) pit (imqx-1) (Th)	100 61 57 74 70 88 88
B8319 B8347 B8346 B8396 B8795 B8795 B810 B8153 B8154 B8164 B8124 B8125 B810	exported prt (tps:%b) (Tp) fitron-edin fibrinogen-BP, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-associated prt p8 (Bb) membrane-associated prt p8 (Bb) cutar membrane prt (Ng) cutar membrane prt (tps:%) (Tp) oral ipoprt A (fbA) (H) surface-loosted membrane prt 1 (fmp1) (Mh) Sc prt (Bb) decorin BP A (dtpA) (Bb) ipoprotein (Bb) ipoprotein (Bb)	50 50 100 100 44 45 45 45 45 40 100 140 154	BB3 04 BB7 67 Sulface end end end BB7 44 BB6 72	igase (murD) (Bs) UDP-NA cruremoylelenyl- Deylthandre-2,8- deminopmelete igase (murE) (Hi) UDP-NA cruremoylelenyl-D- gutemyl-2,8-dismino-pimelete- Delenyl-D-elenine igase frumf (Bb) UDP-NA cylucceemine-N- Acturemyl-pente-peptide) pyr ophosphoryl-undeceprend NA Crase (murd) (Bs) polyseccherioler, ilpopolyseccheriol entigen, ps3/100 (Bb)	100 58 Wer 100	B9567 B9040 B9040 B9414 B9570 B9670 B9872 B9680 B978 B9578 B9578	chemotasia histoline Kees (chell 1) (Bb) chemotasia histoline Kees (chell 2) (Bb) chemotasia pot Millese (chell 1) (Ra) chemotasia pot Millese (chell 1) (Rin) chemotasia response regulator (chell 1) (Tip) chemotasia response regulator (chell 2) (Rin) (MTP-BP (chell (Bd) (MTP-BP (chell 2) (Tim) MC pot (mop-2) (Tid)	100 61 57 74 70 88 88
B8319 B8347 B8345 B8365 B8365 B8763 B8767 B8167 B8167 B8153 B8143 B81424 B81425 B81435 B81435	exported prt (tpnStb) (Tip) fibraneoth (tbntogenEP, put (Sp) inner membrane prt (H) ipopratein LA7 (Bb) membrane-associated prt pss (Bb) membrane-associated prt pss (Bb) outer membrane prt (Ng) outer membrane prt (tpnSt) (Tip) rare ipoprt A (tpA) (H) surface-located membrane prt 1 (imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipopratein (Bb) ipopratein (Bb) ipopratein (Bb)	50 50 100 100 48 48 55 45 80 94 100 154 100	88304 88767 Surfece end end 88744 88672 Ip54	igese (murD) (Bs) UDF-HA cruremoylelenyl- Degitremete-2,6- deminopimetete igese (murE) (Hi) UDF-HA cruremoylelenyl-D- glutemyl-2,6-demino-pimetete- Debryl-D-elenine igese (murF) (Bb) UDF-HA cylucosemine-N- Acmuremyl-(pertapeptide) pyr cyhosphoryl-undeceprend NACTese (murc) (Bs) polysecchericles, ilhopolyseccheric iges: entigen, psis (100 (Bb) glycosyl Tesee (gfD) (Hi)	100 58 Aer 100 58	B9567 B9869 B9040 B9444 B9571 B9572 B9680 B9781 B9678 B9696 B9697	chemichasis histoline Keele (cheul. 1) (Bb) chemichasis histoline Keele (cheul. 2) (Bb) chemichasis pit Miliese (cheil. 2) (Bb) chemichasis pit Miliese (cheil. 2) (Bm) chemichasis preparate regulator (cheil. 1) (Tb) chemichasis response regulator (cheil. 2) (Bm) chemichasis response regulator (cheil. 2) (Bm) chemichasis response regulator (cheil. 2) (Bb) (CTP-BP (cheil. 2) (Bc) (CTP-BP (cheil. 2) (Bc) (CTP-BP (cheil. 2) (Bd) (CTP-BP (cheil. 2) (Bd) (CTP-BP (cheil. 2) (Bd) (CTP-BP (cheil. 2) (Bd) (CTP-BP (cheil. 2) (CTP-B	100 81 57 74 70 88888558
B8319 B8347 B8346 B8396 B8795 B8795 B810 B8153 B8154 B8164 B8124 B8125 B810	exported prt (tps%b) (Tp) throseoth (tbrinogen-Br, put (Sp) inner membrane prt (H) ipoprotein L.47 (Bb) membrane-accodated prt p8 (Bb) membrane-accodated prt p8 (Bb) membrane-accodated prt p8 (Bb) curtar membrane prt (Ng) curtar membrane prt (Ng) curtar membrane prt (Ng) curtar membrane prt (Ng) (Utar membrane prt (Ng)) (Tp) rare ipoprit A (NgA) (H) surface-accasted membrane prt 1 (Imp1) (Mh) sc prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb)	50 50 100 100 44 45 45 45 45 40 100 140 154	BB3 04 BB7 67 Sulface end end end BB7 44 BB6 72	igase (murb) (Bs) UDP-NA cruremoylelenyl- Deylthandruremoylelenyl- Deylthandruremoylelenyl- deminopimelete igase (murb) (Hi) UDP-NA cruremoylelenyl-D- glutemyl-2,8-dismino-pimelete- Delenyl-D-elenine igase frumf (Bb) UDP-NA cglucosemine-N- Acturemyl-pentapopilde) pyr ophosphoryl-undeceprend NA Crase (murd) (Bs) Adjusectherides, ileopolysectherid gless entigen, pss/100 (Bb) glycosyl-Tese (lgtD) (Hi) entigen, PSS (Bb)	100 58 Wer 100	B9567 B9040 B9040 B9414 B9570 B9670 B9872 B9680 B978 B9578 B9578	chamidasse histoline Keele (cheul. 1) (Bb) chamidasse histoline Keele (cheul. 2) (Bb) chamidasse prt Millere (cheil. 2) (Bb) chamidasse prt Millere (cheil. 2) (Bm) chamidasse prt Millere (cheil. 2) (Bm) chamidasse response regulator (cheil. 1) (Bm) chamidasse response regulator (cheil. 2) (Bm) chamidasse response regulator (cheil. 2) (Bm) chamidasse response regulator (cheil. 2) (Bm) (CTP-BP (cheil.) (Bd) (CTP-BP (cheil.) (Bd) (CTP-BP (cheil.) (Bm) MC prt (mip-2) (Td) MC prt (mip-2) (Td) MC prt (mip-2) (Ed) (MC prt (mip-2) (Ed)	100 61 57 74 70 88 88
B8319 B8347 B8345 B8365 B8365 B8767 B8767 B8767 B8167 B8153 B8153 B8153 B8153 B8153 B8154 B8154 B8154 B8154 B8154 B8154 B8154 B8155 B8154	exported prt (truss b) (Tr) fitraneous historinogen EP, put (Sp) inner membrane prt (H) ipopratein LA7 (Bb) membrane-associated prt psk (Bb) membrane-associated prt psk (Bb) cutar membrane prt (Ng) cutar membrane prt (truss) (Tr) rere ipoprt A (frbA) (H) surface-located membrane prt 1 (impl) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipopratein (Bb) ipopratein (Bb) ipopratein (Bb) ipopratein (Bb) cutar membrane-prin (mess) (Bb)	50 53 100 100 48 48 55 45 60 94 100 100 100	88304 88767 Surfece end end 88744 88672 Ip54 883.64	igese (murD) (Bs) UDF-HA cruremoylelenyl- Degitremete-2,6- deminopimetete igese (murE) (Hi) UDF-HA cruremoylelenyl-D- glutemyl-2,6-demino-pimetete- Debryl-D-elenine igese (murF) (Bb) UDF-HA cylucosemine-N- Acmuremyl-(pertapeptide) pyr cyhosphoryl-undeceprend NACTese (murc) (Bs) polysecchericles, ilhopolyseccheric iges: entigen, psis (100 (Bb) glycosyl Tesee (gfD) (Hi)	100 58 46 100 58	B9567 B9040 B9040 B9670 B9670 B9872 B9678 B9678 B9678 B9696 B9696 B9690 B9880	chemichasis histoline Kees (chell 1) (Bb) chemichasis histoline Kees (chell 2) (Bb) chemichasis pit Milies (chell 1) (Rs) chemichasis pit Milies (chell 2) (Rm) chemichasis response regulator (chell 1) (Tb) chemichasis response regulator (chell 2) (Rm) chemichasis response regulator (chell 3) (Rm) chemichasis response regulator (chell 3) (Rb) (CTP-BP (chell) (Bc) (CTP-BP	100 ៩ ភ 14 10 និងសង្សាល់ង្គស្ន
B8319 B8347 B8345 B8365 B8365 B8765 B8167 B8167 B8153 B81424 B81425 B81425 B81435 B81435 B81434 B81434 B81434 B81434 B81434 B81434 B81434 B81434 B81434 B81434 B81434 B81434	exported prt (tps%b) (Tp) fibraneoth (thinogen-Br, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-accordated prt ps% (Bb) membrane-accordated prt ps% (Bb) cuter membrane prt (Ng) cuter membrane prt (Ng) cuter membrane prt (tps%) (Tp) rare ipoprt A (rbA) (H) surface-located membrane prt 1 (imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cuter membrane porin (mass) (Bb) cuter authore prt A (capA) (Bb)	50 53 80 100 100 48 48 53 45 80 94 100 100 100 100 100 100 100	BB3 04 BB7 67 Strife case and and 887 64 BB6 72 Ip54 BB1 64 BB1 68 BB1 73	igese (murb) (Be) UDF-H-A couremoylelenyl- Deglatemate-2,6- deminopmetete ligese (murb) (Hi) UDF-H-A couremoylelenyl-2- glatemyl-2,6-dismino-pmide- Delenyl-2-demine-ligese (murf) (Bb) UDF-H-A cyluccesmine-N- Acouremyl-(pertapepilde) pyriphoephoryl-undeceprend NAG Tese (murd) (Be) polysecoterioles, ilinopolysecoteriol glaces entigen, psi //100 (Bb) glycceyl Tese (grb) (Hi) entigen, RSE (Bb) entigen, RSE (Bb) entigen, RSE, put (Bb)	100 58 46 100 58 100 48	BB667 BB644 BB651 BB670 BB670 BB673 BB673 BB673 BB673 BB697	chamidasse hietstane Keee (chell 1) (Bb) chamidasse hietstane Keee (dhell 2) (Bb) chamidasse pit Millee (dhell 1) (Re) chamidasse pit Millee (dhell 2) (Rm) chamidasse pit Millee (dhell 2) (Rm) chamidasse response regulator (chell 1) (Tip) chamidasse response regulator (chell 2) (Rm) chamidasse response regulator (chell 3) (Rm) MC pat (mip 2) (Tid) MC pat (mip 2) (Tid) MC pat (mip 3) (Tid) MC pat (mip 4) (Ed)	100 ៩ ភ ។ ខ និងនិង្សិស្ត
B8319 B8347 B8345 B8365 B8365 B8705 B8167 B8167 B8163 B8163 B8163 B8163 B8163 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8164 B8166 B8166 B8166 B8166 B8166	exported prt (tps%b) (Tp) throseotin fibrinogen EP, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-escociated prt p8 (Bb) membrane-escociated prt p8 (Bb) membrane-panning prt put (Se) outer membrane prt (Ng) outer membrane prt (tps%) (Tp) rare ipoprt A (rbA) (H) surface-located membrane prt 1 (imp1) (Mh) SC prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer membrane porin (mass) (Bb) outer surface prt A (capA) (Bb) outer surface prt B (capB) (Bb)	50 53 100 100 48 48 53 45 80 94 100 100 100 100 99 99	58304 58767 30/fece 40/d 476 58744 58672 1054 588.64 588.63 588.73 1033	igase (murb) (Bs) UDP-N-A cruremoylelenyl- Deylthandruremoylelenyl- Deylthandruremoylelenyl- Geminopimelete igase (murb) (Hi) UDP-N-A cruremoylelenyl-D- glutemyl-2,8-dismino-pimelete Delenyl-D-elenine igase frumf (Bb) UDP-N-A cylucosemine-N- Acturemyl-(pentapopilde) pyr ophosphoryl-undeceprend NACT-tee (murd) (Bs) pulysescherioler, ilpopolysescheriol glers entigen, pss/100 (Bb) glycosyl Teee (gtD) (Hi) entigen, pss (Bb) entigen, pss, ptr (Bb) entigen, pss, ptr (Bb) entigen, pss, ptr (Bb) entigen, pss, ptr (Bb)	100 58 Aer 100 58 100 48 52	B9667 B8040 B8040 B8444 B9651 B9670 B872 B8660 B9673 B9636 B9636 B9637 B9637 B9637 B9637 B9637 B9637	chamidatio histoline Keele (chell 1) (Bb) chamidatio histoline Keele (chell 2) (Bb) chamidatio pit Miller (chell 2) (Bb) chamidatio pit Miller (chell 2) (Bn) chamidatio pit Miller (chell 2) (Bn) chamidatio preponse regulator (chell 2) (Bn) chamidatio response regulator (chell 2) (Bn) chamidatio response regulator (chell 2) (Bb) (CTP-BP (end) (Bd) (CTP-BP (end) (CTP	100 s 5 14 10 888885558588 8
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B8319 B8347 B8346 B8396 B8396 B8795 B8795 B8167 B8163	exported prt (tm:Stb) (Tip) fibraneoth introngen.ER, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-secolated prt pst (Bb) membrane-secolated prt pst (Bb) outer membrane prt (Ng) outer membrane prt (tm:Str) (Tip) are ipoprt A (ftpA) (H) surface-located membrane prt 1 (fmp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer secolated prt A (capA) (Bb) outer secolated prt A (capA) (Bb) outer secolated prt A (capA) (Bb) outer membrane prt (Bb) surfaced prt B (capB) (Bb) outer membrane prt (Bb) St prt (Bb) St prt (Bb)	50 50 50 100 100 48 48 50 45 100 100 100 100 100 100 100	583.04 587.67 Sulfece 400' 400 587.64 586.72 <u>Ip54</u> 588.64 588.63 588.73 <u>Ip69</u> 588.41 <u>Ip69</u> 588.41	igese (murD) (Be) UDF-H-A cruremoylelenyl- Deyluten to-2,6- deminopmetete igese (murE) (Hi) UDF-H-A cruremoylelenyl-D- glutenyl-2,6-diemino-pmidte- Delenyl-D-alenine igese (murF) (Bb) UDF-H-A cyluccesmine-N- Acruremyl-(pertexpeptide) pyrcphoephoryl-undeceprend NAG-Tese (murG) (Be) pulpsecchericler, ilpopulpseccheric gers entigen, psi/100 (Bb) glycceyl Tese (grD) (Hi) entigen, RSE (Bb) entigen, RSE, put (Bb) entigen, RSE, put (Bb) entigen, RSE, put (Bb) entigen, RSE, put (Bb)	100 58 Aer 100 58 100 48 52 47	B9567 B9040 B9040 B9444 B9571 B9573 B95731 B95731 B95731 B95731 B95731 B9595 B9597 B	chamotasis histoline Kees (chall 1) (Bb) chamotasis histoline Kees (chall 2) (Bb) chamotasis pit Milles (chall 1) (Rs) chamotasis pit Milles (chall 1) (Rm) chamotasis response regulator (chall 1) (Tp) chamotasis response regulator (chall 1) (Tp) chamotasis response regulator (chall 3) (Rm) chamotasis response regulator (chall 3) (Rm) chamotasis response regulator (chall 3) (Rs) MC pit (mq-1) (Rs) MC pit (mq-2) (Td) MC pit (mq-3) (Td) MC pit (mq-4) (Td) MC pit (mq-4	100 s 57 74 70 seesekirksek s 59 59
B8319 B8347 B8345 B8365 B8365 B8765 B8167 B8167 B8153 B81425 B81425 B81425 B81435	exported prt (tps%b) (Tp) throseotin (thinogen-BF, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-accordated prt ps% (Bb) membrane-accordated prt ps% (Bb) membrane-accordated prt ps% (Bb) cutar membrane prt (Ng) cutar membrane prt (Ng) cutar membrane prt (Ng) cutar membrane prt (Ng) surface-located membrane prt 1 (Imp1) (Mh) Sc prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cutar membrane prt (CB) cutar membrane prt (Bb) st prt (Bb)	50 53 83 100 100 48 48 53 46 80 94 100 100 100 100 100 100	583 04 587 67 50/74 09 40 04 00 587 44 586 74 588 164 588 13 1038 588 15 588 15 588 15 588 15	igese (murb) (Be) UDF-H-A cruremoylelenyl- Deyltren febr-2,6- deminopimelete igese (murE) (Hi) UDF-H-A cruremoylelenyl-2- glutemyl-2,6-diemino-pimelete Jederyl-2-dediemino-pimelete Debryl-D-elenine igese fmurF) (Bb) UDF-H-A cglucceamine-N- Acmuremyl-(pertapeptide) pyr cphoephoryl-undeceprend NAG Tese (murb) (Be) polysecchericles, ilinopolyseccheric igens entigen, psis /100 (Bb) glycceyl Tese (grD) (Hi) entigen, RSE (Bb) entigen, RSE, put (Bb) entigen, RSE, put (Bb) entigen, RSE, put (Bb) entigen, RSE, put (Bb) immunogenio-put PSF (Bb) immunogenio-put PSF (Bb) immunogenio-put PSF (Bb)	100 58 46 100 58 100 48 52 47 50	B9567 B9040 B9040 B9444 B9571 B9573	chamchasis histoline Kees (chall 1) (Bb) chamchasis histoline Kees (chall 2) (Bb) chamchasis prt Milles (chall 1) (Rs) chamchasis prt Milles (chall 1) (Rm) chamchasis response regulator (chall 1) (Tp) chamchasis response regulator (chall 1) (Tp) chamchasis response regulator (chall 2) (Rm) MC prt (mp 1) (Tm) MC prt (mp 2) (Td) MC prt (mp 2) (Td) MC prt (mp 3) (Td) MC prt (mp 4) (Ed) prt glutamate mathylectores (chall 2) (Rd) putine 8 chamchasis prt (chall 1) (Bb) putine 8 chamchasis prt (chall 2) (Ed)	100 8 57 74 70 8888855558888 88 59
