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# errata

# The yeast genome directory

Nature 387 (suppl.) (1997)

In the list of authors given on page 5 of this supplement, the names of some authors were omitted or misspelled (asterisks). These were: R. Altmann; W. Arnold\*; M. de Haan\*; K. Hamberg; K. Hinni; L. Jones; W. Kramer; H. Küster\*; K. C. T. Maurer\*; D. Niblett; N. Paricio\*; A. G. Parle-McDermott\*; C. Rebischung; C. Richards; L. Rifkin\*; J. Robben; C. Rodrigues-Pousada\*; I. Schaaff-Gerstenschläger\*; P. H. M. Smits\*; Y. Su\*; Q. J. M. van der Aart\*; J. C. van Vliet-Reedijk\*; A. Wach; M. Yamazaki\*.

# Measurements of elastic anisotropy due to solidification texturing and the implications for the Earth's inner core

# Michael I. Bergman

Nature 389, 60-63 (1997)

Owing to a typographical error, this Letter appeared under the title "Measurements of electric anisotropy due to solidification texturing and the implications for the Earth's inner core". The word 'elastic' in the first line was erroneously replaced with 'electric'.

# cAMP-induced switching in turning direction of nerve growth cones

Hong-jun Song, Guo-li Ming & Mu-ming Poo

Nature 388, 275-279 (1997)

The order of panels in Fig. 3 of this Letter is incorrect as published. Figure 3a-e should be labelled as f-j, and Fig. 3f-j should be labelled a-e.

# corrections

# Synthesis and X-ray structure of dumb-bell-shaped C<sub>120</sub>

Guan-Wu Wang, Koichi Komatsu, Yasujiro Murata & Motoo Shiro

Nature **387**, 583–586 (1997)

In this Letter, we overlooked a citation of G. Oszlanyi *et al.*, *Phys. Rev. B* **54**, 11849 (1996), who reported the observation of covalently bound  $(C_{60})_2^{2-}$  dianions from the X-ray powder diffraction patterns of the metastable phases of  $KC_{60}$  and  $RbC_{60}$ .

# The complete genome sequence of the gastric pathogen *Helicobacter pylori*

Jean-F. Tomb, Owen White, Anthony R. Kerlavage, Rebecca A. Clayton, Granger G. Sutton, Robert D. Fleischmann, Karen A. Ketchum, Hans Peter Klenk, Steven Gill, Brian A. Dougherty, Karen Nelson, John Quackenbush, Lixin Zhou, Ewen F. Kirkness, Scott Peterson, Brendan Loftus, **Delwood Richardson, Robert Dodson,** Hanif G. Khalak, Anna Glodek, Keith McKenney, Lisa M. Fitzegerald, Norman Lee, Mark D. Adams, Erin K. Hickey, Douglas E. Berg, Jeanine D. Gocayne, Teresa R. Utterback, Jeremy D. Peterson, Jenny M. Kelley, Matthew D. Cotton, Janice M. Weidman, Claire Fujii, Cheryl Bowman, Larry Watthey, Erik Wallin, William S. Hayes, Mark Borodovsky, Peter D. Karp, Hamilton O. Smith, Claire M. Fraser & J. Craig Venter

Nature 388, 539-547 (1997)

In this Article, we incorrectly stated that the amino acids lysine and arginine are twice as abundant in *H. pylori* proteins as they are in those of *Haemophilus influenzae* and *Escherichia coli*. This statement was derived from amino-acid analyses that compared absolute differences in abundance, but these do not reflect the frequencies with which amino acids are found in the organisms in question. The actual abundance of arginine in *H. pylori*, *H. influenzae* and *E. coli* is 3.5, 4.5 and 5.5%, respectively; the abundance of lysine in these organisms is 8.9, 6.3 and 4.4%, respectively. This oversight is particularly unfortunate because Russell H. Doolittle, who wrote an accompanying News and Views on our Article and brought this to our attention, was led to comment on the significance of our inaccurate observation. We regret this and any other misunderstanding that our error may have caused.

# The complete genome sequence of the gastric pathogen *Helicobacter pylori*

Jean-F. Tomb\*, Owen White\*, Anthony R. Kerlavage\*, Rebecca A. Clayton\*, Granger G. Sutton\*, Robert D. Fleischmann\*, Karen A. Ketchum\*, Hans Peter Klenk\*, Steven Gill\*, Brian A. Dougherty\*, Karen Nelson\*, John Quackenbush\*, Lixin Zhou\*, Ewen F. Kirkness\*, Scott Peterson\*, Brendan Loftus\*, Delwood Richardson\*, Robert Dodson\*, Hanif G. Khalak\*, Anna Glodek\*, Keith McKenney\*, Lisa M. Fitzegerald\*, Norman Lee\*, Mark D. Adams\*, Erin K. Hickey\*, Douglas E. Berg†, Jeanine D. Gocayne\*, Teresa R. Utterback\*, Jeremy D. Peterson\*, Jenny M. Kelley\*, Matthew D. Cotton\*, Janice M. Weidman\*, Claire Fujii\*, Cheryl Bowman\*, Larry Watthey\*, Erik Wallin‡, William S. Hayes§, Mark Borodovsky§, Peter D. Karp||, Hamilton O. Smith§, Claire M. Fraser\* & J. Craig Venter\*

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Helicobacter pylori, strain 26695, has a circular genome of 1,667,867 base pairs and 1,590 predicted coding sequences. Sequence analysis indicates that *H. pylori* has well-developed systems for motility, for scavenging iron, and for DNA restriction and modification. Many putative adhesins, lipoproteins and other outer membrane proteins were identified, underscoring the potential complexity of host-pathogen interaction. Based on the large number of sequence-related genes encoding outer membrane proteins and the presence of homopolymeric tracts and dinucleotide repeats in coding sequences, *H. pylori*, like several other mucosal pathogens, probably uses recombination and slipped-strand mispairing within repeats as mechanisms for antigenic variation and adaptive evolution. Consistent with its restricted niche, *H. pylori* has a few regulatory networks, and a limited metabolic repertoire and biosynthetic capacity. Its survival in acid conditions depends, in part, on its ability to establish a positive inside-membrane potential in low pH.

For most of this century the cause of peptic ulcer disease was thought to be stress-related and the disease to be prevalent in hyperacid producers. The discovery<sup>1</sup> that *Helicobacter pylori* was associated with gastric inflammation and peptic ulcer disease was initially met with scepticism. However, this discovery and subsequent studies on *H. pylori* have revolutionized our view of the gastric environment, the diseases associated with it, and the appropriate treatment regimens<sup>2</sup>.

Helicobacter pylori is a micro-aerophilic, Gram-negative, slowgrowing, spiral-shaped and flagellated organism. Its most characteristic enzyme is a potent multisubunit urease<sup>3</sup> that is crucial for its survival at acidic pH and for its successful colonization of the gastric environment, a site that few other microbes can colonize<sup>2</sup>. H. pylori is probably the most common chronic bacterial infection of humans, present in almost half of the world population<sup>2</sup>. The presence of the bacterium in the gastric mucosa is associated with chronic active gastritis and is implicated in more severe gastric diseases, including chronic atrophic gastritis (a precursor of gastric carcinomas), peptic ulceration and mucosa-associated lymphoid tissue lymphomas<sup>2</sup>. Disease outcome depends on many factors, including bacterial genotype, and host physiology, genotype and dietary habits<sup>4,5</sup>. H. pylori infection has also been associated with persistent diarrhoea and increased susceptibility to other infectious diseases<sup>6</sup>.

Because of its importance as a human pathogen, our interest in its biology and evolution, and the value of complete genome sequence information for drug discovery and vaccine development, we have

# **Table 1 Genome features**

## General

Coding regions (91.0%) Stable RNA (0.7%) Non-coding repeats (2.3%) Intergenic sequence (6.0%)

## RNA

 Ribosomal RNA
 Coordinates

 235-5S
 445,306-448,642 bp

 23S-5S
 1,473,557-1,473,919 bp

 16S
 1,209,082-1,207,584 bp

 16S
 1,511,138-1,512,635 bp

 5S
 448,041-448,618 bp

## Transfer RNA

36 species (7 clusters, 12 single genes)

Structural RNA

1 species (ssrD)

# 629,845-630,124 bp

## DNA

# Insertion sequences

IS605 13 copies (5 full-length, 8 partial) IS606 4 copies (2 full-length, 2 partial)

## Distinct G + C regions

region 1 (33% G + C) 452-479 kb region 2 (35% G + C) 539-579 kb region 3 (33% G + C) 1,049-1,071 kb region 4 (43% G + C) 1,264-1,276 kb region 5 (33% G + C) 1,590-1,602 kb

cag PAI (Fig. 4)
IS605, 5SRNA and repeat 7
β and β' RNA polymerase, EF-G (fusA)
two restriction/modification systems

IS605, 5SRNA and repeat 7; virB4

Associated genes

## Coding sequences

1,590 coding sequences (average 945 bp)
1,091 identified database match

# articles

sequenced the genome of a representative *H. pylori* strain by the whole-genome random sequencing method as described for *Haemophilus influenzae*<sup>7</sup>, *Mycoplasma genitalium*<sup>8</sup> and *Methanococcus jannaschii*<sup>9</sup>.

# General features of the genome

**Genome analysis.** The genome of H. pylori strain 26695 consists of a circular chromosome with a size of 1,667,867 base pairs (bp) and average G + C content of 39% (Figs 1 and 2). Five regions within the genome have a significantly different G + C composition (Table 1 and Fig. 1). Two of them contain one or more copies of the insertion sequence IS605 (see below) and are flanked by a 5S ribosomal RNA sequence at one end and a 521 bp repeat (repeat 7) near the other. These two regions are also notable because they contain genes involved in DNA processing and one contains 2 orthologues of the virB4/ptl gene, the product of which is required for the transfer of oncogenic T-DNA of Agrobacterium and the secretion of the pertussis toxin by Bordetella pertussis<sup>10</sup>. Another region is the cag pathogenicity island (PAI), which is flanked by 31-bp direct repeats, and appears to be the product of lateral transfer<sup>11</sup>.