B8319 B8347 B8345 B8365 B8365 B8767 B8167 B8167 B8168 B8143 B8143 B8143 B8143 B8143 B8143 B8143 B8143 B8143 B8143 B8143 B8144 B8146 B8146 B8146 B8146 B8146 B8146 B8146 B8146 B8146 B8146 B8146 B8146 B8146	exported prt (tm:Stb) (Tip) fibraneoth introngen.ER, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-secolated prt pst (Bb) membrane-secolated prt pst (Bb) outer membrane prt (Ng) outer membrane prt (tm:Str) (Tip) are ipoprt A (ftpA) (H) surface-located membrane prt 1 (fmp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer secolated prt A (capA) (Bb) outer secolated prt A (capA) (Bb) outer secolated prt A (capA) (Bb) outer membrane prt (Bb) surfaced prt B (capB) (Bb) outer membrane prt (Bb) St prt (Bb) St prt (Bb)	50 50 50 100 100 48 48 50 45 100 100 100 100 100 100 100	B8304 B8767 SUNFACE 4074 407 B8764 B8672 IP54 B83.64 B8673 B83.63 B83.13 ID53 B83.41 ID53 B83.65 B83.65 B83.65 B83.65 B83.65 B83.65 B83.65 B83.65 B83.65	igase (murb) (Bs) UDF-H-A cruremoylelenyl- Deyltemete-2,8- deminopimete-2,8- deminopimete-2,8- deminopimete-2,8- deminopimete-2,8- deminopimete-2,8- deminopimete-2,8- deminopimete- gutemyl-2,8-demino-pimete- Deshyl-Dedemino-pimete- jeace (murf) (Bb) UDF-H-A cylucosemino-N- Acmuremyl-(pentapepide) pyr-chosphoryl-undeceprend NACTese (murc) (Bs) purdprecchericles, inopalyseccheric jeace entigen, pss./100 (Bb) glycosyl Teses (gfD) (Hi) entigen, PSS (Bb) entigen, PSS (Bb) entigen, PSS, put (Bb) entigen, PSS, put (Bb) immunogenio-ptt PST (Bb) immunogenio-ptt PST (Bb) immunogenio-ptt PSS (Bb) immunogenio-ptt PSS (Bb) immunogenio-ptt PSS (Bb) immunogenio-ptt PSS (Bb)	100 58 46 100 58 100 48 52 47 50 99	BB6670 BB6670 BB670 BB670 BB673 BB673 BB673 BB673 BB673 BB673 BB673 BB631 BB631 BB631 BB631 BB631 BB631	chamchasis histoline Kees (chall 1) (Bb) chamchasis histoline Kees (chall 2) (Bb) chamchasis prt Milles (chall 1) (Rs) chamchasis prt Milles (chall 2) (Rm) chamchasis prt milles (chall 2) (Rm) chamchasis response regulator (chall 1) (Tb) chamchasis response regulator (chall 2) (Rm) MC prt (mp 1) (Tm) MC prt (mp 2) (Td) MC prt (mp 2) (Td) MC prt (mp 3) (Td) MC prt (mp 4) (Ed) MC prt (mp 4) (Ed) prt glutamate mathylesterese (chall 2) (Rd) putine B chamchasis prt (chall 4) (Ed) putine B chamchasis prt (chall 4) (Ed) putine B chamchasis prt (chall 4)	100 S 57 74 70 888887575858 88 59 58 88
B8319 B8347 B8345 B8365 B8365 B8765 B8167 B8167 B8163 B8163 B8163 B8163 B8163 B8164 B8165 B8165 B8166	exported prt (tps%b) (Tp) fibraneoth (thinogen-Br, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-accordated prt ps% (Bb) membrane-accordated prt ps% (Bb) membrane-accordated prt ps% (Bb) cutar membrane prt (Ng) cutar membrane prt (tps%) (Tp) rare ipoprt A (rbA) (H) surface-located membrane prt 1 (imp1) (Mh) Sc prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cutar membrane prt (capA) (Bb) cutar auriface prt A (capA) (Bb) cutar membrane prt (Bb) scr (Bb)	50 53 83 100 100 48 48 53 46 80 94 100 100 100 100 100 100 100 100 100 10	B8304 B8767 SWFe-ce 400/460 88744 B8464 B8466 B8473 IDS B8473 IDS B8475 B8475 B8475 B8475 B8475 B8475 B8475	igese (murb) (Be) UDF-H-A cruremoylelenyl- Deglatemate-2,6- deminopmetete igese (murb) (Hi) UDF-H-A cruremoylelenyl-2- glatemyl-2,6-disminopmide- Delenyl-2,6-disminopmide- Delenyl-Delenine igese (murf) (Bb) UDF-H-A cyluccesmine-N- Acnuremyl-(pertappide) pyriphoephoryl-undeceprend NAGTese (murd) (Be) polysectherioler, lipopolysectheriol gess entigen, psi/100 (Bb) glycceyl Tese (grb) (Hi) entigen, RSS, prt (Bb) entigen, RSS, prt (Bb) entigen, RSS, prt (Bb) immunogenioptt RSS, put (Bb)	100 58 465 100 58 100 48 52 47 50 99 97 71	B9567 B9040 B9040 B9444 B9571 B9573	chamchasis histoline Kees (chall 1) (Bb) chamchasis histoline Kees (chall 2) (Bb) chamchasis prt Milles (chall 1) (Rs) chamchasis prt Milles (chall 1) (Rm) chamchasis response regulator (chall 1) (Tp) chamchasis response regulator (chall 1) (Tp) chamchasis response regulator (chall 2) (Rm) MC prt (mp 1) (Tm) MC prt (mp 2) (Td) MC prt (mp 2) (Td) MC prt (mp 3) (Td) MC prt (mp 4) (Ed) prt glutamate mathylectores (chall 2) (Rd) putine 8 chamchasis prt (chall 1) (Bb) putine 8 chamchasis prt (chall 2) (Ed)	100 s 57 74 70 seesekirkstak s 59 58
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B8319 B8347 B8482 B8365 B8003 B8736 B8167 B8167 B8163 B81424 B81424 B81425 B81435 B81436 B81450 B81450 B81450 B81450 B81450 B81406 B81406 B81400 B8150 B8150	exported prt (tpn%b) (Tp) fibraneoth (thinogenER, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-associated prt p8 (Bb) membrane-associated prt p8 (Bb) cutar membrane prt (Ng) cutar membrane prt (tpn9) (Tp) rere ipoprt A (tpA) (H) surface-located membrane 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) cutar membrane prt B (capA) (Bb) cutar surface prt A (capA) (Bb) cutar membrane prt (Bb) cutar membrane prt (Bb) s2 prt (Bb) s2 prt (Bb) cutar membrane prt (Bb) s2 prt (Bb) cutar membrane prt (Bb)	50 53 81 100 100 48 48 48 59 46 60 100 100 100 100 100 100 100 100 100	B8304 B8767 SWMeca 4004 406 B8764 B8672 Ip54 B8A66 B8A73 Ip68 B8A73 Ip68 B8A73 B8A75 B8A75 B8A75 B8A75 B8A75 B8A75 B8A75	igese (murb) (Be) UDP-H-A cruremoylelenyl- Degletemete-2,6- deminopmetete igese (murb) (Hi) UDP-H-A cruremoylelenyl-D- gletemyl-2,6-diemino-pmete- gletemyl-2,6-diemino-pmete- Delaryl-D-demine igese (murb) (Bb) UDP-H-A cglucceamine-N- Acmuremyl-(pertepeptide) pyr-cphosphoryl-undeceprend NAC Tese (murb) (Be) polysecchericles, iliopolyseccheric gess entigen, pss/100 (Bb) glycceyl Tese (gtD) (Hi) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) entigen, RSS, pxt (Bb) immunogenio-pxt RSS, pxt (Bb)	100 58 46 100 58 100 48 52 47 50 99 97 71 49 68	B96-67 B98-69 B90-40 B94-14 B96-51 B96-70 B98-72 B98-60 B96-71 B9	chamchasis histoline Kees (chell 1) (Bb) chamchasis histoline Kees (chell 2) (Bb) chamchasis put Milles (chell 1) (Re) chamchasis put Milles (chell 1) (Rm) chamchasis response regulator (chell 1) (Tp) chamchasis response regulator (chell 1) (Tp) chamchasis response regulator (chell 1) (Rm) chamchasis response regulator (chell 2) (Rm) chamchasis response regulator (chell 2) (Rm) MC put (mcp-1) (Td) MC put (mcp-2) (Td) MC put (mcp-2) (Td) MC put (mcp-2) (Td) MC put (mcp-2) (Ed) put (mcp-3) (Ed) p	100 8 57 74 70 88 88 82 57 52 88 88 98 88 88 100 48 48 4
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B8319 B8347 B8482 B8365 B8705 B8705 B8167 B8165 B8143 B8	exported prt (tpn%b) (Tp) fibraneotin (thinogen-BF, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-associated prt p8 (Bb) membrane-associated prt p8 (Bb) cuter membrane prt (Ng) cuter membrane prt (Ng) cuter membrane prt (tpn20) (Tp) rere ipoprt A (tpA) (H) surface-located membrane prt 1 (imp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cuter membrane prt (appA) (Bb) cuter auriface prt A (capA) (Bb) cuter auriface prt B (appB) (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) st prt (Bb) surface-ipoprt P27 (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb) cuter membrane prt (Bb)	50 53 81 100 100 44 48 48 53 46 60 94 100 100 100 100 100 100 100 100 100 10	B8304 B8767 Sulfece 400'400 B8764 B8672 ID54 B8468 B8A73 ID33 B8H75 B8H75 B8H75 B8H75 B8H87 B8H87 B8H87 B8H87 B8H88	igese (murb) (Be) UDF-H-A cruremoylelenyl- Deglatemice-2,6- deminopmelete igese (murb) (Hi) UDF-H-A cruremoylelenyl-D- glatemyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- purphoephoryl-undeceprend NAG Tese (murd) (Be) pulphoephoryl-undeceprend NAG Tese (murd) (Be) antigen, PSC (Bb) entigen, PSC (Bb) entigen, PSC (Bb) entigen, PSC (ptr (Bb)) entigen, PSC (ptr (Bb)) entigen, PSC (ptr (Bb)) entigen, PSC (ptr (Bb)) immunogenio-ptr PSC (Bb) immunogenio-ptr PSC (Bb) immunogenio-ptr PSC (ptr (Bb)) immunogenio-ptr PSC (ptr (Bb))	100 58 46 100 58 100 48 52 47 50 99 97 71 71 88 49	B8667 B8040 B8040 B8444 B8670 B8670 B8670 B8670 B8600 B8670 B8600	chamchasis histotine Kees (chell 1) (Bb) chamchasis histotine Kees (chell 2) (Bb) chamchasis histotine Kees (chell 2) (Bb) chamchasis pot Milles (chell 1) (Re) chamchasis response regulator (chell 1) (Tp) chamchasis response regulator (chell 2) (Rm) chamchasis response regulator (chell 3) (Rm) chamchasis (Rm) chamchasis response regulator (chell 3) (Rm) chamchasis (Rm) chamchasis (Rm) chamchasis (Re) chamchasis (100 8 57 74 70 8888825528828 88 59 58 88 100 485458
B8319 B8347 B8346 B8396 B8396 B8796 B8197 B8196 B8143 B8	exported prt (tpn%b) (Tp) fibraneoth fibraneopen8p, put (Sp) fibraneoth fibraneopen8p, put (Sp) fibraneopen LA7 (Bb) membrene-seconded prt psk (Bb) membrene-seconded prt psk (Bb) membrene-seconded prt psk (Bb) membrene-spenning prt put (Se) outer membrene prt (Ng) outer membrene prt (tpnSp) (Tp) rere lipoprt A (ripA) (Bi) surfecel coated membrene prt 1 (imp1) (Mh) Sc prt (Bb) decoin BP A (dtpA) (Bb) decoin BP B (dtpB) (Bb) lipoprotein (Bb) lipoprotein (Bb) lipoprotein (Bb) lipoprotein (Bb) outer membrene poin (mssS) (Bb) outer auritece prt A (capA) (Bb) outer auritece prt B (aspB) (Bb) outer membrene prt (Bb) Sc prt (Bb) sc prt (Bb) sc prt (Bb) cuter membrene prt (Bb) outer membrene prt (Bb)	50 53 83 100 100 48 48 53 48 94 100 100 100 100 100 100 100 100 100 10	B8304 B8767 SUMMANA 400/400 B8764 B8469 B8473 ID38 B8475 B8475 B8480 B8475 B8480	igese (murb) (Be) UDF-H-A cruremoylelenyl- Deglatemice-2,6- deminopmelete igese (murb) (Hi) UDF-H-A cruremoylelenyl-D- glatemyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- Delanyl-2,6-dismino-pmide- purphoephoryl-undeceprend NAG Tese (murd) (Be) pulphoephoryl-undeceprend NAG Tese (murd) (Be) antigen, PSC (Bb) entigen, PSC (Bb) entigen, PSC (Bb) entigen, PSC (ptr (Bb)) entigen, PSC (ptr (Bb)) entigen, PSC (ptr (Bb)) entigen, PSC (ptr (Bb)) immunogenio-ptr PSC (Bb) immunogenio-ptr PSC (Bb) immunogenio-ptr PSC (ptr (Bb)) immunogenio-ptr PSC (ptr (Bb))	100 58 46 100 58 100 48 52 47 50 99 97 71 71 88 49	B8687 B8680 B8040 B8444 B8651 B8670 B8731 B8670 C4// 4/1 B8083 B8312 B8670 C4// 4/1 B8083 B8312 B8670 B8730 B8730 B8730 B8257	chandasis histoline Kees (chall 1) (Bb) chandasis histoline Kees (chall 2) (Bb) chandasis pit Milles (chall 1) (Rs) chandasis pit Milles (chall 1) (Rn) chandasis response regulator (chall 1) (Rn) chandasis response regulator (chall 1) (Rn) chandasis response regulator (chall 2) (Rn) MC pet (mp. 1) (Rn) MC pet (mp. 2) (Rd) p	100 S 57 44 70 SESSECTED S 59 55 88 100 48.44 SECTION TO
B8319 B8347 B8345 B8365 B8365 B876 B8167 B8167 B8168 B8143 B8143 B8143 B8145 B8145 B8145 B8145 B8145 B8146 B81	exported prt (tpnStb) (Tip) fibraneoth (thinogenER, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-sessoided prt p8 (Bb) membrane-sessoided prt p8 (Bb) cutar membrane prt (Ng) cutar membrane prt (tpnSt) (Tip) rere ipoprt A (tpA) (H) surfaceloated membrane prt 1 (impl) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cutar membrane prt A (capA) (Bb) cutar veurface prt A (capA) (Bb) cutar veurface prt B (sapB) (Bb) cutar membrane prt (Bb) st prt (Bb) st prt (Bb) st prt (Bb) st prt (Bb) cutar membrane prt (Bb)	50 53 81 100 100 48 48 53 45 46 90 100 100 100 100 100 100 100 100 100	BB3 04 BB7 67 SUNFACE 4074 407 BB3 04 BB3 04 BB3 05 BB3 13 ID33 BB3 11 ID33 BB3 15 BB3	igase (murb) (Be) UDF-H-A couremoylelenyl- Deglatemice-2,6- deminopmetete igase (murb) (Hi) UDF-H-A couremoylelenyl-D- glatemyl-2,6-dismino-pmide- Delanyl-D-alemino-igase (murf) (Bb) UDF-H-A cylucosemine-N- Acouremyl-(pertapepide) pyrophosphoryl-undeceprend NAG Tese (murd) (Be) pulps-coherider, ilpopulps-coherid gers entigen, ps://lio/(Bb) glycosyl Tese (lytb) (Hi) entigen, R86 (Bb) entigen, R86, pxt (Bb) entigen, R86, pxt (Bb) entigen, R86, pxt (Bb) immunogenio-pxt R87, pxt (Bb) entigen, R86, pxt (Bb)	100 58 46 100 58 100 48 52 47 50 99 77 71 49 68 49	B8687 B8040 B8040 B8040 B8041 B8671 B8673 B8673 B8673 B8696 B8696 B8696 B8696 B8196	chandasis histoline Kees (chall 1) (Bb) chandasis histoline Kees (dhall 2) (Bb) chandasis pit Milles (dhall 1) (Re) chandasis pit Milles (dhall 2) (Rin) chandasis pit Milles (dhall 2) (Rin) chandasis response regulator (che'l 1) (Tr) chandasis response regulator (che'l 2) (Rin) MC pit (mp 1) (Tin) MC pit (mp 2) (Tid) MC pit (mp 2) (Tid) MC pit (mp 3) (Tid) MC pit (mp 4) (Ed) pit glutanida mathylectores (chell 1) (80) pit glutanida mathylectores (chell 2) (80) punne-Bichemotasis pit (chell 4) (Bb) punne-Bichemotasis pit (chell 3) (Bb) sion cell division contrid pit 27, pit (M) cell division pit (fit 2) (Bs) cell division pit (fit 2) (Bs) cell division pit (fit 3) (Bb) cell division pit pit (Ed) cell division pit (fit 4) (Bb) cell division pit (fit 4) (Bb)	100 日 57 14 70 38 28 32 57 25 日 28 39 39 38 38 100 48 45 58 72 77 77 700
B8319 B8347 B8346 B8396 B8396 B8796 B8167 B8168 B8168 B8168 B8169 B8	exported prt (truss b) (Tip) fibraneous internepat (H) ipoprotein LA7 (Bb) membrene-seconded prt pss (Bb) membrene-seconded prt pss (Bb) membrene-seconded prt pss (Bb) cutar membrene prt (Ng) surface-located membrene prt 1 (mpl) (Mh) sc prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cutar membrene prt A (capA) (Bb) cutar auritace prt B (acpB) (Bb) cutar membrene prt (Bb) sc prt (Bb) cutar membrene prt (Bb) prt ps3 (Bb) cutar membrene prt (Bb) prt ps3 (Bb)	50 50 50 50 100 100 48 48 50 46 90 100 100 100 100 100 100 100 100 100	B8304 B8767 SUMMAN 4004 4004 4004 4004 4004 4004 4006 883.03 ID54 B83.04 B83.05	igase (murb) (Be) UDF-H-A cruremoylelenyl- Deglatemice-2,6- deminopmetete igase (murb) (Hi) UDF-H-A cruremoylelenyl-D- glatemyl-2,6-disminopmide- Delanyl-D-alemine igase (murf) (Bb) UDF-H-A cylucosemine-N- Acusurenyl-(pertapepide) pyrophosphoryl-undeceprend NAGTese (murd) (Bs) pulps-coherioler, ilpopulps-coheriol igas; entigan, psi/100 (Bb) glycosyl Tese (grb) (Hi) entigan, R85 (Bb) entigan, R85, pxt (Bb) entigan, R85, pxt (Bb) immunoganiopxt R87, pxt (Bb) entigan, R85, pxt (Bb)	100 58 46 100 58 100 48 52 47 50 99 77 49 88 49 55 48	B8667 B8669 B8040 B8444 B8671 B8670 B8712 B8660 B8712 B8660 B8671 B8660 B8671 B8660 B8712 B8660 B8712 B8660 B8712 B8660 B8712 B8660 B8712 B8660 B8710	chamchasis histoline Kees (chell 1) (Bb) chamchasis histoline Kees (chell 2) (Bb) chamchasis pit Milles (chell 1) (Re) chamchasis pit Milles (chell 1) (Re) chamchasis pit Milles (chell 2) (Rm) chamchasis response regulator (chell 1) (Tp) chamchasis response regulator (chell 2) (Rm) chamchasis response regulator (chell 2) (Rm) chamchasis response regulator (chell 2) (Rm) MC pit (mp-1) (Rm) MC pit (mp-2) (Td) MC pit (mp-2) (Td) MC pit (mp-2) (Td) MC pit (mp-2) (Ed) priguitamata mathylectorese (chell 2) (Re) punnels chemchasis pit (chell/1) (Bb) punnels chemchasis pit (chell/2) (Bb) cell division control pit 27, put (Mg cell division pit (fitel) (Be) cell division pit (fitel) (Bb)	100 日 57 14 70 88 88 88 55 55 55 8 8 100 48 45 45 78 77 77 77 100 100
B8319 B8347 B8345 B8365 B8365 B876 B8167 B8167 B8168 B8143 B8143 B8143 B8145 B8145 B8145 B8145 B8145 B8146 B81	exported prt (tpnStb) (Tip) fibraneoth (thinogenER, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-sessoided prt p8 (Bb) membrane-sessoided prt p8 (Bb) cutar membrane prt (Ng) cutar membrane prt (tpnSt) (Tip) rere ipoprt A (tpA) (H) surfaceloated membrane prt 1 (impl) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) cutar membrane prt A (capA) (Bb) cutar veurface prt A (capA) (Bb) cutar veurface prt B (sapB) (Bb) cutar membrane prt (Bb) st prt (Bb) st prt (Bb) st prt (Bb) st prt (Bb) cutar membrane prt (Bb)	50 53 81 100 100 48 48 53 45 46 90 100 100 100 100 100 100 100 100 100	BB3 04 BB7 67 SUNFACE 4074 407 BB3 04 BB3 04 BB3 05 BB3 13 ID33 BB3 11 ID33 BB3 15 BB3	igase (murb) (Be) UDF-H-A couremoylelenyl- Deglatemice-2,6- deminopmetete igase (murb) (Hi) UDF-H-A couremoylelenyl-D- glatemyl-2,6-dismino-pmide- Delanyl-D-alemino-igase (murf) (Bb) UDF-H-A cylucosemine-N- Acouremyl-(pertapepide) pyrophosphoryl-undeceprend NAG Tese (murd) (Be) pulps-coherider, ilpopulps-coherid gers entigen, ps://lio/(Bb) glycosyl Tese (lytb) (Hi) entigen, R86 (Bb) entigen, R86, pxt (Bb) entigen, R86, pxt (Bb) entigen, R86, pxt (Bb) immunogenio-pxt R87, pxt (Bb) entigen, R86, pxt (Bb)	100 58 46 100 58 100 48 52 47 50 99 77 71 49 68 49	B8687 B8040 B8040 B8040 B8041 B8671 B8673 B8673 B8673 B8696 B8696 B8696 B8696 B8196	chandasis histoline Kees (chall 1) (Bb) chandasis histoline Kees (dhall 2) (Bb) chandasis pit Milles (dhall 1) (Re) chandasis pit Milles (dhall 2) (Rin) chandasis pit Milles (dhall 2) (Rin) chandasis response regulator (che'l 1) (Tr) chandasis response regulator (che'l 2) (Rin) MC pit (mp 1) (Tin) MC pit (mp 2) (Tid) MC pit (mp 2) (Tid) MC pit (mp 3) (Tid) MC pit (mp 4) (Ed) pit glutanida mathylectores (chell 1) (80) pit glutanida mathylectores (chell 2) (80) punne-Bichemotasis pit (chell 4) (Bb) punne-Bichemotasis pit (chell 3) (Bb) sion cell division contrid pit 27, pit (M) cell division pit (fit 2) (Bs) cell division pit (fit 2) (Bs) cell division pit (fit 3) (Bb) cell division pit pit (Ed) cell division pit (fit 4) (Bb) cell division pit (fit 4) (Bb)	100 8 57 74 70 38 28 32 57 22 81 22 82 83 83 84 84 100 48 45 58 72 77 77 71 71 71 71 71 71 71 71 71 71 71
B8319 B8347 B8346 B8366 B8367 B8376	exported prt (tpn:Stb) (Tip) fibronedminibrinogen-BP, put (Sp) finner membrane prt (H) fipoprotein LA7 (Bb) membrane-associated prt pst (Bb) membrane-associated prt pst (Bb) outer membrane prt (Ng) outer membrane prt (tpn:St) (Tip) rare fipoprt A (fbtA) (H) surface-located membrane prt 1 (fmp1) (Mh) St prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpA) (Bb) fipoprotein (Bb) fipoprotein (Bb) fipoprotein (Bb) fipoprotein (Bb) fipoprotein (Bb) outer nembrane prt (Bb) outer auritace prt B (depB) (Bb) outer membrane prt (Bb) St prt (Bb) surface fipoprt P27 (Bb) outer membrane prt (Bb) prt ps3 (Bb)	50 50 50 50 100 100 48 48 50 46 90 100 100 100 100 100 100 100 100 100	B8304 B8767 SUMMANA B8767 B8764 B88672 ID54 B8868 B8873 ID58 B8875	igese (murb) (Be) UDF-H-A cruremoylelenyl- Deglatemate-2,6- deminopmetete igese (murb) (Hi) UDF-H-A cruremoylelenyl-D- glatemyl-2,6-dismino-pridete- Delanyl-D-elenine igese (murb) (Bb) UDF-H-A cyluccesmine-N- Acruremyl-(pertapepilde) pyriphoephoryl-undeceprend NAGTese (murb) (Bb) pdysectherider, ilinopalysectheria gess entigen, psi/100 (Bb) glycceyl Tese (grb) (Hi) entigen, R65 (Bb) entigen, R65, pxt (Bb) entigen, R65, pxt (Bb) immunogenio-pxt R65, pxt (Bb) immunogenio-pxt R67, pxt (Bb) entigen, R65, pxt (Bb)	100 58 100 58 100 58 100 48 52 47 50 99 77 49 88 49 55 48	B8667 B8689 B8040 B8444 B8670 B8771 B8670 B8771 B8690 B8771 B8690 B8711 B8690 B8711 B8690 B8712 B8690 B8712 B8690 B8712 B8690 B8710 B8700 B8700 B8700 B8001 B8001 B8001	chamchasis histidine Kese (chell 1) (Bb) chamchasis histidine Kese (chell 2) (Bb) chamchasis histidine Kese (chell 2) (Bb) chamchasis ptt MTese (chell 1) (Re) chamchasis response regulator (chell 1) (Tp) chamchasis response regulator (chell 1) (Tp) chamchasis response regulator (chell 2) (Rm) chamchasis (Rm) chamchasis response regulator (chell 2) (Rm) chamchasis (Rm) chamchasis response regulator (chell 2) (Rm) chamchasis	100 日 57 74 70 多数数数57数目数 85 59 85 86 100 148.44数72777771000 1000 1000 1000 1000 1000 100
B8319 B8347 B8346 B8366 B8367 B8376	exported prt (tpnStb) (Tip) fibraneoth (thinogenEP, put (Sp) inner membrane prt (H) ipoprotein LA7 (Bb) membrane-sessolated prt p8 (Bb) membrane-sessolated prt p8 (Bb) outer membrane prt (Ng) outer membrane prt (tpnS) (Tip) auter membrane prt (tpnS) (Tip) rere ipoprt A (tpA) (H) surfacel costed membrane prt 1 (impl) (Mh) Sc prt (Bb) decorin BP A (dtpA) (Bb) decorin BP B (dtpB) (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) ipoprotein (Bb) outer sembrane prt (Bb) outer sembrane prt (Bb) outer membrane prt (Bb) sc prt (Bb) surface ipoprt P27 (Bb) outer membrane prt (Bb)	50 53 81 100 100 44 48 53 46 60 94 100 100 100 100 100 100 100 100 100 10	B8304 B8767 SUMMANA B8767 B8764 B88672 ID54 B8868 B8873 ID58 B8875	igese (murb) (Be) UDF-H-A cruremoylelenyl- Degletenete-2,6- deminopmelete igese (murb) (Hi) UDF-H-A cruremoylelenyl-Degletenete-2,6- gletenyl-2,6-diemino-pmelete gletenyl-2,6-diemino-pmelete gletenyl-2,6-diemino-line igese fmurf (Bb) UDF-H-A cglucceamine-N- Acnuremyl-(pentapepilde) pyr-choephoryl-undeceprend NA Grace (murb) (Be) polysecchericles, iliopolyseccheric gens entigen, PSS (Bb) glycosyl Tese (IgfD) (Hi) entigen, PSS, pxt (Bb) entigen, PSS, pxt (Bb) entigen, PSS, pxt (Bb) immunogenio-pxt PST (Bb) immunogenio-pxt PST, pxt (Bb) entigen, PSS, pxt (Bb) entigen, PSS, pxt (Bb) entigen, PSS, pxt (Bb)	100 58 46 100 58 100 48 52 47 50 99 77 49 88 49 55 48	B9667 B9869 B9040 B9444 B9671 B9670 B9871 B96781 B96781 B96786 B9696 B9697 B9880	chandasis histoline Kees (chall 1) (Bb) chandasis histoline Kees (chall 2) (Bb) chandasis pit Milles (chall 1) (Re) chandasis pit Milles (chall 1) (Re) chandasis pit Milles (chall 2) (Rin) chandasis response regulator (chall 1) (Rp) chandasis response regulator (chall 2) (Rin) MC pit (Ring 2) (Rin) MC pit (Rin) MC pi	100 8 57 74 70 88 88 82 57 52 81 82 83 85 88 100 48 45 53 72 72 77 77 1000 1000 1000

l <u>p28-2</u> BBG08	stage 0 sporulation prt J (spoOJ)		ATP-pro	ton motive force interconversion V-type ATPase, sub A (atpA) {Mb}	64	BB575	CTP Sase (pyrG) {Mj}	71
вваоо	{Bb}	66	BB093 BB092	V-type ATPase, sub B (atpB) {Mb}	62 51	Salvage BB777	of nucleosides and nucleotides adenine phosphoribosylTase	
Cell killi		00	BB096	V-type ATPase, sub E (atpE) {Mj}	54		(apt) {Ta}	63
BB143 BB117	-hemolysin (hlyA) {Ah} hemolysin III (ypIQ) {Bs}	62 61	BB091 BB090	V-type ATPase, sub I (atpl) {Eh} V-type ATPase, sub K (atpK) {Mj}	53 54	BB618 BB239	cytidine deaminase (cdd) {Mp} deoxyguanosine/deoxyadenosine	61
BB506 BB059	hemolysin (tlyA) {Sh} hemolysin (tlyC) {Sh}	59 65	Electron	transport		BB375	kinase(I) sub 2 (dck) {La} pfs prt (pfs-1) {Ec}	59 64
BB202	hemolysin, put {Syn}	54	BB061 BB515	thioredoxin (trxA) {Ec} thioredoxin RDase (trxB) {Bb}	59 99	BB588 BB791	pfs prt (pfs-2) {Hi} thymidine kinase (tdk) {Bs}	59 47
Chapero BB741	ones chaperonin (groES) {Pg}	77	Ferment	, , , ,		BB015	uridine kinase (udk) {Bb}	100
BB602	chaperonin, put {Cb}	72	BB622	acetate kinase (ackA) {Ec}	63	<u>lp36</u>	adanias dassinas (adaO) (Da)	
BB519 BB295	grpE prt (grpE) {Bb} heat shock prt (hsIU) {Bb}	100 100	BB589	P AcTase (pta) {Tt}	65	BBK17	adenine deaminase (adeC) {Bs}	57
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 BB518	heat shock prt 70 (dnaK-1) {Bb} heat shock prt 70 (dnaK-2) {Bb}	61 100	BB057	glyceraldehyde 3-P DHase (gap) {Bb}	99	BB647	ferric uptake regulation prt (fur) {Sp}	48
BB560	heat shock prt 90 (htpG) {Bb}	100	BB630	1-phosphofructoKase (fruK) {Hi}	52	BB198	guanosine-3',5'-bis(diP) 3'-	
Detoxifi			BB056 BB658	phosphoglycerate Kase (pgk) {Bb} phosphoglycerate mutase (gpmA)	99	BB737	pyrophosphohydrolase (spoT) {Ec} histidine phosphoKase/PPase,	
BB153	superoxide dismutase (sodA) {Hi}	68	BB348	{Ec} pyruvate Kase (pyk) {Bs}	79 62	BB176	put {MI} methanol DHase regulator	49
BB690 BB179	neutrophil activating prt (napA) {Hi} thiophene and furan oxidation	57	BB727	pyroP-fructose 6-P 1-PPTase (pfk) {Eh}	65	BB416	(moxR) {Bb} pheromone shutdown prt	99
	prt (thdF) {Bb}	100	BB020	pyroP-fructose 6-P 1-PPTase, sub (pfpB) {Bb}	100	BB042	(traB) {Ef} P transport system regulatory	61
	and peptide secretion	100	BB055		100		prt (phoU) {Pa}	57
BB154 BB395		62		phosphate pathway		BB379 BB419	prt Kase C1 inhibitor (pkcl) {Bb} response regulatory prt	100
BB498 BB362	preprt translocase sub (secY) {Sc} prolipoprt diacylglyceryl Tase	64	BB222 BB636	glucose-6-P 1-DHase, put {As} glucose-6-P 1-DHase (zwf) {Hi}	48 64	BB763	(rrp-1) {Syn} response regulatory prt	57
BB652	(lgt) {Ec} prt-export membrane prt	56	BB561	phosphogluconate DHase (gnd) {Sd}	71	BB764	(rrp-2) {Ec} sensory transduction histidine	67
BB653	(secD) {Ec} prt-export membrane prt	63	BB657	ribose 5-P isomerase (rpi) {Mj}	61	BB420	Kase, put {Bs} sensory transduction	60
	(secF) {Hi}	63	Sugars	0 D :			histidine Kase, put (Syn)	61
BB030	signal peptidase I (lepB-1) {Bs}	51	BB407		54	BB693	xylose operon regulatory prt (xylR-1) {Th.}	48
BB031 BB263	signal peptidase I (lepB-2) {Syn} signal peptidase I (lepB-3) {St}	57 57	BB444 BB676	nucleotide sugar epimerase {Vc} phosphoglycolate PPase (gph) {Hi}	69 50	BB831	xylose operon regulatory prt (xylR-2) {Syn}	51