RNA and repeat elements. Thirty-six tRNA species were identified using tRNAscan-SE<sup>12</sup>. These are organized into 7 clusters plus 12 single genes. Two separate sets of 23S–5S and 16S ribosomal RNA (rRNA) genes were identified, along with one orphan 5S gene and one structural RNA gene (Table 1). Associated with each of the two 23S–5S gene clusters is a 6-kilobase (kb) repeat containing a possible operon of 5 ORFs that have no database matches.

Eight repeat families (>97% identity) varying in length from 0.47 to 3.8 kb were found in the chromosome (Figs 1 and 2). Members of repeat 7 are found in intergenic regions, while the others are associated with coding sequences and may represent gene duplications. Repeats 1, 2, 3 and 6 are associated with genes that encode outer-membrane proteins (OMP) (Fig. 3).

Two distinct insertion sequence (IS) elements are present. There are five full-length copies of the previously described IS605<sup>11,13</sup> and two of a newly discovered element designated IS606. In addition, there are eight partial copies of IS605 and two partial copies of IS606. Both elements encode two divergently transcribed transposases (TnpA and TnpB). IS606 has less than 50% nucleotide identity with IS605 and the IS606 transposases have 29% amino-acid identity with their IS605 counterpart. Both copies of the IS606 TnpB may be non-functional owing to frameshifts.

**Origin of replication.** As a typical eubacterial origin of replication was not identified<sup>14</sup>, we arbitrarily designated basepair one at the start of a 7-mer repeat, (AGTGATT)<sub>26</sub>, that produces translational stops in all reading frames, as this repeated DNA is unlikely to contain any coding sequence.

Open reading frames. One thousand five hundred and ninety predicted coding sequences were identified. They were searched against a non-redundant protein database resulting in 1,091 putative identifications that were assigned biological roles using a classification system adapted from Riley<sup>15</sup> (Table 2). The 1,590 predicted genes had an average size of 945 bp, similar to that observed in other prokaryotes<sup>7–9</sup>, and no genome-wide strand bias was observed (Fig. 2). More than 70% of the predicted proteins in *H. pylori* have a calculated isoelectric point (pI) greater than 7.0, compared to  $\sim$ 40% in *H. influenzae* and *E. coli*. The basic amino acids, arginine and lysine, occur twice as frequently in *H. pylori* proteins as in those of *H. influenzae* and *E. coli*, perhaps reflecting an adaptation of *H. pylori* to gastric acidity.

Paralagous families. Ninety-five paralogous gene families comprising 266 gene products (16% of the total) were identified (www.tigr.org/tdb/mdb/hpdb/hpdb.html). Of these, 67 (173 proteins) have an assigned role. Sixty-four have only 2 members, while the porin/adhesin-like outer membrane protein family (Fig. 2) is the largest with 32 members. The largest number of paralogues with assigned roles fall into the functional categories of cell

envelope, transport and binding proteins, and proteins involved in replication. The large number of cell envelope proteins might reflect either a reduced biosynthetic capacity or a need to adapt to the challenging gastric environment.

# **Cell division and protein secretion**

The gene content of *H. pylori* suggests that the basic mechanisms of replication, cell division and secretion are similar to those of *E. coli* and *H. influenzae*. However, important differences are noted. For example, apparently missing from the *H. pylori* genome are orthologues of DnaC, MinC, and the secretory chaperonin, SecB. In oriC-type primosome formation, the DnaB and DnaC proteins form a B–C complex that delivers the DnaB helicase to the developing primosome complex<sup>16</sup>. The apparent absence of DnaC in *H. pylori* suggests that either a novel mechanism for recruiting DnaB exists or a DnaC orthologue with no detectable sequence similarity is present. Similar arguments can be made for other seemingly missing important functions.

H. pylori has a classical set of bacterial chaperones (DnaK, DnaJ, CbpA, GrpE, GroEL, GroES, and HtpG). The transcriptional regulation of H. pylori chaperone genes is likely to be different from that in E. coli, as it seems not to have the sigma factors that upregulate chaperone synthesis in E. coli (heat-shock sigma 32 and stationary-phase sigma S).

In addition to the SecA-dependent secretory pathway, *H. pylori* has two specialized export systems. One is associated with the *cag* pathogenicity island<sup>11</sup> and the other is the flagellar export pathway which is assembled from orthologues of FliH, FliI, FliP, FlhA, FlhB, FliQ, FliR and FliP<sup>17</sup>. Apparently absent from *H. pylori* is a type IV signal peptidase and orthologues of the dsbABC system, which in other species are required for the maturation of pili and pilin-like structures<sup>18</sup> and assembly of surface structures involved in virulence and DNA transformation<sup>19</sup>.

# **Recombination, repair and restriction systems**

Systems for homologous recombination and post-replication, mismatch, excision and transcription-coupled repair appear to be present in *H. pylori*. Also present are genes with similarity to DNA glycosylases which have associated AP endonuclease activity. The RecBCD pathway, which mediates homologous recombination and double-strand break repair, and RecT and RecE orthologues, proteins involved in strand exchange during recombination<sup>20</sup>, seem to be absent. The ability of *H. pylori* to perform mismatch repair is suggested by the presence of methyl transferases, mutS and uvrD. However, orthologues of MutH and MutL were not identified. Components of an SOS system also appear to be absent.

Bacteria commonly use restriction and modification systems to degrade foreign DNA. In *H. pylori*, this defence system is well developed with eleven restriction-modification systems identified on the basis of gene order and similarity to endonucleases, methyltransferases, and specificity subunits. Three type I, one type II, and three type IIS systems were identified, as well as four type III systems, including the recently identified epithelial responsive

**Figure 1** Linear representation of the *H. pylori* 26695 chromosome illustrating the location of each predicted protein-coding region, RNA gene, and repeat elements in the genome. Symbols are as follows: ++, Co<sup>2+</sup>, Zn<sup>2+</sup>, Cd<sup>2+</sup>; ?, unknown; A/G/S, p-alanine/glycine/p-serine; B12, B12/ferric siderophores; E, glutamate; Mo, molybdenum; P, proline; P/G, proline/glycine betaine; Q, glutamine; S, serine; a-k, α-ketoglutarate; a/o, arginine/ornithine; aa, amino acids (specificity unknown); aa2, dipeptides; aaX, oligopeptides; fum, fumarate, succinate; glu, glucose/galactose; h, hemin; lac, μ-lactate; mal, malate 2-oxoglutarate; nic, nicotinamide mononucleotides; pyr, pyrimidine nucleosides. 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 TopPred<sup>47</sup>.

endonuclease, *iceA1*, and its associated DNA adenine methyltransferase (M. HypI) genes<sup>21,22</sup>. In addition to the complete systems, seven adenine-specific, and four cytosine-specific methyltransferases, and one of unknown specificity were found. Each of these has an adjacent gene with no database match, suggesting that they may function as part of restriction-modification systems.

# **Transcription and translation**

Although analysis of gene content suggests that *H. pylori* has a basic transcriptional and translational machinery similar to that of *E. coli*, interesting differences are observed. For example, no genes for a catalytic activity in tRNA maturation (*rnd*, *rph*, or *rnpB*) were identified and of the three known ribonucleases involved in mRNA degradation, only polyribonucleotide phosphorylase was found. Twenty-one genes coding for 18 of the 20 tRNA synthetases normally required for protein biosynthesis were found.

As in most other completely sequenced bacterial genomes, the gene for glutaminyl-tRNA synthetase, glnS, is missing, and the existence of a transamidation process is assumed. It is also possible that the product of the second glutamyl-tRNA synthetase gene, *gltX*, present in H. pylori, may have acquired the glutaminyl-tRNA synthetase function. H. pylori provides the first example of a bacterial genome apparently lacking an asparaginyl-tRNA synthetase gene, asnS. A transamidation process to form Asn-tRNAAsn from Asp-tRNAAsn has been reported for the archaeon Haloferax volcanii<sup>22</sup> and may also operate in H. pylori. Most intriguing, however, is the finding that in H. pylori the genes encoding the  $\beta$ and β' subunits of RNA polymerase are fused. In all studied prokaryotes the two genes are contiguous, but separate, and are part of the same transcriptional unit. Whether this gene fusion in H. pylori results in a fused protein, or whether the transcriptional or translational product of the fusion is subject to splicing, is currently not known. It is worth noting that an artificial fusion of the E. coli

*rpoB* and *rpoC* genes is viable and results in a transcriptional complex, which has the same stoichiometry as the native complex (K. Severinov, personal communication).