BB469 BB694	signal peptidase II (Isp) {Sc} signal recognition particle	60	BB207	UTP-glucose-1-P uridylylTase (gtaB) {Bs}	63	<u>lp54</u>		
	prt (ffh) {Bs}	70 50	BB545	xylulokinase (xylB) {Bs}	43	BBA07	chpAl prt, put {Ec}	55
BB610	prt (ffh) {Bs} trigger factor (tig) {Hi}	70 50	Fatty ac			BBA07	on	55
BB610 <i>Transfo</i> BB591	prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs}	50 54	Fatty ac General	xylulokinase (xylB) {Bs} d and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase	43	BBA07	ion ation of DNA endonuclease precursor	
BB610 <i>Transfo</i> BB591 BB798	prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi}	50	Fatty ac General	xylulokinase (xylB) {Bs} d and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase		BBA07 Replicati Degrada	ion ation of DNA	5553
BB610 <i>Transfo</i> BB591 BB798	prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism	50 54	Fatty ac General BB037	xylulokinase (xylB) {Bs} d and phospholipid metabolism 1-acyl-sn-glycerol-3-P AcTase (plsC) {Bb} 3-OH-3-methylglutaryl-CoA RDase (mvaA) {Pm}	43	Replicati Degrada BB411	ion ation of DNA endonuclease precursor	
BB610 Transfor BB591 BB798 Central General BB241	prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol kinase (glpK) {Ec}	50 54	Fatty ac General BB037 BB685 BB683	xylulokinase (xylB) {Bs} d 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}	431005253	Replicati Degrada BB411	ion ation of DNA endonuclease precursor (nucA) {As} blication, restriction, modification, nation, and repair 3-methyladenine DNA	53
BB610 Transfor BB591 BB798 Central General BB241 BB243	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}	50 54 52 74 52	Fatty ac General BB037 BB685 BB683 BB109 BB704	xylulokinase (xylB) {Bs} d 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}	4310052	BBA07 Replicati Degrada BB411 DNA reprecombit BB422 BB827	ion ation of DNA endonuclease precursor (nucA) (As) colication, restriction, modification, nation, and repair 3-methyladenine DNA glycosylase (mag) (At) ATP-dep helicase (hrpA) {Ec}	
BB610 Transfor BB591 BB798 Central General BB241 BB243 BB376	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}	50 54 52 74	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721	xylulokinase (xylB) {Bs} d 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 pt {Syn} CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase {Bs}	100 52 53 67 65 55	Replicati Degrada BB411 DNA reprecombin BB422 BB827 BB437	ion ation of DNA endonuclease precursor (nucA) {As} blication, restriction, modification, nation, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init prt (dnaA) {Bb}	53 56 61 100
BB610 Transfor BB591 BB798 Central General BB241 BB243	prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism glycerol-3-P DHase, anaerobic (glpA) {Hi} SAM Sase (metK) {Bs} sugars glucosamine-6-P isomerase	50 54 52 74 52 72	Fatty ac General BB037 BB685 BB683 BB109 BB704	xylulokinase (xylB) {Bs} d 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	43 100 52 53 67 65 55 50	BBA07 Replicati Degrada BB411 DNA representati BB422 BB827 BB437 BB435 BB436	on stion of DNA endonuclease precursor (nucA) {As} clication, restriction, modification, ination, and repair 3-methyladenine DNA glycosylase (mag) {At} ATP-dep helicase (hrpA) {Ec} chromosomal replication init pt (dnaA) {Bb} DNA gyrase, sub A (gyrA) {Bs} DNA gyrase, sub B (gyrB) {Bb}	53 56 61 100 67 99
BB610 Transfol BB591 BB798 Central General BB241 BB243 BB376 Amino s	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}	50 54 52 74 52	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327	xylulokinase (xylB) {Bs} d 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}	43 100 52 53 67 65 55 50	BBA07 Replicati Degrada BB411 DNA reprecombi BB422 BB827 BB437 BB435	on ation of DNA endonuclease precursor (nucA) (As) colication, restriction, modification, nation, 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)	53 56 61 100 67
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino & BB152	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}	50 54 52 74 52 72	Fatty ac General B8037 BB685 BB683 BB109 BB704 BB721 BB327 BB368	xylulokinase (xylB) {Bs} d 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}	43 100 52 53 67 65 55 50	BBA07 Replicati Degrada BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB344	on ation of DNA endonuclease precursor (nucA) (As) colication, restriction, modification, mation, 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	53 56 61 100 67 99 55 56
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada	prt (ffh) {Bs} trigger factor (tig) {Hi} tri	50 54 52 74 52 72 79 54	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593	xylulokinase (xylB) {Bs} d 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}	100 52 53 67 65 55 50) 54 54	BBA07 Replicati Degrada BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB344 BB552	idion intion of DNA endonuclease precursor (nucA) {As} blication, restriction, modification, nation, 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	53 56 61 100 67 99 55 56 55
BB610 Transfol BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151	prt (ffh) {Bs} trigger factor (tig) {Hi} rmation competence locus E, put {Bs} competence prt F, put {Hi} intermediary metabolism 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}	50 54 52 74 52 72	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB693 BB688 BB686	xylulokinase (xylB) {Bs} d 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}	100 52 53 67 65 55 50) 54	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB436 BB344 BB552 BB211	on ation of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, mation, 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 (luyD) {Ec} DNA mismatch repair prt (mutL) {Hi} DNA mismatch repair prt (mutS) (Hi) DNA mismatch repair prt,	53 56 61 100 67 99 55 56 55 57
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosphi	prt (ffh) {Bs} trigger factor (tig) {Hi} tri	50 54 52 74 52 72 79 54 58 54	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119	xylulokinase (xylB) {Bs} d 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 pyroP DCase {Sc} phosphatidate cytidylylTase (cdsA), AFS(Ec)	43 100 52 53 67 65 55 50) 54 56 51 52 61	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB436 BB436 BB344 BB552 BB211 BB797 BB098 BB548	istion of DNA endonuclease precursor (nucA) (As) blication, restriction, modification, nation, 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)	53 56 61 100 67 99 55 56 55
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosphi BB533	prt (ffh) {Bs} trigger factor (tig) {Hi} sompetence 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} porus compounds phnP prt (phnP) {Ec}	50 54 52 74 52 72 79 54 58	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB693 BB688 BB686	xylulokinase (xylB) {Bs} d 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 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),	43 100 52 53 67 65 55 50) 54 54 56 51 52 61 52	BBA07 Replicati Degrada BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB548 BB579	on stion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, mation, 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}	53 56 61 100 67 99 55 56 55 57
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosphi BB533	prt (ffh) {Bs} trigger factor (tig) {Hi} tri	50 54 52 74 52 72 79 54 58 54	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687	xylulokinase (xylB) {Bs} d 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} phosphatidylTase {Hp}	43 100 52 53 67 65 55 50) 54 56 51 52 61 52 61 52 61 52 61 62 63 63 64 65 65 65 65 65 65 65 65 65 65	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB436 BB436 BB344 BB552 BB211 BB797 BB098 BB548	con ation of DNA endonuclease precursor (nucA) (As) colication, restriction, modification, mation, 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) DNA polymerase III, sub	53 56 61 100 67 99 55 56 55 57 51 61
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysac BB166 BB166 BB004	prt (ffh) {Bs} trigger factor (tig) {Hi} trigger factor (final factor	50 54 52 74 52 72 79 54 58 54 48	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoti	xylulokinase (xylB) {Bs} d 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 Kase {Mj} mevalonate cytidylylTase (cdsA), AFS(Ec) phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion	43 100 52 53 67 65 55 50) 54 54 56 51 52 61 52 53 61 52 63 65 65 65 65 65 65 65 65 65 65	BBA07 Replicati Degrada BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB548 BB579	ion stion of DNA endonuclease precursor (nucA) {As} colication, restriction, modification, mation, 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} DNA polymerase III, sub (dnaN) {Bb} DNA polymerase III, sub	53 56 61 100 67 99 55 56 55 57 51 61 62 100
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosph BB533 Polysac BB166 BB004 BB835	prt (ffh) {Bs} trigger factor (tig) {Hi} trigger (tig) {Hi} tri	50 54 52 74 52 72 79 54 58 54 48	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoth BB128	xylulokinase (xylB) {Bs} d 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 pyroP DCase {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion adenylate kinase (cmk-1) {Bs}	43 100 52 53 67 65 55 50) 54 56 51 52 61 52 61 52 63 63 64 65 65 65 65 65 65 65 65 65 65	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710	endonuclease precursor (nucA) (As) colication, restriction, modification, nation, 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) DNA polymerase III, sub (dnaE) (Ec) DNA polymerase III, sub (dnaN) (Bb) DNA polymerase III, sub / (dnaX) (Bs) DNA primase (dnaG) (Bs)	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysac BB166 BB004 BB835 Energy Aerobic	prt (ffh) {Bs} trigger factor (tig) {Hi} tri	50 54 52 74 52 72 79 54 58 54 48	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoti BB417 BB128 BB819 BB463	xylulokinase (xylB) {Bs} d 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 kase {Mj} mevalonate cytidylylTase (cdsA), AFS{Ec} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj} nucleoside-diP kinase (mdk) {Bs}	43 100 52 53 67 65 55 50) 54 54 56 51 52 53 61 52 53 61 52 53 63 64 65 57 77 70 70 70 70 70 70 70 70 7	BBA07 Replicati Degrada BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB828	endonuclease precursor (nucA) (As) colication, restriction, modification, mation, 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) DNA polymerase III, sub (dnaN) (Bb) DNA polymerase III, sub (dnaN) (Bs) DNA primase (dnaG) (Bs) DNA recombinase (recG) (Syn) DNA recombinase (recG) (Syn) DNA topoisomerase I (topA) (Syn)	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 60 64
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosphi BB533 Polysac BB166 BB004 BB835 Energy	prt (ffh) {Bs} trigger factor (tig) {Hi} sompetence 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} phnP prt (phnP) {Ec} charides - (cytoplasmic) 4glucanoTase (malQ) {Syn} phosphoglucomutase (femD) {Mj} phosphomannomutase (cpsG) {Hi} metabolism	50 54 52 74 52 72 79 54 58 54 48	Patty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoth BB417 BB128 BB1819	xylulokinase (xylB) {Bs} d 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) phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj}	43 100 52 53 67 65 55 50) 54 54 55 56 61 52 53 61 52 61 52 63 65 65 65 65 65 65 65 65 65 65	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB828 BB035 BB036	endonuclease precursor (nucA) (As) colication, restriction, modification, nation, 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 (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 IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb)	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 64 58 56