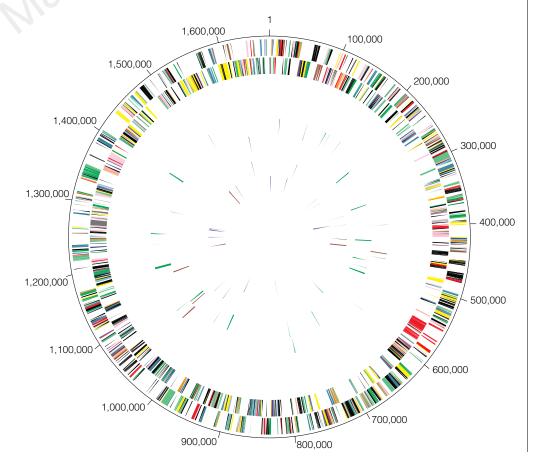
# Adhesion and adaptive antigenic variation

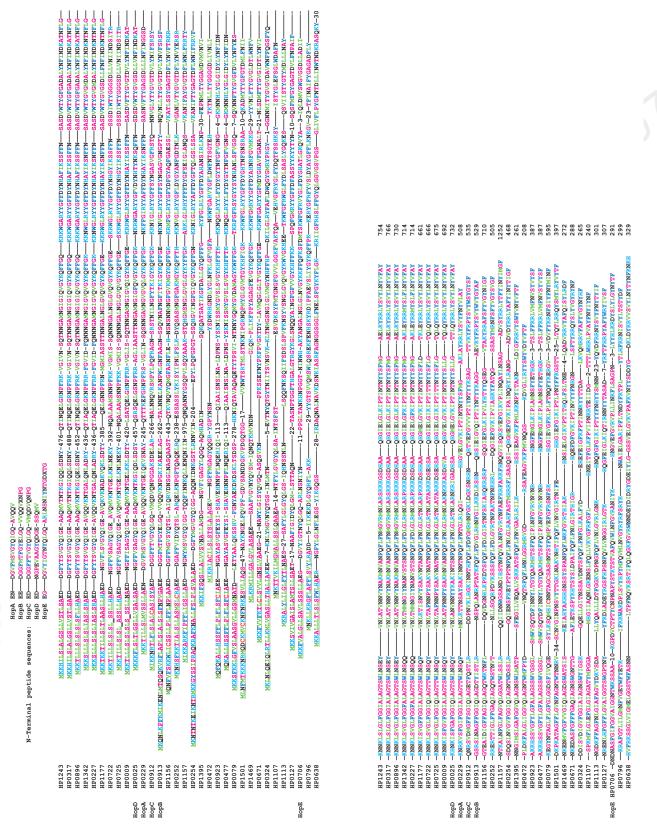
Most pathogens show tropism to specific tissues or cell types and often use several adherence mechanisms for successful attachment. *H. pylori* may use at least five different adhesins to attach to gastric epithelial cells<sup>5</sup>. One of them, HpaA (HP0797), was previously identified as a lipoprotein in the flagellar sheath and outer membrane<sup>5,23</sup>. In addition to the HpaA orthologue, we have identified 19 other lipoproteins. Few have an identifiable function, but some are likely to contribute to the adherence capacity of the organism.

Two adhesins<sup>24–26</sup>, one of which mediates attachment to the Lewis<sup>b</sup> histo-blood group antigens, belong to the large family of outer membrane proteins (OMP) (Fig. 3) (T. Boren and R. Haas, personal communication). It is conceivable that other members of these closely related proteins also act as adhesins. Given the large number of sequence-related genes encoding putative surface-exposed proteins, the potential exists for recombinational events leading to mosaic organization. This could be the basis for antigenic variation in *H. pylori* and an effective mechanism for host defence evasion, as seen in *M. genitalium*<sup>27</sup>.

At least one other mechanism for antigenic variation could operate in *H. pylori*. The DNA sequence at the beginning of eight genes, including five members of the OMP family, contain stretches of CT or AG dinucleotide repeats (Table 3a). In addition, poly(C) or poly(G) tracts occur within the coding sequence of nine other genes (Table 3b). Slipped-strand mispairing within such repeats are documented features of one mechanism of genotypic variation<sup>28,29</sup>. These mechanisms may have evolved in bacterial pathogens to increase the frequency of phenotypic variation in genes involved in

Figure 2 Circular representation of the H. pylori 26695 chromosome. Outer concentric circle: predicted coding regions on the plus strand classified as to role according to the colour code in Fig. 1 (except for unknowns and hypotheticals, which are in black). Second concentric circle: predicted coding regions on the minus strand. Third and fourth concentric circles: IS elements (red) and other repeats (green) on the plus and minus strand, respectively. Fifth and sixth concentric circles: tRNAs (blue), rRNAs (red), and sRNAs (green) on the plus and minus strand, respectively.





**Figure 3** Multiple sequence alignment of members of the outer membrane protein family of *H. pylori*. These proteins were identified as OMPs based on the characteristic alternating hydrophobic residues at their carboxy termini. All members of this family have one domain of similarity at the amino-terminal end and seven domains of similarity at their carboxy-terminal end. Note that the first 11 of these OMPs share extensive similarity over their entire length. Four of the OMPs were identified as porins (Hops) based on identity to published aminoterminal sequences, represented at the top of the alignment<sup>50</sup>. The most likely

candidate for HopD is HP0913, which has 15 matches to the first 20-residue N-terminal peptide sequence<sup>50</sup>. These differences may be due to strain variability. The program Signal-P<sup>48</sup> was used to identify cleavage sites and signal peptides (underlined). Four of the OMPs have TTG start codons (HP1156, HP0252, HP1113, HP0796). Numbers embedded in the sequences represent amino acids omitted from the alignment. The star symbols indicate that HP722, HP725 and HP9 proteins contain a frameshift in their signal-peptide-coding region. These frameshifts are associated with the presence of dinucleotide repeats (Table 3).

critical interactions with their hosts<sup>28</sup>. Such 'contingency' genes encode surface structures like pilins, lipoproteins or enzymes that produce lipopolysaccharide molecules<sup>28</sup>. Our analysis suggests that the seventeen genes reported in Table 3a,b belong to this category and thus may provide an example of adaptive evolution in *H. pylori*.

Phenotypic variation at the transcriptional level may also operate in *H. pylori*. Examples of repetitive DNA mediating transcriptional control have been documented by the presence of oligonucleotide repeats in promoter regions<sup>29</sup>. Homopolymeric tracts of A or T in potential promoter regions of eighteen genes were found, including eight members of the OMP family (Table 3c).

#### **Virulence**

The virulence of individual *H. pylori* isolates has been measured by their ability to produce a cytotoxin-associated protein (CagA) and

an active vacuolating cytotoxin (VacA)<sup>5</sup>. The *cagA* gene, though not a virulence determinant, is positioned at one end of a pathogenecity island containing genes that elicit the production of interleukin (IL)-8 by gastric epithelial cells<sup>11,30</sup>. Consistent with its more virulent character, *H. pylori* strain 26695 contains a single contiguous PAI region<sup>11</sup> (Fig. 4).

VacA induces the formation of acidic vacuoles in host epithelial cells, and its presence is associated epidemiologically with tissue damage and disease<sup>31</sup>. VacA may not be the only ulcer-causing factor as 40% of *H. pylori* strains do not produce detectable amounts of the cytotoxin *in vitro*<sup>5</sup>. Sequence differences at the amino terminus and central sections are noted among VacA proteins derived from Tox<sup>+</sup> and Tox<sup>-</sup> strains<sup>31</sup>. This Tox<sup>+</sup> *H. pylori* strain contains the more toxigenic S1a/m1 type cytotoxin and three additional large proteins with moderate similarities to the carboxy-terminal end of the active

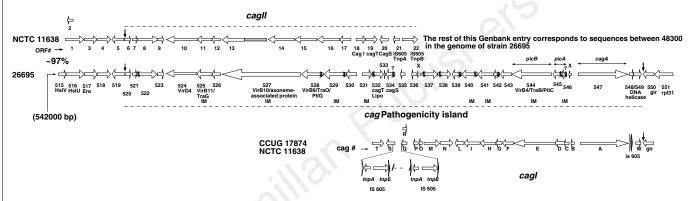
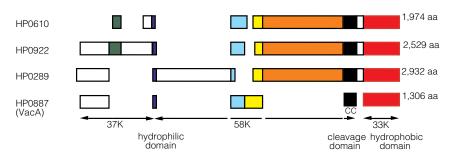


Figure 4 Comparison between the Cag pathogenicity islands of the sequenced strain, 26695 and the NCTC11638 strain. The twenty nine ORFs of the contiguous PAI in strain 26695 are represented together with the corresponding ORFs from the PAI present in NCTC11638 (AC000108 and U60176). The PAI in NCTC11638 is divided by the IS 605 elements into two regions, cagl and cagll. The PAI in NCTC11638 is flanked by a 31-bp (TTACAATTTGAGCCCATTCTTTAGCTTGTTTT) direct repeat (vertical arrows) as described11. Some of the genes encode proteins with similarity to proteins involved either in DNA transfer (Vir and Tra proteins) or in export of a toxin (Ptl protein)10. However, these genes do not have the conserved contiguous arrangement found in the VirB, Tra and Ptl operons, suggesting that this PAI is not derived from these systems. Most genes of the PAI have no database match, contrary to a previous suggestion<sup>11</sup>. Thirteen of the proteins have a signal peptide (squiggle line), three of them with a weaker probability (squiggled line+?). The average length of the signal peptides is 25 amino acids, suggesting that this PAI is of Gram-negative origin. Eight proteins are predicted to have at least two membrane-spanning domains and to be integral membrane proteins

(IM)<sup>47</sup>. Although the two PAI are ~97% identical at the nucleotide level, there are several notable and perhaps biologically relevant differences between the two sequences. Four of the genes differ in size. In the PAI of strain 26695, HP 520 and 521 are shorter, whereas HP523 is longer, and HP 527 actually spans both ORF13 and 14. In addition, the N-terminal part of HP527 is 129 amino acids longer than the corresponding region in ORF14. HP548/549 contains a frameshift and is therefore probably inactive in strain 26695. The stippled box preceding ORF13 represents an N-terminal extension not annotated in the Genbank entry for the PAI of NCTC11638. The 'x' indicates ORFs that are neither GeneMark-positive nor GeneSmith-positive, so were not included in our gene list. However, these ORFs may be biologically significant. We do not represent cagR as an ORF, because it is completely contained within ORFQ, and is GeneMark-negative.



**Figure 5** Conserved domains of VacA and related proteins. HP887 is the vacuolating cytotoxin (vacA) gene from *H. pylori* 26695 strain. HP610, HP922 and HP289 are related proteins. Blocks of aligned sequence and the length of each protein are shown. Arrows designate the extents of each VacA domain. The hydrophilic domain (blue boxes) contains the site in VacA at which the N-terminal domain is cleaved into 37K and 58K fragments. The putative cleavage site (ANNNQQNS) differs from that of three cytotoxic strains (CCUG 1784, 60190, G39;

AKNDKXES) and is not conserved in the other three VacA-related proteins. The cleavage domain (black boxes) of VacA contains a pair of Cys residues 60 residues upstream from the site at which the C terminus is cleaved. These residues are not conserved in the other three proteins. The 33K C-terminal hydrophobic domain (red boxes) in VacA is thought to form a pore through which the toxin is secreted. The other three proteins show 26–31% sequence similarity to VacA in this region. The other coloured boxes represent regions of similarity.

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cytotoxin ( $\sim$ 26–31%) (Fig. 5). However, they lack the paired-cysteine residues and the cleavage site required for release of the VacA toxin from the bacterial membrane<sup>31</sup> (Fig. 5). We propose that these proteins may be retained on the outside surface of the cell membrane and contribute to the interaction between *H. pylori* and host cells.

The surface-exposed lipopolysaccharide (LPS) molecule plays an important role in *H. pylori* pathogenesis<sup>32</sup>. The LPS of *H. pylori* is several orders of magnitude less immunogenic than that of enteric bacteria<sup>33</sup> and the O antigen of many *H. pylori* isolates is known to mimic the human Lewis<sup>x</sup> and Lewis<sup>y</sup> blood group antigen<sup>32</sup>. Genes for synthesis of the lipid A molecule, the core region, and the O antigen were identified. Two genes with low similarity to fucosyltransferases (HP379, HP651) were found and may play a role in the LPS-Lewis antigen molecular mimicry. Our analysis also suggests that three genes, two glycosyltransferases (HP208 and HP619) and one fucosyltransferase (HP379), may be subject to phase variation (Table 3a, b).

As with other pathogens, H. pylori probably requires an ironscavenging system for survival in the host<sup>5</sup>. Genome analysis suggests that H. pylori has several systems for iron uptake. One is analogous to the siderophore-mediated iron-uptake fec system of E. coli<sup>34</sup>, except that it lacks the two regulatory proteins (FecR and FecI) and is not organized in a single operon. Unlike other studied systems, H. pylori has three copies of each of fecA, exbB and exbD. A second system, consisting of a feoB-like gene without feoA, suggests that H. pylori can assimilate ferrous iron in a fashion similar to the anaerobic feo system of *E. coli*. Other systems for iron uptake present in H. pylori consist of the three frpB genes which encode proteins similar to either haem- or lactoferrin-binding proteins. Finally, H. pylori contains NapA, a bacterioferritin<sup>34</sup>, and Pfr, a non-haem cytoplasmic iron-containing ferritin used for storage of iron<sup>35</sup>. The global ferric uptake regulator (Fur) characterized in other bacteria is also present in H. pylori. Consensus sequences for Fur-binding boxes were found upstream of two *fecA* genes, the three *frnB* genes and *fur*.

*H. pylori* motility is essential for colonization<sup>36</sup>. It enables the bacterium to spread into the viscous mucous layer covering the gastric epithelium. At least forty proteins in the *H. pylori* genome appear to be involved in the regulation, secretion and assembly of the flagellar architecture. As has bene reported for the *flaA* and *flaB* genes, we identified sigma 28 and sigma 54-like promoter elements upstream of many flagellar genes, underscoring the complexity of the transcriptional regulation of the flagellar regulon<sup>5</sup>.

# Acidity, pH and acid tolerance

H. pylori is unusual among pathogenic bacteria in its ability to colonize host cells in an environment of high acidity. As it enters the gastric environment by oral ingestion, the organism is transiently subjected to the extreme pH of the lumen side of the gastric mucous layer (pH  $\sim$ 2). The survival of *H. pylori* in acidic environments is probably due to its ability to establish a positive inside-membrane potential<sup>37</sup> and subsequently to modify its microenvironment through the action of urease and the release of factors that inhibit acid production by parietal cells<sup>5</sup>. A switch in membrane polarity provides an electrical barrier that prevents the entry of protons (H<sup>+</sup>). A positive cell interior can be created by the active extrusion of anions or by a proton diffusion potential. The latter model appears more likely as no clear mechanism for electrogenic anion efflux is apparent in the genome. A proton diffusion potential would require the anion permeability of the cytoplasmic membrane to be low and, thus far, only three anion transporters have been identified. However, it remains to be determined whether anion conductances are associated with other proteins: the MDR-like transporters (HP600, HP1082 and HP1206) or hypotheticals. Although it has been suggested that proton-translocating P-type ATPases could mediate survival in acid conditions by the extrusion of protons from the cytoplasm<sup>38</sup>, this idea is not supported by the identified transporter

HP no.	ID	No. of repeats	Gene status	Poly(A) or Poly(	T) tracts in 5' interg	genic region
9	OMP	11 CT	Off	-	Poly(A)	
208	glycos. transf.	11 AG	Truncated		Poly(A)	
638	OMP	6 CT	On		No	
722	OMP	8 CT	Off		Poly(T)	
725	OMP	6 CT	Off		Poly(T)	
744	Нуро	9 AG	Truncated		No	
896	OMP	11 CT	On		Poly(A)	
1417	Cons. Hypo	9 AG	Truncated		No ´	
Nucleotide sec	uence at the beginning of HP072	2 showing the CT dinucleotide repe	eat and the poly T tract. The put	ative ribosome binding	site is shown in gr	een. Translation
		truncated product. The addition o			ring', will restore th	e frame.
		CTCGCTTCATCGCTCTTGCACGC				
Y F K F		<u> </u>	F D N G F F V	S A G Y		
MKK	TIIISISI	SIHRSCTI	K T T A F I *			
		0 2 0 0 . 2				
(b) Homopolyn	neric poly(C) and poly(G) tracts w	ithin codina seauence				
(b) Homopolyn HP no.	neric poly(C) and poly(G) tracts w	ithin coding sequence ID	Tract len	gth		Gene status
	neric poly(C) and poly(G) tracts w		Tract len C15	gth		Gene status Off
HP no. 58 217	neric poly(C) and poly(G) tracts w	ID	C15 G12	gth		
HP no. 58 217 379	neric poly(C) and poly(G) tracts w	ID Hypo Hypo fucosyl transf.	C15 G12 C13	gth		Off On On
HP no. 58 217 379 464	neric poly(C) and poly(G) tracts w	ID Hypo Hypo	C15 G12 C13 C15	gth		Off On On On
HP no. 58 217 379 464 619	neric poly(C) and poly(G) tracts w	ID Hypo Hypo fucosyl transf. Typel R glycos. transf.	C15 G12 C13 C15 C15	gth		Off On On On Truncated
HP no. 58 217 379 464 619 651	neric poly(C) and poly(G) tracts w	ID Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo	C15 G12 C13 C15 C13 C13	gth		Off On On On Truncated On
HP no. 58 217 379 464 619 651 1353	neric poly(C) and poly(G) tracts w	ID Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo	C15 G12 C13 C15 C13 C13 C15	gth		Off On On On Truncated On Truncated
HP no. 58 217 379 464 619 651 1353 1471	neric poly(C) and poly(G) tracts w	Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R	C15 G12 C13 C15 C13 C13 C15 G14	gth		Off On On On Truncated On Truncated On
HP no. 58 217 379 464 619 651 1353	neric poly(C) and poly(G) tracts w	ID Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo	C15 G12 C13 C15 C13 C13 C15	gth		Off On On On Truncated On Truncated
HP no. 58 217 379 464 619 651 1353 1471 1522 Genes possibl		ID Hypo Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo TypellS-R Methyl ase	C15 G12 C13 C15 C13 C13 C15 G14 G12			Off On On On Truncated On Truncated On
HP no. 58 217 379 464 619 651 1353 1471 1522		Hypo Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase	C15 G12 C13 C15 C13 C13 C15 G14 G12	gth HP no.	ID	Off On On On Truncated On Truncated On
HP no. 58 217 379 464 619 651 1353 1471 1522 Genes possibl	y regulated by homopolymeric po	ID Hypo Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo TypellS-R Methyl ase	C15 G12 C13 C15 C13 C13 C15 G14 G12		ID rfaJ	Off On On On Truncated On Truncated On Truncated
HP no. 58 217 379 464 619 651 1353 1471 1522 Genes possibl HP no.	y regulated by homopolymeric po ID Tract	ID Hypo Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase ly(A) or poly(T) tracts in 5' interger HP no.	C15 G12 C13 C15 C13 C13 C15 G14 G12  Dic regions ID Tract	HP no.	rfaJ	Off On On On Truncated On Truncated On Truncated
HP no. 58 217 379 464 619 651 1353 1471 1522 Genes possibl HP no. 9	y regulated by homopolymeric po ID Tract OMP A14	ID Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo Hypo TypelIS-R Methyl ase ly(A) or poly(T) tracts in 5' interger HP no.	C15 G12 C13 C13 C13 C13 C15 G14 G12  Aic regions ID Tract  OMP T15	HP no. 208		Off On On On Truncated On Truncated On Truncated Truncated Truncated
HP no. 58 217 379 464 619 651 1353 1471 1522 Genes possibl HP no. 9 227	y regulated by homopolymeric po ID Tract OMP A14 OMP T14	ID Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo TypelIS-R Methyl ase lly(A) or poly(T) tracts in 5' interger HP no.  25 228	C15 G12 C13 C13 C15 C13 C15 G14 G12   Dic regions ID Tract  OMP T15 IMP A14	HP no. 208 349	rfaJ pyrG	Off On On On Truncated On Truncated On Truncated Truncated Truncated
HP no. 58 217 379 464 619 651 1353 1471 1522 Genes possibl HP no. 9 227 350	y regulated by homopolymeric po ID Tract OMP A14 OMP T14 IMP A15	ID Hypo Hypo Hypo fucosyl transf. Typel R glycos. transf. Hypo TypelIS-R Methyl ase  ly(A) or poly(T) tracts in 5' interger HP no.  25 228 547	C15 G12 C13 C15 C13 C13 C15 G14 G14 G12  Dic regions ID Tract  OMP T15 IMP A14 CagA A14	HP no. 208 349 629	<i>rfaJ</i> <i>pyrG</i> Hypo	Off On On On Truncated On Truncated Tract A11 T15

genes. The P-type ATPase sequences in *H. pylori* (*copAP*, HP791, and HP1503) are more closely related to divalent cation transporters than to ATPases with specificity for protons or monovalent cations. One of them, HP0791, is involved in Ni<sup>2+</sup> supply, an essential component of urease activity<sup>39</sup>. The others may be involved in the elimination of toxic metals from the cytoplasm and not in pH regulation.