BB610 Transfor BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysac BB166 BB004 BB835 Energy Aerobic BB728	prt (ffh) (Bs) trigger factor (tig) {Hi} trigger (tig)	50 54 52 74 52 72 79 54 58 54 48 55 52 57	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleott BB417 BB128 BB819 BB463 BB793 BB793 BB793 BR793 BR793 Purine of	xylulokinase (xylB) {Bs} d 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 pt {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 pyroP DCase {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} tymidylate kinase (cmk-1) {Mj} uridylate kinase (smbA) {Mj} ibonucleotide biosynthesis	43 100 52 53 67 65 55 50 54 54 56 51 52 61 52 53 67 68 58 68 68 68 68 68 68 68 68 68 6	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB436 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB710 BB5828 BB035	endonuclease precursor (nucA) (As) polication, restriction, modification, mation, 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 (dnaE) (Ec) DNA polymerase III, sub (dnaN) (Bb) DNA primase (dnaG) (Bs) DNA primase (dnaG) (Bs) DNA teromismase (recG) (Syn) DNA topoisomerase I (topA) (Syn) DNA topoisomerase IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb) endonuclease III (nth) (Syn) excinuclease ABC, sub A	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 64 58 56 60 64 59
BB610 Transfo. BB591 BB798 Central General BB241 BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysac BB166 BB004 BB835 Energy Aerobic BB728	prt (ffh) {Bs} trigger factor (tig) {Hi} trigger (tig) {Hi}	50 54 52 74 52 72 79 54 58 54 48 55 52 57	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoth BB417 BB128 BB319 BB463 BB793 BB793 BB791	xylulokinase (xylB) {Bs} d 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 pyroP DCase {Sc} phosphatidylTase {Hp} phosphotidate cytidylylTase (cdsA), AFS{Ec} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj} nucleoside-diP kinase (mkk) {Bs} thymidylate kinase (smbA) {Mj} ibonucleotide biosynthesis phosphoribosyl pyroP Sase	43 100 52 53 67 65 55 50 54 56 51 52 61 52 53 67 65 55 50 65 54 56 55 53 67 67 67 67 67 67 67 67 67 67	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB348 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB828 BB036 BB036 BB745	endonuclease precursor (nucA) (As) colication, restriction, modification, nation, 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 polymerase (lig) (Bs) DNA polymerase (lig) (Hi) DNA polymerase III, sub / (dnaX) (Bs) DNA polymerase III, sub / (dnaX) (Bs) DNA topoisomerase IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb) Endonuclease ABC, sub A (uvrA) (Ec)	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 64 58 56
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosph BB533 Polysac BB166 BB004 BB835 Energy Aerobic BB728 Amino a BB841	prt (ffh) {Bs} trigger factor (tig) {Hi} tri	50 54 52 74 52 72 79 54 58 54 48 55 52 57	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoth BB417 BB128 BB819 BB463 BB793 BB571 Purine r BB544	xylulokinase (xylB) {Bs} d 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 pt {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 pyroP DCase {Sc} phosphatidylTase {Hp} phosphomevalonate Kase, put {Sc} pyrimidines, nucleosides, nucleotide de and nucleoside interconversion adenylate kinase (adk) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} tymidylate kinase (cmk-1) {Mj} uridylate kinase (smbA) {Mj} ibonucleotide biosynthesis	43 100 52 53 67 65 55 50 54 54 56 51 52 61 52 53 63 64 55 55 50 65 55 50 65 55 55 55 55 55 55 55 55 55	BBA07 Replicati Degrada BB411 DNA reprecemble BB422 BB827 BB437 BB436 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB611 BB710 BB581 BB710 BB581 BB710 BB828 BB035 BB036 BB036 BB745 BB837	endonuclease precursor (nucA) (As) colication, restriction, modification, mation, 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) (Bb) DNA polymerase III, sub (dnaN) (Bs) DNA topoisomerase I (topA) (Syn) DNA topoisomerase I (topA) (Syn) DNA topoisomerase IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb) excinuclease ABC, sub B (uvrB) (Ec)	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 64 58 56 60 64 59
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phosph BB533 Polysac BB166 BB004 BB835 Energy Aerobic BB728 Amino a BB841 BB842 Anaerola	prt (ffh) (Bs) trigger factor (tig) (Hi) trigger factor (Hi) trigger factor (tig) (Hi) trigger (tig)	50 54 52 74 52 72 79 54 58 54 48 55 52 57 59 75 74	Patty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoth BB417 BB128 BB819 BB463 BB793 BB793 BB793 Cp26 BBB18	xylulokinase (xylB) {Bs} d 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} phosphatidylTase {Hp} phosphatidylTase {Hp} phosphatidylTase {Hp} phosphatidylTase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj} nucleoside-diP kinase (mk) {Bs} cytidylate kinase (tmk) {Mj} uridylate kinase (smbA) {Mj} ibonucleotide biosynthesis phosphoribosyl pyroP Sase (prs) {Mp} GMP Sase (guaA) {Bb}	43 100 52 53 67 65 55 50 54 54 55 55 50 61 52 53 61 52 61 52 53 63 63 63 63 64 65 65 65 65 65 65 65 65 65 65	BBA07 Replicati Degrade BB411 DNA reprecombi BB422 BB827 BB437 BB435 BB436 BB436 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB461 BB710 BB581 BB828 BB461 BB710 BB581 BB828 BB461 BB710 BB581 BB828 BB461 BB710 BB581 BB828 BB461 BB710 BB581 BB837 BB8581	endonuclease precursor (nucA) (As) colication, restriction, modification, mation, 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 mismatch repair prt, put (Syn) DNA polymerase I (polA) (Hi) DNA polymerase III, sub (dnaE) (Ec) DNA polymerase III, sub (dnaN) (Bb) DNA polymerase III, sub / (dnaX) (Bs) DNA polymerase III, sub / (dnaX) (Bs) DNA topoisomerase IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb) DNA topoisomerase IV (parC) (Bb) endonuclease III (nth) (Syn) excinuclease ABC, sub A (uvrA) {Ec} excinuclease ABC, sub C (uvrC) (Syn)	53 56 61 100 67 99 55 56 55 57 51 61 62 100 64 58 56 60 64 58 58 58 58 58 58 58 58 58 58
BB610 Transfo. BB591 BB798 Central General BB241 BB243 BB376 Amino s BB152 BB151 Degrada BB620 BB002 Phospha BB533 Polysac BB166 BB004 BB805 BB004 BB805 BB728 Amino s BB8841 BB842	prt (ffh) (Bs) trigger factor (tig) (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) trigger factor (Hi) trigger factor (Interpretation of polysaccharides -glucosidase, put (Syn) -N-Achexosaminidase, put (As) trigger factor (Interpretation of polysaccharides -glucosidase, put (Syn) -N-Achexosaminidase, put (As) trigger factor (Interpretation of polysaccharides -glucosidase, put (Syn) -N-Achexosaminidase, put (As) trigger factor (Interpretation of polysaccharides -glucosidase, put (Syn) -N-Achexosaminidase, put (As) trigger factor (Interpretation of polysaccharides -glucosidase, put (Syn) -N-Achexosaminidase, (malQ) (Syn) phosphoglucomutase (femD) (Mj) phosphomannomutase (cpsG) (Hi) metabolism NADH oxidase, water-forming (nox) (Sh) trigger factor (Itg) (Itg) trigger factor (Itg) trigger (Itg) trigger factor (Itg) trigger (Itg	50 54 52 74 52 72 79 54 58 54 48 55 52 57 59	Fatty ac General BB037 BB685 BB683 BB109 BB704 BB721 BB327 BB368 BB137 BB593 BB688 BB686 BB119 BB249 BB687 Purines, Nucleoti BB417 BB128 BB819 BB463 BB793 BB571 Purine r BB544	xylulokinase (xylB) {Bs} d 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} phosphatidylTase {Hp} phosphatidylTase {Hp} phosphatidylTase {Hp} phosphatidylTase (cmk-1) {Bs} cytidylate kinase (cmk-1) {Bs} cytidylate kinase (cmk-2) {Mj} nucleoside-diP kinase (mk) {Bs} tytidylate kinase (tmk) {Mj} uridylate kinase (smbA) {Mj} ibonucleotide biosynthesis phosphoribosyl pyroP Sase (prs) {Mp} GMP Sase (guaA) {Bb}	43 100 52 53 67 65 55 50 54 54 56 51 52 61 52 53 67 65 55 50 65 54 55 55 55 55 55 55 55 55 5	BBA07 Replicati Degrada BB411 DNA reprecemble BB422 BB827 BB437 BB436 BB436 BB344 BB552 BB211 BB797 BB098 BB548 BB579 BB438 BB611 BB710 BB581 BB710 BB581 BB710 BB828 BB035 BB036 BB036 BB745 BB837	endonuclease precursor (nucA) (As) polication, restriction, modification, mation, 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 primase (dnaG) (Bs) DNA recombinase (recG) (Syn) DNA topoisomerase I (topA) (Syn) Endonuclease III (nth) (Syn) excinuclease ABC, sub B (uvrA) (Ec) excinuclease ABC, sub B	53 56 61 100 67 99 55 56 55 57 51 61 62 100 61 56 60 64 58 56 60 64 59 4 71

	(recD) {Ec}	54	BB833	isoleucyl-tRNA Sase (ileS) {Sc}	66	BB703	ribosomal prt L32 (rpmF) {Bs}	62
BB633	exodeoxyribonuclease V, chain	E1	BB251	leucyl-tRNA Sase (leuS) {Bs}	70 E 4	BB396	ribosomal prt L33 (rpmG) {Bs}	76
BB634	(recB) {Hi} exodeoxyribonuclease V,	51	BB659 BB587	lysyl-tRNA Sase (Mj) methionyl-tRNA Sase (metG) (Sc)	54 67	BB440 BB189	ribosomal prt L34 (rpmH) {Bb} ribosomal prt L35 (rpml) {Ba}	100 74
DD034	chain (recC) {Hi}	51	BB514	phenylalanyl-tRNA Sase, sub	07	BB499	ribosomal prt L36 (rpmJ) {Bs}	89
BB829	exonuclease SbcD (sbcD) {Ec}	55	DDOTT	(pheT) {Bb}	100	BB127	ribosomal prt S1 (rpsA) {Ec}	55
BB830	exonuclease SbcC (sbcC) {Ec}	52	BB513	phenylalanyl-tRNA Sase, sub		BB123	ribosomal prt S2 (rpsB) {Pa}	79
BB177	glucose-inhibited div prt B (gidB)			(pheS) {Bb}	100	BB484	ribosomal prt S3 (rpsC) {Hi}	71
	{Bb}	99	BB402	prolyl-tRNA Sase (proS) {Sc}	65	BB615	ribosomal prt S4 (rpsD) {Hi}	63
BB178	glucose-inhibited div prt A		BB226	seryl-tRNA Sase (serS) {Bs}	62	BB495	ribosomal prt S5 (rpsE) {Bs}	77
DDOOO	(gidA) {Bb}	100	BB720	threonyl-tRNA Sase (thrZ) {Bs}	67	BB115	ribosomal prt S6 (rpsF) {Os}	50
BB022	Holliday junction DNA helicase	100	BB005 BB370	tryptophanyl-tRNA Sase (trsA) {Cl} tyrosyl-tRNA Sase (tyrS) {Bs}	65	BB386	ribosomal prt S7 (rpsG) (Sc)	75
BB023	(ruvB) {Bb} Holliday junction DNA helicase	100	BB738	valyl-tRNA Sase (valS) {Bs}	62 67	BB492 BB338	ribosomal prt S8 (rpsH) {Syn} ribosomal prt S9 (rpsI) {Hi}	66 71
DD020	(ruvA) {Bb}	100	DD700	valyi titivi Codac (valo) (baj	07	BB477	ribosomal prt S10 (rpsJ) {Bb}	100
BB014	primosomal prt N (priA) {Bb}	100	Degrada	ation of proteins, peptides, and gly-		BB501	ribosomal prt S11 (rpsK) {Hi}	77
BB131	recA prt (recA) {Bb}	100	copeption			BB387	ribosomal prt S12 (rpsL) (An)	89
BB607	rep helicase, ss DNA-dep		BB608	aminoacyl-histidine dipeptidase		BB500	ribosomal prt S13 (rpsM) (Cp)	76
	ATPase (rep) {Hi}	61		(pepD) {Hi}	55	BB491	ribosomal prt S14 (rpsN) {Bs}	72
BB111	replicative DNA helicase	F0	BB366	aminopeptidase I (yscl) {Bb}	100	BB804	ribosomal prt S15 (rpsO) {Tt}	77
BB114	(dnaB) {Ec} ss DNA-BP (ssb) {Syn}	58 62	BB069 BB611	aminopeptidase II (Bs) ATP-dep Clp protease proteolytic	57	BB695 BB487	ribosomal prt S16 (rpsP) {Bs} ribosomal prt S17 (rpsQ) {Mc}	70 76
BB254	ss-DNA-specific exonuclease	02	DDOTT	component (clpP-1) {Hi}	79	BB113	ribosomal prt S17 (rpsQ) (Mc)	78
	(recJ) {Hi}	52	BB757	ATP-dep Clp protease proteolytic		BB482	ribosomal prt S19 (rpsS) {Bb}	99
BB623	transcription-repair coupling factor			component (clpP-2) {Hi}	67	BB233	ribosomal prt S20 (rpsT) {Bb}	100
	(mfd) {Hi}	60	BB369	ATP-dep Clp protease, sub A		BB256	ribosomal prt S21 (rpsU) {Mx}	68
BB053	uracil DNA glycosylase (ung) {Hi}	68		(clpA) {Ec}	56	BB516	rRNA methylase (yacO) {Mc}	66
L- 00 0			BB612	ATP-dep Clp protease, sub X	1 C	+DA/A	a difference	
<u>lp28-2</u> BBG32	replicative DNA helicase, put {Bs}	59	BB834	(clpX) {Ec} ATP-dep Clp protease, sub C	75	BB821	nodification 2-methylthio-N6-isopentyladenosine	
DDGGZ	replicative DNA fielicase, put (DS)	00	DD004	(clpC) {Pp}	67	DDOZI	tRNA modification enzyme	
<u>lp25</u>			BB253	ATP-dep protease LA (lon-1) {Bb}	100		(miaA) {Ec}	53
BBE29	adenine specific DNA MTase, put		BB613	ATP-dep protease LA (lon-2) {Hi}	65	BB084	AT (nifS) {Syn}	61
	{Hp}	57	BB359	carboxyl-terminal protease (ctp)		BB343	glu-tRNA amidoTase, sub C (gatC)	
_				{Syn}	65		{Bs}	56
Transcri			BB203	Lambda CII stability-governing	F0	BB341	glu-tRNA amidoTase, sub B (gatB)	00
General BB052		54	BB204	prt (hflK) {Ec} Lambda CII stability-governing prt	56	BB342	{Bs}	63
DDU02	spoo pit (spoo) {EC}	54	DD2U4	(hflC) {Ec}	56	DD342	glu-tRNA amidoTase, sub A (gatA) {Bs}	61
Degrada	ation of RNA		BB248	oligoendopeptidase F (pepF) {LI}	58	BB064	methionyl-tRNA formylTase	01
BB805	polyribonucleotide nucleotidylTase	68	BB067	peptidase, put {Sc}	56		(fmt) {Ec}	56
	(pnpA) {Bs}		BB104	periplasmic serine protease		BB787	peptidyl-tRNA hydrolase (pth) {Bb}	100
BB046	ribonuclease H (rnhB) {Hi}	66		DO (htrA) {Hi}	60	BB012	pseudouridylate Sase I (hisT) {Bb}	100
BB705	ribonuclease III (rnc) {Bs}	62	BB430	proline dipeptidase (pepQ) {Hi}	49	BB021	SAM: tRNA ribosylTase-isomerase	
BB441	ribonuclease P prt component	100	BB769	sialoglycoprotease (gcp) {Hi}	60	DDOOO	{Bb}	96
	(rnpA) {Bb}	100	BB627	vacuolar X-prolyl dipeptidyl aminopeptidase		BB809	tRNA-guanine transglycosylase (tgt) (Zm)	60
DNA-de	pendent RNA polymerase			I (pepX) {MI	55	BB698	tRNA (guanine-N1)-MTase (trmD)	00
BB502	DNA-directed RNA polymerase			West 7 C			{Mg}	68
	(rpoA) {Bs}	64	BB118	zinc protease, put {Hi}	54	BB803	tRNA pseudouridine 55 Sase	
BB389	DNA-directed RNA polymerase		BB536	zinc protease, put {Hi}	52		(truB) {Ec}	57
	(rpoB) {Bb}	97						
BB388	DNA-directed RNA polymerase	74	Nucleon		400		tion factors	70
BB771	(rpoC) {Ec}						GTP-B membrane prt (lepA) {Hi}	76
וווטט		71	DDZ3Z	hbbU prt {Bb}	100	BB088	nantida chain ralagea factor 1 (nrfA	