Additional mechanisms of pH homeostasis may well contribute to *H. pylori* survival. A change in protein content observed in response to a shift of extracellular pH from 7.5 to 3.0 suggests the presence of an acid-inducible response<sup>40</sup>. Although *H. pylori* lacks most orthologues of the genes that are acid-induced in *E. coli* and *Salmonella typhimurium*, including the amino-acid decarboxylases and formate hydrogen lyase, certain virulence factors, outer membrane

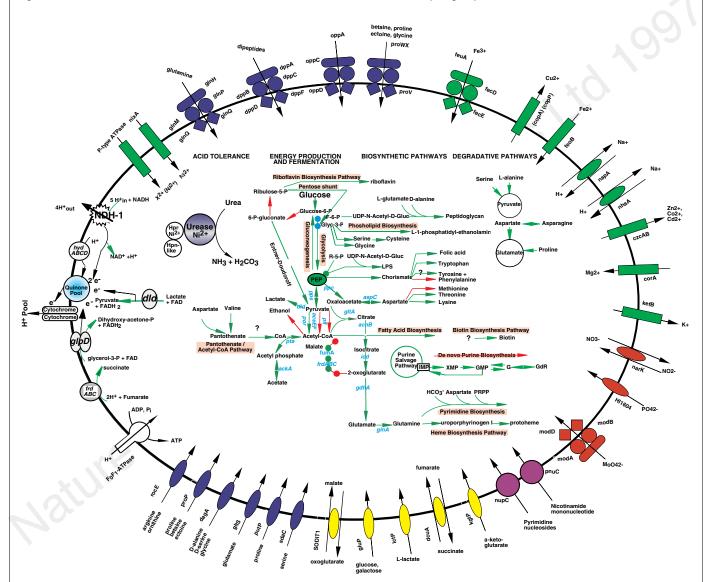


Figure 6 Solute transport and metabolic pathways of Helicobacter pylori. Transporters identified by sequence comparisons are characterists of Gramnegative bacteria. Colours correspond to transport role categories defined by Riley<sup>15</sup>: blue, amino acids, peptides and amines; red, anions; yellow, carbohydrates, organic alcohols and acids; green, cations; and purple, nucleosides, purines and pyrimidines. Numerous permeases (ovals) with specificity for amino acids (recE, proP, dagA, gltS, putP and sdaC) or carbohydrates (SODiTI, gluP, lactP, cduA, kgtP) import organic nutrients. Structurally related permease proteins maintain ionic homeostasis by transporting HPO<sub>4</sub><sup>2-</sup> (HI1604), NO<sub>3</sub><sup>2-</sup> (narK), and Na+ (nhA, napA). Primary active-transport systems, independent of the proton cycle, are also apparent. Included in this group are ATP-binding proteincassette (ABC) transporters (composite figures of 2 diamonds, 2 circles, 1 oval) for the uptake of oligopeptides (oppACD), dipeptides (dppABCDF), proline (proVWX), glutamine (glnHMPQ), molybdenum (modABD), and iron III (fecED), Ptype ATPases that extrude toxic metals from the cell (copAP and cadA), and the glutathione-regulated potassium-efflux protein (kefB). Transporters for the accumulation of ionic cofactors are encoded by nixA (Ni<sup>2+</sup> for urease activation), corA (Mg<sup>2+</sup> for phosphohydrolases, phosphotransferases, ATPases) and feoB (Fe<sup>2+</sup>

import under anaerobic conditions for cytochromes, catalase). An integrated view of the main components of the central metabolism of *H. pylori* strain 26695 is presented. The use of glucose as the sole carbohydrate source is emphasized. Urease, a multisubunit Ni2+-binding enzyme, is crucial for colonization and for survival of H. pylori at acid pH, and is indicated as a complex (purple circle) with Hpn, a Ni<sup>2+</sup>-binding cofactor, and a newly identified Hpn-like protein (HP1432). A question mark is attached to pathways that could not be completely elucidated. Pathways or steps for which no enzymes were identified are represented by a red arrow. Pathways for macromolecular biosynthesis (RNA, DNA and fatty acids) have been omitted. ackA, acetate kinase; acnB, aconitase B; aspC, aspartate aminotransferase; dld, p-lactate dehydrogenase; gdhA, glutamate dehydrogenase; glnA, glutamine synthetase; gltA citrate synthase; HydABC, hydrogenase complex; icd, isocitrate dehydrogenase; pfl, pyruvate formate lyase; por, pyruvate ferredoxin oxidoreductase; ppc, phosphoenolpyruvate carboxylase; pps, phosphoenolpyruvate synthase; pta, phosphate acetyltransferase; gldD, glycerol-3-phosphate dehydrogenase; NDH-1, NADH-ubiquinone oxidoreductase complex.

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proteins, sensor-regulator pairs and other proteins may be acidinduced.

# **Regulation of gene expression**

Bacteria regulate the transcription of their genes in response to many environmental stimuli, such as nutrient availability, cell density, pH, contact with target tissue, DNA-damaging agents, temperature and osmolarity. In the case of pathogens, the regulated expression of certain key genes is essential for successful evasion of host responses and colonization, adaptation to different body sites, and survival as the pathogen passes to new hosts. In H. pylori, global regulatory proteins are less abundant than in *E. coli*. For example, orthologues of many DNA-binding proteins that regulate the expression of certain operons such as OxyR (oxidative stress), Crp (carbon utilization), RpoH (heat shock), and Fnr (fumarate and nitrate regulation) are absent. Only four H. pylori proteins have a perfect match to helix-turn-helix (HTH) motifs, a signature of transcription factors; a putative heat-shock protein (HspR), two proteins with no database match (HP1124 and HP1349) and SecA, a component of the general secretory machinery. In contrast, 34 proteins containing an HTH motif were found in H. influenzae and 148 in E. coli. We identified several other putative regulatory functions, including SpoT and CstA for 'stringent response' to amino-acid starvation and to carbon starvation, respectively.

Environmental response requires sensing changes and transmission of this information to cellular regulatory networks. Two-component regulator systems, consisting of a membrane histidine kinase sensor protein and a cytoplasmic DNA-binding response regulator, provide a well studied mechanism for such signal transduction. Four sensor proteins and seven response regulators were found in *H. pylori*, similar to the number found in *H. influenzae*<sup>7</sup>. This is approximately one third the number found in *E. coli* which, in contrast to *H. pylori* and *H. influenzae*, may be exposed to more environments.

## Metabolism

Metabolic pathway analysis of the H. pylori genome suggests the following features. H. pylori uses glucose as the only source of carbohydrate and the main source for substrate-level phosphorylation. It also derives energy from the degradation of serine, alanine, aspartate and proline. The glycolysis-gluconeogenesis metabolic axis constitutes the backbone of energy production and the start point of many biosynthetic pathways. The biosynthesis of peptidoglycan, phospholipids, aromatic amino acids, fatty acids and cofactors is derived from acetyl-CoA or from intermediates in the glycolytic pathway (Fig. 6). The metabolism of pyruvate reflects the microaerophilic character of this organism. Neither the aerobic pyruvate dehydrogenase (aceEF) nor the strictly anaerobic pyruvate formate lyase (pfl) associated with mixed-acid fermentation are present. The conversion of pyruvate to acetyl CoA is performed by the pyruvate ferrodoxin oxidoreductase (POR), a four-subunit enzyme thus far only described in hyperthermophilic organisms<sup>41</sup>. The tricarboxylic acid cycle (TCA) is incomplete and the glyoxylate shunt is absent. The analysis of degradative pathways, uptake systems and biosynthetic pathways for pyrimidine, purine and haem suggests that H. pylori uses several substrates as nitrogen source, including urea, ammonia, alanine, serine and glutamine. The assimilation of ammonia, an abundant product of urease activity, is achieved by the glutamine synthase enzyme and  $\alpha$ ketoglutarate is transformed into glutamate by glutamate dehydrogenase rather than by the glutamate synthase enzyme.

In *H. pylori*, proton translocation is mediated by the NDH-1 dehydrogenase and the different cytochromes, including the primitive-type cytochrome cbb3 (Table 2). Four respiratory electron-generating deydrogenases have been identified, glycerol-3-phosphate dehydrogenase (GlpD), D-lactate dehydrogenase, NADH-ubiquinone oxidoreductase complex (NDH-1), and a hydrogenase complex (HydABC). Our analysis also suggests that

H. pylori is not able to use nitrate, nitrite, dimethylsulphoxide, trimethylamine N-oxide or thiosulphate as electron acceptors. Much of our metabolic analysis is supported by experimental evidence<sup>41,42</sup>.