	RNA polymerase sigma factor (rpoS) (Pa)				100	BB088 BB196	peptide chain release factor 1 (prfA	
BB712	(rpoS) {Pa}	61		modification	100		Hi}	73
			Protein	modification methionine aminopeptidase	68	BB196		73
	(rpoS) {Pa} RNA polymerase sigma-70 factor	61 100	Protein BB105 (map) {E BB065	modification methionine aminopeptidase 3s} polypeptide deformylase	68	BB196 BB074 BB121	Hi) peptide chain release factor 2 (prfB {Sc} ribosome releasing factor (frr) {Mt}	73) 70
BB712	(rpoS) {Pa} RNA polymerase sigma-70 factor (rpoD) {Bb}	61	Protein BB105 (map) {E BB065 (def) {Sy	modification methionine aminopeptidase 3s} polypeptide deformylase n)	68 67	BB196 BB074	Hi) peptide chain release factor 2 (prfB {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA)	73 70 68
BB712 BB450	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) (Av)	61 100	Protein BB105 (map) {E BB065	modification methionine aminopeptidase 3s} polypeptide deformylase	68	BB196 BB074 BB121 BB169	Hi) peptide chain release factor 2 (prfB {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec}	73) 70
BB712 BB450	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) (Av) iption factors	61 100	Protein BB105 (map) {E BB065 (def) {Sy BB648	modification methionine aminopeptidase 3s} polypeptide deformylase nn} serine/threonine kinase, put {Pf}	68 67 51	BB196 BB074 BB121	Hi) peptide chain release factor 2 (prfB {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB)	73 70 68 87
BB712 BB450	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B	61 100 57	Protein BB105 (map) {E BB065 (def) {Sy BB648	modification methionine aminopeptidase 3s} polypeptide deformylase rn} serine/threonine kinase, put {Pf} nal proteins: synthesis and modification	68 67 51 tion	BB196 BB074 BB121 BB169 BB801	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs}	73 70 68
BB712 BB450 Transcr. BB107	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec}	61 100	Protein BB105 (map) {E BB065 (def) {Sy BB648 Riboson BB392	modification methionine aminopeptidase 3s} polypeptide deformylase /n} serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs}	68 67 51 <i>tion</i> 71	BB196 BB074 BB121 BB169	Hi) peptide chain release factor 2 (prfB {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC)	73 70 68 87 73
BB712 BB450	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B	61 100 57	Protein BB105 (map) {E BB065 (def) {Sy BB648	modification methionine aminopeptidase 3s} polypeptide deformylase rn} serine/threonine kinase, put {Pf} nal proteins: synthesis and modification	68 67 51 tion	BB196 BB074 BB121 BB169 BB801	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs}	73 70 68 87
BB712 BB450 Transcr. BB107	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination	61 100 57 62 62	Protein BB105 (map) {I BB065 (def) {Sy BB648 Riboson BB392 BB481 BB478 BB479	modification methionine aminopeptidase 3s} polypeptide deformylase m} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb}	68 67 51 <i>tion</i> 71 99 99	BB196 BB074 BB121 BB169 BB801 BB190 BB691	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm}	73 70 68 87 73
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec}	61 100 57	Protein BB105 (map) {I BB065 (def) {Sy BB648 Ribosor BB392 BB481 BB478 BB479 BB490	modification methionine aminopeptidase 3s} polypeptide deformylase rn} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) (Bb} ribosomal prt L5 (rplE) {Hi}	68 67 51 <i>tion</i> 71 99 99 100 80	BB196 BB074 BB121 BB169 BB801 BB190	Hi) peptide chain release factor 2 (prf8 {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P	73 70 68 87 73 72 67
BB712 BB450 Transcr BB107 BB800	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor	61 100 57 62 62 64	Protein BB105 (map) {{ BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB493	modification methionine aminopeptidase as polypeptide deformylase m) serine/threonine kinase, put {Pf} serine/threonine kinase, put {Pf} serine/threonine kinase, put {Bs} ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc}	68 67 51 tion 71 99 99 100 80 72	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214	Hi) peptide chain release factor 2 (prf8 {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec}	73 70 68 87 73
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) (Bs) transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec}	61 100 57 62 62 64 56	Protein BB105 (map) {I BB065 (def) {Sy BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB493 BB493 BB493	modification methionine aminopeptidase 3s} polypeptide deformylase ns) serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7 (rplL) {Sc}	68 67 51 tion 71 99 100 80 72 75	BB196 BB074 BB121 BB169 BB801 BB190 BB691	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor P	73 70 68 87 73 72 67
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx}	61 100 57 62 62 64	Protein BB105 (map) {E BB065 (def) {Sy BB648 Ribosor BB392 BB478 BB479 BB490 BB493 BB490 BB493 BB390 BB112	modification methionine aminopeptidase 3s} polypeptide deformylase m} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L9 (rplI) {Ec}	68 67 51 tion 71 99 100 80 72 75 57	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) {Bb}	73 70 68 87 73 72 67
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor	61 100 57 62 62 64 56 47	Protein BB105 (map) [8 BB065 (def) [5] BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB493 BB391 BB391	modification methionine aminopeptidase as} polypeptide deformylase ml serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L5 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplI) {Sc} ribosomal prt L9 (rplI) {Sc} ribosomal prt L10 (rplJ) {Bs}	68 67 51 tion 71 99 99 100 80 72 75 57 61	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214	Hi) peptide chain release factor 2 (prf8 {Sc} ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) {Bb} translation elongation factor	73 70 68 87 73 72 67 56
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx}	61 100 57 62 62 64 56	Protein BB105 (map) {I BB065 (def) {S} BB648 Ribosor BB392 BB481 BB478 BB490 BB490 BB493 BB490 BB112 BB391 BB393 BB339	modification methionine aminopeptidase 3s} polypeptide deformylase m} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L9 (rplI) {Ec}	68 67 51 tion 71 99 100 80 72 75 57	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) {Bb}	73 70 68 87 73 72 67
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355 BB230	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor (Rbo) {Bb}	61 100 57 62 62 64 56 47	Protein BB105 (map) {I BB065 (def) {Sy BB648 Ribosor BB392 BB478 BB479 BB490 BB493 BB393 BB391 BB393 BB399 BB393 BB393 BB393 BB3848	modification methionine aminopeptidase as} polypeptide deformylase yn} serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L9 (rplI) {Eo} ribosomal prt L9 (rplI) {Eo} ribosomal prt L10 (rplI) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L13 (rplM) {Hi} ribosomal prt L14 (rplM) {Tm}	68 67 51 tion 71 99 100 80 72 75 57 61 73 72 79	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) (Bs) translation initiation factor 3 (infC) (Pv) translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi}	73 70 68 87 73 72 67 56
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355 BB230	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) (Bb)	61 100 57 62 62 64 56 47 100	Protein BB105 (map) {E BB065 (def) {Sy BB648 Ribosor BB392 BB493 BB493 BB493 BB493 BB391 BB393 BB393 BB393 BB393 BB393 BB398 BB488 BB498	modification methionine aminopeptidase ass} polypeptide deformylase ms serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) (Bs) ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L9 (rplI) {Ec} ribosomal prt L10 (rplJ) (Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L13 (rplM) {Hi} ribosomal prt L14 (rplN) {Tm} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs}	68 67 51 tion 71 99 100 80 72 57 61 73 72 79 68	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) (Bs) translation initiation factor 3 (infC) (Pv) translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm}	73 70 68 87 73 72 67 56 100
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355 BB230	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor (Rbo) {Bb}	61 100 57 62 62 64 56 47	Protein BB105 (map) {E BB065 (def) {S) BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB493 BB390 BB112 BB391 BB393 BB393 BB393 BB393 BB488 BB497 BB488	modification methionine aminopeptidase 3s} polypeptide deformylase ns) serine/threonine kinase, put {Pf} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L6 (rplE) {Hi} ribosomal prt L6 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplI) {Ec} ribosomal prt L10 (rplI) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L13 (rplM) {Hi} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn}	68 67 51 tion 71 99 100 80 72 75 57 61 73 72 79 68 81	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpo	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins	73 70 68 87 73 72 67 56 100
BB712 BB450 Transcr BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor (Rb) (Bb) cocessing polynucleotide adenylylTase (papS) {Bs}	61 100 57 62 62 64 56 47 100	Protein BB105 (map) {E BB065 (def) {S} BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB112 BB391 BB393 BB393 BB393 BB393 BB393 BB393 BB488 BB497 BB485 BB495 BB485 BB503	modification methionine aminopeptidase 3s} polypeptide deformylase ns) serine/threonine kinase, put {Pf} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplL) {Ec} ribosomal prt L10 (rplJ) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L11 (rplK) {Tm} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L15 (rplO) {Bs} ribosomal prt L15 (rplO) {Ec}	68 67 51 tion 71 99 100 80 72 75 57 61 73 72 79 68 81 63	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpa	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} port and binding proteins	73 70 68 87 73 72 67 56 100 57 68
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355 BB230 <i>RNA pro</i> BB706	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) {Bb} ccessing polynucleotide adenylylTase (papS) {Bs}	61 100 57 62 62 64 56 47 100	Protein BB105 (map) {{I BB065 (def) {{S}} BB648 Ribosor BB392 BB493 BB499 BB490 BB493 BB391 BB391 BB391 BB393 BB393 BB393 BB393 BB393 BB485 BB485 BB494	modification methionine aminopeptidase Bs} polypeptide deformylase rn} serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L9 (rplI) {Ec} ribosomal prt L10 (rplJ) (Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L13 (rplM) (Hi) ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn} ribosomal prt L16 (rplP) {Syn} ribosomal prt L16 (rplP) {Ec} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L18 (rplR) {Bs}	68 67 51 tion 71 99 99 100 80 72 75 61 73 72 79 68 81 63 69	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpp Genera BB573	Hi) peptide chain release factor 2 (prf8 (Sc) ribosome releasing factor (frr) (Mt) translation initiation factor 1 (infA) (Ec) translation initiation factor 2 (infB) (Bs) translation initiation factor 3 (infC) (Pv) translation elongation factor G (fus-2) (Tm) translation elongation factor P (efp) (Ec) translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) (Hi) translation elongation factor G (fus-1) (Tm) port and binding proteins ABC transporter, ATP-BP (Bs)	73 70 68 87 73 72 67 56 100 57 68
BB712 BB450 Transcr BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) {Bb} ccessing polynucleotide adenylylTase (papS) {Bs}	61 100 57 62 62 64 56 47 100	Protein BB105 (map) {E BB065 (def) {S} BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB112 BB391 BB393 BB393 BB393 BB393 BB393 BB393 BB488 BB497 BB485 BB495 BB485 BB503	modification methionine aminopeptidase 3s} polypeptide deformylase ns) serine/threonine kinase, put {Pf} serine/threonine kinase, put {Pf} nal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplL) {Ec} ribosomal prt L10 (rplJ) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L11 (rplK) {Tm} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L15 (rplO) {Bs} ribosomal prt L15 (rplO) {Ec}	68 67 51 tion 71 99 100 80 72 75 57 61 73 72 79 68 81 63	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpa	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} port and binding proteins	73 70 68 87 73 72 67 56 100 57 68