# Evolutionary relationships of H. pylori

H. pylori is currently classified in the Proteobacteria, a large, diverse division of Gram-negative bacteria which includes two other completely sequenced species, H. influenzae and E. coli. Given this taxonomic placement, based primarily on 16S rRNA sequence comparisons, one might expect the proteins of *H. pylori* more closely to resemble their H. influenzae and E. coli homologues rather than those in other genomes such as Synechocystis sp., M. genitalium, M. pneumoniae, M. jannaschii, and Saccharomyces cerevisae. This is indeed the case for many proteins. There are, however, many examples of H. pylori proteins in amino-acid biosynthesis, energy metabolism, translation and cellular processes that have greater sequence similarity to those found in non-Proteobacteria. For example, Dhs1, the initial enzyme in the chorismate biosynthesis pathway is 75.5% similar to Arabidopsis thaliana chloroplast Dhs1 gene product, and has minimal sequence similarity to the equivalent E. coli AroH, AroF or AroG gene products. The remaining enzymes in this pathway have strong sequence similarity to their E. coli counterpart. Similarly, the H. pylori prephenate dehydrogenase (TyrA), which converts chorismate to tyrosine, and six out of 15 enzymes in the aspartate amino acid biosynthetic pathways, resemble those from B. subtilis. A similar pattern can be seen in a different functional category. Nearly all H. pylori tRNA synthetases have eubacterial homologues, mostly with best matches to Proteobacteria species. However, histidyl-tRNA synthetase shows several amino-acid sequence signatures in common with eukaryotic and archaeal (M. jannaschii)

Such observations of discordant sequence similarity are often interpreted as evidence of lateral gene transfer in the evolutionary history of an organism. It is also possible that *H. pylori* diverged early from the lineage that led to the gamma Proteobacteria, and retained more ancient forms of enzymes that have been subsequently replaced or have diverged extensively in *H. influenzae* and *E. coli*.

## Conclusion

Our whole-genome analysis of *H. pylori* gives new insight into its pathogenesis, acid tolerance, antigenic variation and microaerophilic character. The availability of the complete genome sequence will allow further assessment of *H. pylori* genetic diversity. This is an important aspect of *H. pylori* epidemiology as allelic polymorphism within several loci has already been associated with disease outcome<sup>5,21,31</sup>. The extent of molecular mimicry between *H. pylori* and its human host, an underappreciated topic, can now be fully explored<sup>43</sup>. The identification of many new putative virulence determinants should allow critical tests of their roles and thus new insight into mechanisms of initial colonization, persistence of this bacterium during long-term carriage, and the mechanisms by which it promotes various gastroduodenal diseases.

## Methods

H. pylori strain 26695 (ref. 44) was originally isolated from a patient in the United Kingdom with gastritis (K. Eaton, personal communication) and was chosen because it colonizes piglets and elicits immune and inflammatory responses. It is also toxigenic, and transformable, and thus amenable to mutational tests of gene function.

The *H. pylori* genome sequence was obtained by a whole-genome random sequencing method previously applied to genomes of *Haemophilus influenzae*<sup>7</sup>, *Mycoplasma genitalium*<sup>8</sup>, and *Methanococcus jannaschii*<sup>9</sup>. Ninety-two per cent of the genome was covered by at least one  $\lambda$  clone and only 0.56% of the genome had single-fold coverage.

Open reading frames (ORFs) and predicted coding regions were identified using three methods. The predicted protein-coding regions were initially defined by searching for ORFs longer than 80 codons. Coding potential analysis of the entire genome was performed with a version of GeneMark<sup>45</sup> trained with a set of H. pylori ORFs longer than 600 nucleotides. Coding sequences and potential starts of translation were also determined using GeneSmith (H.S., unpublished), a program that evaluates ORF length, separation of ORFs and overlap and quality of ribosome binding site. ORFs with low GeneMark coding potential, no database match, and not retained by GeneSmith were eliminated. GeneSmith identified 25 ORFs that are smaller than 100 codons, had no database match and were GeneMark negative. Frameshifts were detected by inspecting pairwise alignments, families of orthologues (similar proteins derived from different species) and paralogues (similar proteins from within the same organism), and regions containing homopolymer stretches and dinucleotide repeats. Ambiguities were resolved by an alternative sequencing chemistry (terminator reactions), and by sequencing PCR products obtained using the genomic DNA as template. Frameshifts that remain in the genome are considered authentic and not sequencing artefacts.

To determine their identity, ORFs were searched against a non-redundant amino-acid database as previously described. ORFs were also analysed using 175 hidden Markov models constructed for a number of conserved protein families (pfam v1.0) using hmmer. In addition, all ORFs were searched against the prosite motif database using MacPattern. Families of paralogues 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 unix version of the program TopPred<sup>47</sup> was used to identify membrane-spanning domains (MSD) in proteins. Six hundred and sixty three proteins containing at least one MSD were found; of these, 300 had 2 potential MSDs or more. The presence of signal peptides and the probable position of the cleavage site in secreted proteins were detected using Signal-P, a neural net program that had been trained on a curated set of secreted proteins from Gram-negative bacteria<sup>48</sup>. 367 proteins were predicted to have a signal peptide. Lipoproteins were identified by scanning for the presence of a lipobox in the first 30 amino acids of every protein; 20 lipoproteins were identified, eighteen of which were Signal-P positive. Outer-membrane proteins were found by searching for aromatic amino acids at the end of the proteins.

Homopolymer and dinucleotide repeats were found by using RepScan (H.O.S., unpublished) which finds direct repeats of any length. All features identified using these programs were validated by visual inspection to remove false positives. Metabolic pathways were curated by hand and by reference to EcoCyc<sup>49</sup>.

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Correspondence and requests for materials should be addressed to J.-ET. (e-mail: ghp@tigr.org). The annotated genome sequence and gene family alignments are available on the World-Wide Web site at http://www.tigr.org/tdb/mdb/hpdb/hpdb.html. The sequence has been deposited with GenBank under accession number AE000511.

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Table 2. List of *H.* pylori genes with putative identifications. Gene numbers correspond to those in Fig. 1. Each identified gene has been assigned a putative role category adapted from ref. 15. Percentages represent per cent identities.