BB712 BB450 <i>Transcr</i> BB107 BB800 BB394 BB132 BB355 BB230 <i>RNA pro</i> BB706 Translat <i>General</i> BB590	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor (preA) (Ec) transcription detor, put {Mx} transcription termination factor Rho (rho) (Bb) cocessing polynucleotide adenylylTase (papS) {Bs} dion dimethyladenosine Tase (ksgA) {Bs}	61 100 57 62 62 64 56 47 100 57	Protein BB105 (map) {I BB065 (def) {Sy BB648 BB392 BB478 BB479 BB490 BB493 BB393 BB399 BB399 BB399 BB399 BB393 BB393 BB393 BB393 BB398 BB494 BB494 BB698 BB188 BB778	modification methionine aminopeptidase as} polypeptide deformylase yn} serine/threonine kinase, put {Pf} sinal proteins: synthesis and modification ribosomal prt L2 (rpID) {Bb} ribosomal prt L3 (rpIC) {Bb} ribosomal prt L4 (rpID) {Bb} ribosomal prt L6 (rpIF) {Sc} ribosomal prt L7/L12 (rpIL) {Sc} ribosomal prt L10 (rpII) {Bc} ribosomal prt L10 (rpII) {Bs} ribosomal prt L11 (rpIN) {Tm} ribosomal prt L14 (rpIN) {Tm} ribosomal prt L15 (rpIO) {Bs} ribosomal prt L16 (rpIP) {Syn} ribosomal prt L17 (rpIQ) {Ec} ribosomal prt L18 (rpIR) {Bs} ribosomal prt L19 (rpIS) {Ec} ribosomal prt L20 (rpIT) {Ec} ribosomal prt L21 (rpIU) {Ec}	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 79 68 81 63 69 74 70 58	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpt Genera BB573 BR742 BB466 BB754	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} port and binding proteins ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {BI}	73 70 68 87 73 72 67 56 100 57 68
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BB712 BB450 Transcr BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706 Translate General BB590 BB802 Amino a BB220	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) (Bb) Decessing polynucleotide adenylylTase (papS) {Bs} ition dimethyladenosine Tase (ksgA) (Bs) ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec}	61 100 57 62 62 64 56 47 100 57	Protein BB105 (map) {I BB065 (def) {Sy BB648 Ribosor BB392 BB493 BB499 BB493 BB391 BB393 BB391 BB393 BB393 BB393 BB393 BB393 BB494 BB485 BB503 BB494 BB699 BB188 BB778 BB483 BB778 BB483 BB489 BB489	modification methionine aminopeptidase as} polypeptide deformylase m) serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplI) {Bc} ribosomal prt L10 (rplI) {Bs} ribosomal prt L10 (rplI) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L11 (rplK) {Tm} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L18 (rplR) {Bs} ribosomal prt L19 (rplS) {Ec} ribosomal prt L19 (rplT) {Ec} ribosomal prt L20 (rplT) {Ec} ribosomal prt L21 (rplU) {Bb} ribosomal prt L22 (rplV) {Bb} ribosomal prt L23 (rplW) {Bb} ribosomal prt L24 (rplX) {Ec}	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 58 100	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpt Genera BB573 BB742 BB466 BB754 BB080 BB269 BB726	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor P (tuf) {Bb} translation elongation factor TU (tuf) {Bb} translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins / ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Mj} ABC transporter, ATP-BP {Mj} ATP-BP (y xH-1) {Bb}	73 70 68 87 73 72 67 56 100 57 68
BB712 BB450 Transcr. BB107 BB800 BB394 BB132 BB355 BB230 Translat General BB590 BB802 Amino a BB220 BB594	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) {Bb} coessing polynucleotide adenylylTase (papS) {Bs} dion dimethyladenosine Tase (ksgA) {Bs} ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec} arginyl-tRNA Sase (argS) {Mj}	61 100 57 62 62 64 56 47 100 57	Protein BB105 (map) {E BB065 (def) {Sy BB648 Ribosor BB392 BB481 BB478 BB479 BB493 BB390 BB112 BB391 BB391 BB393 BB391 BB393 BB398 BB488 BB497 BB485 BB503 BB485 BB503 BB485 BB699 BB188 BB778 BB699 BB188 BB778 BB699 BB188 BB778 BB699 BB188 BB783 BB783 BB784 BB699 BB188 BB783 BB784 B	modification methionine aminopeptidase ass} polypeptide deformylase ms serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) (Bs) ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L10 (rplJ) (Bs) ribosomal prt L11 (rplK) {Tm} ribosomal prt L11 (rplK) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn} ribosomal prt L16 (rplP) {Syn} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L18 (rplR) {Bs} ribosomal prt L19 (rplC) {Ec} ribosomal prt L19 (rplC) {Ec} ribosomal prt L19 (rplC) {Ec} ribosomal prt L21 (rplV) {Ec} ribosomal prt L22 (rplV) {Bb} ribosomal prt L23 (rplW) {Bb} ribosomal prt L24 (rplX) {Ec} ribosomal prt L27	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 70 70 70 70 70 70 70 70 70	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpe Genera BB573 BB742 BB466 BB726 BB269 BB726	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {EC} translation initiation factor 2 (infB) (Bs) translation initiation factor 3 (infC) (Pv) translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TU (tuf) (Bb) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins / ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Mj} ATP-BP (yixH-1) {Bb} ATP-BP (yixH-2) {Bb}	73 70 68 87 73 72 67 56 100 57 68 53 57 74 60 63 100 54
BB712 BB450 Transcr BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706 Translate General BB590 BB802 Amino a BB220	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) {Bs} transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) (Bb) Decessing polynucleotide adenylylTase (papS) {Bs} ition dimethyladenosine Tase (ksgA) (Bs) ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec}	61 100 57 62 62 64 56 47 100 57	Protein BB105 (map) {I BB065 (def) {Sy BB648 Ribosor BB392 BB493 BB499 BB493 BB391 BB393 BB391 BB393 BB393 BB393 BB393 BB393 BB494 BB485 BB503 BB494 BB699 BB188 BB778 BB483 BB778 BB483 BB489 BB489	modification methionine aminopeptidase as} polypeptide deformylase m) serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplI) {Bc} ribosomal prt L10 (rplI) {Bs} ribosomal prt L10 (rplI) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L11 (rplK) {Tm} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L18 (rplR) {Bs} ribosomal prt L19 (rplS) {Ec} ribosomal prt L19 (rplT) {Ec} ribosomal prt L20 (rplT) {Ec} ribosomal prt L21 (rplU) {Bb} ribosomal prt L22 (rplV) {Bb} ribosomal prt L23 (rplW) {Bb} ribosomal prt L24 (rplX) {Ec}	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 58 100 100	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpt Genera BB573 BB742 BB466 BB754 BB080 BB269 BB726	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor P (tuf) {Bb} translation elongation factor TU (tuf) {Bb} translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins / ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Mj} ABC transporter, ATP-BP {Mj} ATP-BP (y xH-1) {Bb}	73 70 68 87 73 72 67 56 100 57 68
BB712 BB450 Transcr. BB107 BB800 BB394 BB132 BB355 BB230 Translat General BB590 BB802 Amino a BB220 BB594 BB101 BB446 BB599	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) (Bs) transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) (Bb) Decessing polynucleotide adenylylTase (papS) {Bs} ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec} arginyl-tRNA Sase (agrS) {Mi} asparaginyl-tRNA Sase (agrS) {Ec} cysteinyl-tRNA Sase (cysS) {Hi}	61 100 57 62 62 64 56 47 100 57 61 62 62 55 73 66 58	Protein BB105 (map) {{I BB065} (def) {{S}} BB648 Ribosor BB392 BB481 BB478 BB490 BB493 BB390 BB112 BB391 BB393 BB393 BB393 BB398 BB497 BB485 BB497 BB485 BB498 BB188 BB497 BB485 BB499 BB188 BB497 BB485 BB480 BB480 BB480 BB480 BB480	modification methionine aminopeptidase as} polypeptide deformylase m) serine/threonine kinase, put {Pf} mal proteins: synthesis and modificat ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L6 (rplF) {Sc} ribosomal prt L9 (rplI) {Ec} ribosomal prt L10 (rplI) {Bs} ribosomal prt L10 (rplI) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L11 (rplK) {Tm} ribosomal prt L13 (rplM) {Hi} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L18 (rplR) {Bs} ribosomal prt L19 (rplS) {Ec} ribosomal prt L19 (rplS) {Ec} ribosomal prt L20 (rplT) {Ec} ribosomal prt L22 (rplV) {Bb} ribosomal prt L23 (rplW) {Bb} ribosomal prt L24 (rplX) {Ec} ribosomal prt L27 (rpmA) {Hi} ribosomal prt L28 (rpmB) {Ec}	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 58 100 100 64 82 62	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpt Genera BB573 BB742 BB466 BB754 BB080 BB269 BB726 Ip38 BBJ26 Amino	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {EC} translation initiation factor 2 (infB) (Bs) translation initiation factor 3 (infC) (Pv) translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) (Bb) translation elongation factor TU (tuf) (Bt) translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins / ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Mj} ATP-BP (ylxH-1) {Bb} ATP-BP (ylxH-2) {Bb} ABC transporter, ATP-BP {Mj} ATP-BP (glxH-2) {Bb} ABC transporter, ATP-BP {Mj} ATP-BP (glxH-2) {Bb}	73 70 68 87 73 72 67 56 100 57 68 53 57 74 60 63 100 54 62
BB712 BB450 Transcr. BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706 Translat General BB590 BB802 Amino a BB220 BB594 BB101 BB446 BB599 BB372	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) (Bs) transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription factor, put {Mx} transcription termination factor Rho (rho) {Bb} coessing polynucleotide adenylylTase (papS) {Bs} ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec} arginyl-tRNA Sase (asnS) {Ec} aspartyl-tRNA Sase (asnS) {Ec} cysteinyl-tRNA Sase (cysS) {Hi} glutamyl-tRNA Sase (cysS) {Hi} glutamyl-tRNA Sase (gltX) {Rm}	61 100 57 62 62 64 56 47 100 57	Protein BB105 (map) {E BB065 (def) {Sy BB648 Riboson BB392 BB478 BB479 BB493 BB493 BB390 BB112 BB393 BB393 BB393 BB393 BB393 BB398 BB485 BB503 BB485 BB699 BB188 BB780 BB489 BB780 BB780 BB780 BB350 BB350 BB350 BB350	modification methionine aminopeptidase ass} polypeptide deformylase ms polypeptide deformylase mibosomal prt L1 (rplA) (Bs) ribosomal prt L2 (rplB) (Bb) ribosomal prt L3 (rplC) (Bb) ribosomal prt L4 (rplD) (Bb) ribosomal prt L5 (rplE) (Hi) ribosomal prt L6 (rplF) (Sc) ribosomal prt L9 (rplI) (Ec) ribosomal prt L10 (rplI) (Bs) ribosomal prt L11 (rplK) (Tm) ribosomal prt L13 (rplM) (Hi) ribosomal prt L14 (rplN) (Tm) ribosomal prt L16 (rplP) (Syn) ribosomal prt L16 (rplP) (Syn) ribosomal prt L16 (rplP) (Ec) ribosomal prt L19 (rplS) (Ec) ribosomal prt L20 (rplT) (Ec) ribosomal prt L20 (rplT) (Ec) ribosomal prt L22 (rplW) (Bb) ribosomal prt L23 (rplW) (Bb) ribosomal prt L24 (rplX) (Ec) ribosomal prt L27 (rpmA) (Hi) ribosomal prt L28 (rpmB) (Ec) ribosomal prt L29 (rpmC) (Bs)	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 58 100 100 64 82 65 65	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpa Genera BB573 BB742 BB466 BB754 BB080 BB269 BB726 Lp38 BBJ26 Amino BB729	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) (Mt) translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor P (tfp) {Eb} translation elongation factor TU (tuf) {Bb} translation elongation factor TU (tuf) {Bb} translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins / ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Mj} ATP-BP (yixH-1) {Bb} ATP-BP (yixH-2) {Bb} ABC transporter, ATP-BP {Mj} acids, peptide, and amines glutamate transporter (gltP) {Bs}	73 70 68 87 73 72 67 56 100 57 68 53 57 74 60 63 100 54
BB712 BB450 Transcr. BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706 Translat General BB590 BB802 Amino a BB220 BB594 BB101 BB446 BB599 BB372 BB371	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) (Bs) transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription termination factor Rho (rho) {Bb} coessing polynucleotide adenylylTase (papS) {Bs} ition dimethyladenosine Tase (ksgA) {Bs} ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec} arginyl-tRNA Sase (alaS) {Ec} asparaginyl-tRNA Sase (aspS) {Ec} cysteinyl-tRNA Sase (gytX) {Rm} glycyl-tRNA Sase (glyX) {Ta}	61 100 57 62 62 64 56 47 100 57 61 62 62 62 55 73 66 58 63 63 68	Protein BB105 (map) {I BB065 (def) {Sy BB065 (def) {Sy BB648 Ribosor BB392 BB481 BB478 BB479 BB490 BB493 BB391 BB391 BB393 BB488 BB497 BB488 BB496 BB489	modification methionine aminopeptidase as} polypeptide deformylase yn} serine/threonine kinase, put {Pf} mal proteins: synthesis and modifications ribosomal prt L1 (rplA) {Bs} ribosomal prt L2 (rplB) {Bb} ribosomal prt L3 (rplC) {Bb} ribosomal prt L4 (rplD) {Bb} ribosomal prt L5 (rplE) {Hi} ribosomal prt L6 (rplF) {Sc} ribosomal prt L7/L12 (rplL) {Sc} ribosomal prt L9 (rplI) {Bc} ribosomal prt L10 (rplI) {Bs} ribosomal prt L10 (rplI) {Bs} ribosomal prt L11 (rplK) {Tm} ribosomal prt L14 (rplN) {Tm} ribosomal prt L15 (rplO) {Bs} ribosomal prt L16 (rplP) {Syn} ribosomal prt L16 (rplP) {Syn} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L17 (rplQ) {Ec} ribosomal prt L18 (rplR) {Bs} ribosomal prt L19 (rplS) {Ec} ribosomal prt L20 (rplT) {Ec} ribosomal prt L21 (rplU) {Ec} ribosomal prt L23 (rplW) {Bb} ribosomal prt L24 (rplW) {Ec} ribosomal prt L27 (rpmA) {Hi} ribosomal prt L28 (rpmB) {Ec} ribosomal prt L29 (rpmC) {Bs}	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 58 100 100 64 82 65 60	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpic Genera BB573 BB742 BB466 BB754 BB080 BB269 BB756 BB269 BB756 BB269 BB756 BB766 BB767 BB768 BB7799 BB401	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) {Mt} translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {PV} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor TU (tuf) {Bb} translation elongation factor TU (tuf) {Bb} translation elongation factor TS (tsf) {Hi} translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} Port and binding proteins ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Bl} ABC transporter, ATP-BP {Mi} ABC transporter, ATP-BP {Mj} ATP-BP (ylxH-1) {Bb} ATP-BP (ylxH-1) {Bb} ABC transporter, ATP-BP {Mj} ATP-BP (ylxH-2) {Bb} ABC transporter, ATP-BP {Mj} ATP-BP (ylxH-2) {Bb} ABC transporter, ATP-BP {Mj} ATP-BP (ylxH-2) {Bb}	73 70 68 87 73 72 67 56 100 57 68 53 57 74 60 63 100 54 62