AMINO-ACID BIOSYNTHESIS		HP0841	pantothenate metabolism flavoprotein (dfp)		HP0855		41.8%
General		D. of decides			HP0326	CMP-N-acetylneuraminic acid synthetase	04.00/
HP0695 hydantoin utilization protein A (hyuA)	28.6%	Pyridoxine HP1583	pyridoxal phosphate biosynthetic protein		HP0230	(neuA) CTP:CMP-3-deoxy-D-manno-octulosonate-	31.9%
Aromatic amino-acid family		111 1000	A (pdxA)	34.2%	111-0230	cytidylyl-transferase (kdsB)	36.2%
HP1038 3-dehydroquinase type II (aroQ)	99.4%	HP1582	pyridoxal phosphate biosynthetic protein J	011270			25.7%
HP0283 3-dehydroquinate synthase (aroB)	38.1%		(pdxJ)		HP0379		39.2%
HP0134 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (dhs1)	54.6%	Riboflavin	. ,		HP0651	fucosyltransferase	39.2%
HP0401 3-phosphoshikimate	34.070	HP0802	GTP cyclohydrolase II (ribA)		HP0044		62.1%
1-carboxyvinyltransferase (aroA)	53.6%	HP0804	GTP cyclohydrolase II/3,4-dihydroxy-2-butar		HP0867		32.0%
HP1279 anthranilate isomerase (trpC)	47.0%		4-phosphate synthase (ribA, ribB)	11.070	HP0159	lipopolysaccharide 1,2-glucosyltransferase (rfal)	28.9%
HP1282 anthranilate synthase component I (trpE)	47.9%	HP1505	riboflavin biosynthesis protein (ribG)	33.1%	HP0208	lipopolysaccharide 1,2-glucosyltransferase	20.9%
HP1280 anthranilate synthase component II (trpD)	42.5%	HP1087	riboflavin biosynthesis regulatory protein (ribC)	28.9%	111 0200		26.7%
HP1281 anthranilate synthase component II (trpD)	40.2%	HP1574		32.8%	HP0805	lipooligosaccharide 5G8 epitope biosynthes	
HP0663 chorismate synthase (aroC)	47.2% 30.2%			52.4%			36.9%
HP1380 prephenate dehydrogenase (tyrA) HP1249 shikimate 5-dehydrogenase (aroE)	36.6%		, glutaredoxin and glutathione	02.170	HP0826	lipooligosaccharide 5G8 epitope biosynthes	
HP0157 shikimic acid kinase I (aroK)	36.1%	HP1118	gamma-glutamyltranspeptidase (ggt)	53.2%			39.2%
HP1277 tryptophan synthase, alpha subunit (trpA)	46.5%	HP1458	thioredoxin	38.3%	HP1416	lipopolysaccharide 1,2-glucosyltransferase	00.00/
HP1278 tryptophan synthase, beta subunit (trpB)	66.1%	HP0824	thioredoxin (trxA)	E1 E0/-	1100070		29.2%
Aspartate family		HP1164	thioredoxin reductase (trxB)	28.5%	HP0679	lipopolysaccharide biosynthesis protein (wbpB)	42.8%
HP0649 aspartate ammonia-lyase (aspA)	55.5%	Thiamine			HP1475	lipopolysaccharide core biosynthesis proteil	
HP1189 aspartate-semialdehyde dehydrogenase		HP0814	thiamin biosynthesis protein (thiF)	34.6%		(kdtB)	49.0%
(asd)	45.7%	HP0843	thiamin phosphate pyrophosphorylase/		HP0279	lipopolysaccharide heptosyltransferase-1	
HP1229 aspartokinase (lysC) 48.0%	4770	1100015	hyroxyethylthiazole kinase (thiB)	35.7%			31.7%
HP0106 cystathionine gamma-synthase (metB)	47.7%	HP0845	thiamin phosphate pyrophosphorylase/	0700/	HP0619	lipopolysacharide biosynthesis glycosyl	
HP0290 diaminopimelate decarboxylase	42.7%	HP0844	hyroxyethylthiazole kinase (thiM)	37.9% 41.0%	LIBALOS		37.2%
(dap decarboxylase) (lysA) HP0566 diaminopimelate epimerase (dapF)	30.0%		thiamine biosynthesis protein (thi)		HP1105		28.7%
HP0510 dihydrodipicolinate reductase (dapi)	95.3%	Pyridine nud HP0329	NH(3)-dependent NAD+ synthetase (nadE)		HP1578 HP1581		28.1% 29.2%
HP1013 dihydrodipicolinate synthetase (dapA)	39.5%	HP1355	nicotinate-nucleotide pyrophosphorylase		HP0857		44.5%
HP0822 homoserine dehydrogenase (metL)	37.7%	111 1000	(nadC)		HP1275	phosphomannomutase (algC)	
HP1050 homoserine kinase (thrB)	27.7%	HP1356	quinolinate synthetase A (nadA)	34.2%			39.6%
HP0672 solute-binding signature and mitochondria	4700				HP1429	polysialic acid capsule expression protein	
signature protein (aspB)	47.3%	CELL ENVE	LOPE				46.0%
HP0212 succinyl-diaminopimelate desuccinylase (dapE)	42.3%		s, lipoproteins and porins		HP0366	spore coat polysaccharide biosynthesis	05.00/
HP0626 tetrahydrodipicolinate N-succinyltransferas			60 kDa inner-membrane protein	40.0%	HP0178		35.3%
(dapD)	36.1%	HP0180	apolipoprotein N-acyltransferase (cute)	20.070	וורטו/8	spore coat polysaccharide biosynthesis protein E	36.2%
HP0098 threonine synthase (thrC)	32.9%	HP0175	cell binding factor 2	34.9%	HP0421	type 1 capsular polysaccharide biosynthesis	
Glutamate family			Hypothetical protein	20.470		protein J (capJ)	29.0%
HP0380 glutamate dehydrogenase (gdhA)	59.0%	HP0567 HP1456		26.4% 98.9%	HP0196	UDP-3-0-(3-hydroxymyristoyl) glucosamine	
HP0512 glutamine synthetase (glnA)	48.6%	HP1456 HP1564	outer membrane protein (Ipp2U)	39 9%		N-acyltransferase (lpxD)	39.5%
HP1158 pyrroline-5-carboxylate reductase (proC)	28.9%	HP0009		0.0%	HP1052	UDP-3-0-acyl N-acetylglcosamine deacetylas	se
Pyruvate family		HP0324		0.0%			44.6%
HP0941 alanine racemase, biosynthetic (alr)	32.4%	HP0472	outer membrane protein (omp11)	99.5%	HP1375	UDP-N-acetylglucosamine acyltransferase	
HP1468 branched-chain-amino-acid		HP0477	outer membrane protein (omp12)	0.0%			41.8%
aminotransferase (ilvE)	63.5%	HP0638	outer membrane protein (omp13)		Surface stru		
HP0330 ketol-acid reductoisomerase (ilvC)	48.1%	HP0671	outer membrane protein (omp14)		HP0840		60.2%
Serine family		HP0706	outer membrane protein (omp15)		HP0325		32.7%
HP0107 cysteine synthetase (cysK)	45.7%	HP0722	outer membrane protein (omp16)		HP0351		34.4%
HP0096 phosphoglycerate dehydrogenase	31.0%	HP0725	outer membrane protein (omp17)		HP0246		37.9%
HP0397 phosphoglycerate dehydrogenase (serA)	32.5%	HP0796	outer membrane protein (omp18)		HP1557		37.0%
HP0736 phosphoserine aminotransferase (serC)	30.7%	HP0896	outer membrane protein (omp19)	36.6% 0.0%	HP1559	flagellar basal-body rod protein (flgB) (proximal rod protein)	31.0%
HP0652 phosphoserine phosphatase (serB)	36.5%	HP0025 HP0912	outer membrane protein (omp2) outer membrane protein (omp20)		HP1558	flagellar basal-body rod protein (flgC)	31.070
HP1210 serine acetyltransferase (cysE)	98.2%	HP0913	outer membrane protein (omp21)	38.2%	111 1000	(proximal rod protein)	46.0%
HP0183 serine hydroxymethyltransferase (glyA)	54.0%	HP0923	outer membrane protein (omp21)	0.0%	HP1092		35.5%
BIOSYNTHESIS OF COFACTORS, PROSTHETIC GROU	PS	HP1107	outer membrane protein (omp23)				47.7%
AND CARRIERS	10,	HP1113	outer membrane protein (omp24)	36.0%	HP1041		43.1%
General		HP1156	outer membrane protein (omp25)		HP1035		35.5%
HP0220 synthesis of [Fe-S] cluster (nifS)	48.0%	HP1157	outer membrane protein (omp26)		HP0684		43.4%
Biotin	10.070	HP1177	outer membrane protein (omp27)		HP0770		38.7%
HP0598 8-amino-7-oxononanoate synthase (bioF)	34.9%	HP1243	outer membrane protein (omp28)		HP0685		55.6%
HP0976 adenosylmethionine-8-amino-7-oxononano		HP1342 HP0079	outer membrane protein (omp29)		HP1419 HP0173		52.3% 26.4%
aminotransferase (bioA)	49.2%	HP10079 HP1395	outer membrane protein (omp3) outer membrane protein (omp30)		HP0353		29.1%
HP1140 biotin operon repressor/biotin acetyl coen		HP1395 HP1469	outer membrane protein (omp30) outer membrane protein (omp31)		HP1420		47.6%
A carboxylase synthetase (birA)	36.9%	HP1501	outer membrane protein (omp31)		HP0870		98.9%
HP0407 biotin sulfoxide reductase (bisC)	42.7%	HP0127	outer membrane protein (omp4)		HP0908		30.5%
HP1254 biotin synthesis protein (bioC)	32.1%	HP0227	outer membrane protein (omp5)		HP1119	flagellar hook-associated protein 1	
HP1406 biotin synthetase (bioB)	36.2%	HP0229	outer membrane protein (omp6)	38.4%		(HĂP1) (flgK)	27.6%
HP0029 dethiobiotin synthetase (bioD)	36.0%	HP0252	outer membrane protein (omp7)		HP0752		28.9%
Folic acid		HP0254	outer membrane protein (omp8)		HP0815		32.9%
HP1036 7, 8-dihydro-6-hydroxymethylpterin-		HP0317	outer membrane protein (omp9)		HP0816		29.7%
pyrophosphokinase (folK)	34.6%	HP0839	outer membrane protein P1 (ompP1)	23.3%	HP0352	flagellar motor switch protein (fliG)	37.0%
HP0587 aminodeoxychorismate lyase (pabC)	32.4%	HP0955	prolipoprotein diacylglyceryl transferase (lgt		HP1031 HP0753		34.4%
HP1232 dihydropteroate synthase (foIP)	34.5%	HP0655 HP1571	protective surface antigen D15 rare lipoprotein A (rlpA)		HP0327		32.3% 23.3%
HP1545 folylpolyglutamate synthase (folC) HP0928 GTP cyclohydrolase I (folE)	35.2% 50.9%	HP0610	toxin-like outer membrane protein				98.5%
HP0577 methylene-tetrahydrofolate dehydrogenase		HP0922			HP0/9/		
(foID)	48.4%		toxin-like outer membrane protein		HP0797 HP0584	flagellar switch protein (fliN)	39.7%
HP0293 para-aminobenzoate synthetase (pabB)		HP0289	toxin-like outer membrane protein toxin-like outer membrane protein	29.5%			
Haem and porphyrin	35.1%		toxin-like outer membrane protein	29.5% 30.6%	HP0584 HP0601 HP0115	flagellin A (flaA) flagellin B (flaB)	39.7% 99.8% 99.0%
HP0163 delta-aminolevulinic acid dehydratase		Murein sace	toxin-like outer membrane protein culus and peptidoglycan	29.5% 30.6%	HP0584 HP0601 HP0115 HP0295	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla)	39.7% 99.8% 99.0% 32.9%
(hemB)		Murein saco HP0830	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddlA)	29.5% 30.6% 40.6% 28.5%	HP0584 HP0601 HP0115 HP0295 HP1575	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flhB protein (flhB)	39.7% 99.8% 99.0% 32.9% 40.5%
HP0376 ferrochelatase (hemH)	35.1% 50.5%	Murein saco HP0830 HP0738 HP0549	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddIA) glutamate racemase (glr)	29.5% 30.6% 40.6% 28.5% 36.6%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flhB protein (flhB) fliY protein (fliY)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3%
HP0306 glutamate-1-semialdehyde 2,1-aminomutas	35.1% 50.5% 33.4%	Murein saco HP0830 HP0738 HP0549 HP0772	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddIA) glumante racemase (glr) N-acetylmuramoyl-L-alanine amidase (amiA	29.5% 30.6% 40.6% 40.6% 36.6% 4)26.8%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flhB protein (flhB) flip protein (flf) Hook assembly protein, flagella (flgD)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5%
(hemL)	35.1% 50.5% 33.4% e	Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (glr) N-acetylmuramoyl-L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A)	29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flihB protein (flhB) fliy protein (flhB) fly protein (flhB) flook assembly protein, flagella (flgD) paralysed flagella protein (pflA)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9%