BB712 BB450 Transcr. BB107 BB800 BB394 BB132 BB355 BB230 RNA pro BB706 Translat General BB590 BB802 Amino a BB220 BB594 BB101 BB446 BB599 BB372	(rpoS) (Pa) RNA polymerase sigma-70 factor (rpoD) (Bb) RNA polymerase sigma-54 factor (ntrA) {Av} iption factors N utilization substance prt B (nusB) {Ec} N-utilization substance prt A (nusA) (Bs) transcription antitermination factor (nusG) {Ec} transcription elongation factor (greA) {Ec} transcription factor, put {Mx} transcription factor, put {Mx} transcription termination factor Rho (rho) {Bb} coessing polynucleotide adenylylTase (papS) {Bs} ribosome-B factor A (rbfA) {Bs} acyl tRNA synthetases alanyl-tRNA Sase (alaS) {Ec} arginyl-tRNA Sase (asnS) {Ec} aspartyl-tRNA Sase (asnS) {Ec} cysteinyl-tRNA Sase (cysS) {Hi} glutamyl-tRNA Sase (cysS) {Hi} glutamyl-tRNA Sase (gltX) {Rm}	61 100 57 62 62 64 56 47 100 57	Protein BB105 (map) {E BB065 (def) {Sy BB648 Riboson BB392 BB478 BB479 BB493 BB493 BB390 BB112 BB393 BB393 BB393 BB393 BB393 BB398 BB485 BB503 BB485 BB699 BB188 BB780 BB489 BB780 BB780 BB780 BB350 BB350 BB350 BB350	modification methionine aminopeptidase ass} polypeptide deformylase ms polypeptide deformylase mibosomal prt L1 (rplA) (Bs) ribosomal prt L2 (rplB) (Bb) ribosomal prt L3 (rplC) (Bb) ribosomal prt L4 (rplD) (Bb) ribosomal prt L5 (rplE) (Hi) ribosomal prt L6 (rplF) (Sc) ribosomal prt L9 (rplI) (Ec) ribosomal prt L10 (rplI) (Bs) ribosomal prt L11 (rplK) (Tm) ribosomal prt L13 (rplM) (Hi) ribosomal prt L14 (rplN) (Tm) ribosomal prt L16 (rplP) (Syn) ribosomal prt L16 (rplP) (Syn) ribosomal prt L16 (rplP) (Ec) ribosomal prt L19 (rplS) (Ec) ribosomal prt L20 (rplT) (Ec) ribosomal prt L20 (rplT) (Ec) ribosomal prt L22 (rplW) (Bb) ribosomal prt L23 (rplW) (Bb) ribosomal prt L24 (rplX) (Ec) ribosomal prt L27 (rpmA) (Hi) ribosomal prt L28 (rpmB) (Ec) ribosomal prt L29 (rpmC) (Bs)	68 67 51 tion 71 99 99 100 80 72 75 57 61 73 72 79 68 81 63 69 74 70 58 100 100 64 82 65 65	BB196 BB074 BB121 BB169 BB801 BB190 BB691 BB214 BB476 BB122 BB540 Transpa Genera BB573 BB742 BB466 BB754 BB080 BB269 BB726 Lp38 BBJ26 Amino BB729	Hi) peptide chain release factor 2 (prfB (Sc) ribosome releasing factor (frr) (Mt) translation initiation factor 1 (infA) {Ec} translation initiation factor 2 (infB) {Bs} translation initiation factor 3 (infC) {Pv} translation elongation factor G (fus-2) {Tm} translation elongation factor P (efp) {Ec} translation elongation factor P (tfp) {Eb} translation elongation factor TU (tuf) {Bb} translation elongation factor TU (tuf) {Bb} translation elongation factor TS (tsf) {Hi} translation elongation factor G (fus-1) {Tm} ort and binding proteins / ABC transporter, ATP-BP {Bs} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Hi} ABC transporter, ATP-BP {Mj} ATP-BP (yixH-1) {Bb} ATP-BP (yixH-2) {Bb} ABC transporter, ATP-BP {Mj} acids, peptide, and amines glutamate transporter (gltP) {Bs}	73 70 68 87 73 72 67 56 100 57 68 53 57 74 60 63 100 54

	(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	40	BB558	phosphoenolpyruvate-prt PPase	0.5	BBI26	multidrug-efflux transporter {Hp}	55
BB334	(proX) {Ec}	43	BB408	(ptsl) {Sc}	65	I 0F		
BB334	OP ABC transporter, ATP-BP (oppD) {Bs}	75	BB408	PTS system, fru-specific IIABC (fruA-1) {Ec}	65	<u>lp25</u> BBE22	pyrazinamidase/nicotinamidase	
BB335	OP ABC transporter, ATP-BP	75	BB629	PTS system, fru-specific IIABC	00	DDEZZ	(pncA) {Mt}	56
DDSSS	(oppF) {Bs}	80	DD029	(fruA-2) {Ec}	68		(blicy) fivit	30
BB332	OP ABC transporter, permease prt	00	BB559	PTS system, glu-specific IIA	00	Transno	oson-related functions	
55002	(oppB-1){Ec}	68	55000	(crr) {Bb}	100		recon related rametiene	
BB747	OP ABC transporter, permease prt		BB645	PTS system, glu-specific IIBC		lp38		
	(oppB-2){Bs}	54		(ptsG) {Sc}	67	BBJ05	transposase-like prt, put {Bb}	89
BB333	OP ABC transporter, permease		BB116	PTS system, mal/glu-specific				
	prt (oppC-1){Hi}	64		IIABC (malX) {Ec}	56	<u>lp36</u>		
BB746	OP ABC transporter, permease		BB677	RG ABC transporter, ATP-BP		BBK25	transposase-like prt, put {Bb}	80
DDooo	prt (oppC-2){Bs}	52	DD070	(mglA) {Mg}	68			
BB328	OP ABC transporter,		BB678	RG ABC transporter,	F4	<u>lp28-1</u> BBF18	trananagaa lika art aut (Dh)	96
	periplasmic BP (oppA-1) {Bb}	74	BB679	permease prt (rbsC-1) {Mg} RG ABC transporter,	51	BBF19	transposase-like prt, put {Bb} transposase-like prt, put {Bb}	96
BB329	OP ABC transporter,	74	00079	permease prt (rbsC-2) {Mp}	52	DDF 19	transposase-like prt, put {bb}	90
DDSZS	periplasmic BP (oppA-2) {Bb}	94		permease pit (1030-2) (wp)	JZ	lp28-2		
BB330	OP ABC transporter,	J-T	cp26				transposase-like prt {Bb}	99
55000	periplasmic BP (oppA-3) {Bb}	81	BBB04	PTS system, cello-specific			, and a control in the (2-2)	
BB642	SP ABC transporter, ATP-BP			IIC (celB) {Bs}	62	lp28-3		
	(potA) {Ec}	69	BBB05	PTS system, cello-specific		BBH40	transposase-like prt, put {Bb}	57
BB641	SP ABC transporter, permease prt			IIA (celC) {Bs}	61			
	(potB) {Ec}	65	BBB06	PTS system, cello-specific		<u>lp17</u>		
BB640	SP ABC transporter, permease prt			IIB (celA) {Bs}	73		transposase-like prt, put {Bb}	99
DDooo	(potC) {Ec}	63	BBB29	PTS system, glu-specific	70	BBD23	transposase-like prt, put {Bb}	88
BB639	SP ABC transporter, periplasmic			IIBC, put {Ec}	70			
	BP (potD) {Ec}	53	Cationa			Unknow		57
In54	BP (potD) {Ec}	53	Cations BB724	K+ transport prt (ntpl) {Fh}	60	BB528	aldose RDase, put {Bs}	57 58
<u>lp54</u> BBA34		53	BB724	K+ transport prt (ntpJ) {Eh} Mg2+ transport prt (mgtE) {Bb}	60 100	BB528 BB684	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss}	58
<u>lp54</u> BBA34	OP ABC transporter,	53 66	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
			BB724			BB528 BB684	aldose RDase, put {Bs} carotenoid biosyn prt, put {Ss}	58 99 54 53
	OP ABC transporter,		BB724 BB380 BB164	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}	58 99 54 53 59
BBA34	OP ABC transporter, periplasmic BP (oppA-4) {Bc} 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	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other ca Adaptat	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 c: <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	66 78	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other ca Adaptat	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) P ABC transporter, permease	66787458	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other ca Adaptat 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 BB036	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
EBA34 CD26 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)	66787458	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 BB336 BB336 BB333 BB033 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} P115 prt {Mh} P26 {Bb} periplasmic prt {Bb}	58 99 54 53 59 54 58 47 49 62 53 100 100 70 100
CD26 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 <i>Other</i> BB451 Other c: 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 BB045 BB336 BB336 BB363 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} P115 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 C <i>Adaptat</i> BB237 BB785 BB785 BB785 Colicin-1	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
CD26 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 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 70 100 56
EBA34 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	78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other C <i>Adaptat</i> BB237 BB785 BB785 BB785 Colicin-1	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) vdrates, 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 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 BB363 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 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 70 100 56
EBA34 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, permease prt (pstA) {Syn} P ABC transporter, periplasmic P-BP (pstB) {Syn} **drates, organic alcohols, and acids glycerol uptake facilitator (glpF) {Bs} L-lactate permease (lctP) {Ec} methylgalactoside	78 74 58 63 48	BB724 BB380 BB164 BB447 BB637 BB638 <i>Other</i> BB451 Other c: <i>Adaptat</i> BB237 BB786 BB785 BB810 <i>Colicin-</i> 1 BB766 BB546	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) 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)	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB454 BB702 BB045 BB336 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 {Mi} P116 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 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) **Orland transporter alcohols, and acids glycerol uptake facilitator (glpF) (Bs) L-lactate permease (lctP) (Ec) methylgalactoside ABC transporter, ATP-BP	66 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 BB766 BB766	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} rel analog sensitivity	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB168 BB508 BB219 BB421 BB524 BB454 BB702 BB045 BB336 BB363 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 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 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) **Cortansporter**, pe	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 BB766 BB766	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) 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)	100 59 57 48 50 58 45 51 74 51	BB528 BB684 BB671 BB250 BB168 BB528 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 {Mi} P116 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 70 100 56
Cp26 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) **Transporter** **Transporter* **Transporter*	66 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 BB766 BB766	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} ad analog sensitivity acriflavine 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 BB363 BB033 BB297 BB443 Ip54 BBA76 Ip28-4 BBI06 Cp9	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 {Mi} P116 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 70 100 56
Cp26 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, 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)	66 78 74 58 63 48 57 57	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other Cc Adaptat BB237 BB785 BB810 Colicin-1 BB766 BB546 Drug ar 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) Na+/H+ antiporter (nhaC-2) (Hi) chromate transport prt, put (Mi) 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 BB299 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB336 BB336 BB336 BB336 BB336 BB336 BB336 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} 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 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} vdrates, 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}	66 78 74 58 63 48 57 57	BB724 BB380 BB164 BB447 BB637 BB638 Other BB451 Other Cc Adaptat BB237 BB785 BB810 Colicin-1 BB766 BB546 Drug ar 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} bacitracin resistance prt	100 59 57 48 50 58 45 51 74 51 52 44	BB528 BB684 BB671 BB250 BB168 BB299 BB421 BB524 BB454 BB702 BB045 BB336 BB336 BB336 BB336 BB336 BB336 BB336 BB336 BB336 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 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