	35.1% 50.5% 33.4% e 51.3%	Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanineiD-alanine ligase A (ddIA) glutamate racemase (glr) N-acetylmuramoyl-L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 2 (pbp2)	29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7% 35.0%	HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP0907 HP1274 HP0751	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) fliB protein (flhB) fliP protein (flhB) fliP protein (fliY) Hook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5%
HP0239 glutamyl-tRNA reductase (hemA)	35.1% 50.5% 33.4% e 51.3% 32.7%	Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanine-D-alanine ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyl-Lalanine amidase (amiA penicillin-binding protein 12 (pbp2) penicillin-binding protein 2 (pbp2) peptidoglycan associated lipoprotein precur	29.5% 30.6% 40.6% 28.5% 36.6% )/26.8% 33.7% 35.0% (sor	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274	flagellin A (flaA) flagellin A (flaB) flagellin B (flaB) flagellin B homologue (fla) flith B protein (flhB) flith P protein (flhB) flith P protein (fltr) Hook assembly protein, flagella (flgD) paralysed flagellia protein (pflA) polar flagellin (flaG) putative neureminyllactose-binding	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9%
HP0665 oxygen-independent coproporphyrinogen	35.1% 50.5% 33.4% e 51.3% 32.7%	Murein sace HP0830 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125	toxin-like outer membrane protein culus and peptidoglycan amidase D-alanine:D-alanine ligase A (ddlA) glutamate racemase (gir) N-acetylmuramoyl-L-alanine amidase (amiA penicillin-binding protein 1A (PBP-1A) peptidoglycan associated lipoprotein precui (omp18)	29.5% 30.6% 40.6% 28.5% 36.6% )26.8% 33.7% 35.0% rsor	HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP0907 HP1274 HP0751	flagellin A (flaA) flagellin B (flaB) flagellin B (homologue (fla) flagellin B homologue (fla) fliN protein (fliN) fliv protein (fliN) Hook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyflactose-binding haemagglutinin homologue (hpaA)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN)	35.1% 50.5% 33.4% e e 51.3% 32.7% IIII	Murein sacc HP0830 HP0738 HP0549 HP0772 HP0597 HP1565	toxin-like outer membrane protein   uulus and peptidoglycan  amidase D-alanine:D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetylmuramoylalanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  peptidoglycan associated lipoprotein precu  (cmp18)  phospho-N-acetylmuramoyl-pentapeptide-	29.5% 30.6% 40.6% 40.6% 36.6% 36.6% 33.7% 35.0% rsor 42.6%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462	flagellin A (flaA) flagellin B (flaB) flagellin B (homologue (fla) flagellin B homologue (fla) fliNB protein (fliNB) fliY protein (fliNB) flow assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (fipaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen	35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4%	Murein sacci HP0830 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493	toxin-like outer membrane protein  culus and peptidoglycan  amidase  D-alanine:D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetylmuramoyl-Lalanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  peptidoglycan associated lipoprotein precui  (omp18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mrary)	29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 37.7% 35.7% 35.7% 42.6% 45.2%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flihB protein (flhB) fliY protein (flhB) fliY protein (flhC) pralysed flagella protein (flfA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN)	35.1% 50.5% 3.4% e e 51.3% 32.7% III 42.4% III 37.9%	Murein sacci HP0830 HP0738 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493 HP0743	toxin-like outer membrane protein   uulus and peptidoglycan  amidase D-alanine:D-alanine ligase A (ddlA)  glutamate racemase (girl)  N-acetylmuramoylalanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  peptidoglycan associated lipoprotein precu  (omp 18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)	29.5% 30.6% 40.6% 28.6% 36.6% 33.7% 35.0% 55.0% 42.6% 42.6% 45.2%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462 HP0232	flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flagellin B homologue (fla) fliNB protein (fliNB) fliY protein (fliNB) flood assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC)	35.1% 50.5% 33.4% 6 6 51.3% 32.7% III 42.4% IIII 37.9% 45.7%	Murein sacci HP0830 HP0738 HP0549 HP0772 HP0597 HP1565 HP1125 HP0493	toxin-like outer membrane protein  culus and peptidoglycan  amidase  D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetylmuramoyl-Lalanine amidase (amiA  penicillin-binding protein 14 (PBP-1A)  penicillin-binding protein 12 (pbp2)  peptidoglycan associated lipoprotein precui  (omp18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)	29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 33.7% 35.0% 42.6% 45.2% 37.7% 51.9%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462 HP0232 CELLULAR	flagellin A (flaA) flagellin B (flaB) flagellin B (homologue (fla) flagellin B homologue (fla) fliNB protein (fliNB) fliY protein (fliNB) flow assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (fipaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% 772.5% 96.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN)	35.1% 50.5% 3.4% e e 51.3% 32.7% III 42.4% III 37.9%	Murein sacci HP0830 HP0738 HP0778 HP0597 HP1565 HP1125 HP0493 HP0743 HP1373 HP1373 HP1372 HP0645	toxin-like outer membrane protein  culus and peptidoglycan  amidase D-alanine:D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetylmuramoyi-L-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein precur  (cmp18)  phospho-N-acetylmuramoyi-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)	29.5% 30.6% 40.6% 28.5% 36.6% 28.8% 35.7% 35.0% 42.6% 47.7% 51.9% 33.6% 33.7% 35.9%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462 HP0232 CELLULAR General	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flish protein (flhB) fly protein (flhB) fly protein (flhB) Hook assembly protein, flagella (flgD) paralysed flagellin (flaG) polar flagellin (flaG) putative neurominyllactose-binding haemagglutinin homologue (fppaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES	39.7% 99.8% 99.8% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% /7.5% /96.2% /99.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 porphobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemK)	35.1% 50.5% 33.4% e 51.3% 32.7% III 42.4% III 37.9% 45.7% 35.9%	Murein sack HP0830 HP0738 HP0778 HP0597 HP1565 HP1125 HP0493 HP0743 HP1373 HP1372 HP0645 HP1543	toxin-like outer membrane protein  culus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acelyimuramoyl-alanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lylic murein transglycosylase (sti)  toxR-activated gene (tagE)	29.5% 30.6% 40.6% 28.5% 36.6% 28.5% 36.6% 35.7% 42.6% 42.6% 42.6% 51.7% 51.9% 32.2% 32.2%	HP0584 HP0601 HP0115 HP0295 HP1575 HP1030 HP0907 HP1274 HP0751 HP0410 HP1192 HP1462 HP0232 CELLULAR General HP0019	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) flix protein (flaY) brook assembly protein, flagella (flgD) paralysed flagellin (flaG) putative neuraminyflactose-binding haemagglutnin homologue (hpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 21.9% 24.2% (72.5% 96.2% (99.2%)
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 porphobilinogen deaminase (nemC) HP0381 protoporphyrinogen oxidase (nemS) HP0604 uroporphyrinogen deamoxylase (hemE) HP1224 uroporphyrinogen deamoxylase (hemD) Menaquinone and ubiquinone	35.1% 50.5% 33.4% e 51.3% 32.7% III 37.9% 42.4% III 37.9% 45.7% 35.9% 46.3%	Murein sact HP0830 HP0738 HP0749 HP0772 HP0597 HP1665 HP1125 HP0493 HP0743 HP1373 HP1373 HP1372 HP0645 HP1544 HP1544	toxin-like outer membrane protein  culus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetylmuramoyi-L-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein precur  (cmp18)  protespho-N-acetylmuramoyi-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining  rotein (mreB)  rote	29.5% 30.6% 40.6% 28.5% 36.6% 28.8% 36.6% 28.35.7% 35.0% 42.6% 47.7% 51.9% 33.6% 33.7% 33.6% 33.7% 33.6% 33.7%	HP0584 HP0601 HP0015 HP0295 HP1575 HP1576 HP1030 HP0907 HP1274 HP0410 HP1192 HP1462 HP1462 HP0232 CELLULAR General HP0019	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) flish protein (flhB) floretin (flhB) floretin (flhB) floretin (flhB) protein (flhB) protein (flhB) prarlysed flagellin (flaG) prarlysed flagellin (flaG) putative neureminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES	39,7% 99,8% 99,9% 99,9% 99,9% 32,9% 40,5% 22,9% 42,5% 23,9% 21,9% 27,25% 99,2% 24,2% 99,2% 26,8% 31,7% 26,8% 31,7%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 porphobilinogen deaminase (nemC) HP0381 protoporphyrinogen oxidase (nemS) HP0604 uroporphyrinogen deamoxylase (hemE) HP1224 uroporphyrinogen deamoxylase (hemD) Menaquinone and ubiquinone	35.1% 50.5% 33.4% e 51.3% 32.7% III 37.9% 42.4% III 37.9% 45.7% 35.9% 46.3%	Murein sack HP0830 HP0738 HP0778 HP0597 HP1565 HP1125 HP0493 HP0743 HP1373 HP1372 HP0645 HP1543	toxin-like outer membrane protein  culus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acety/muramoyl-alanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding sosciated lipop2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  protein protein protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lytic murein transglycosylase (st)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis	29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 36.6% 33.7% 35.0% 42.6% 42.6% 47.7% 51.9% 37.7% 51.9% 32.2% 37.2% 31.2%	HP0584 HP0601 HP0151 HP0295 HP1030 HP0907 HP1030 HP0907 HP0410 HP1474 HP0751 HP0410 HP1462 HP1462 CELLULAR General HP0393 HP0393 HP0393	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) flix protein (flaY) brook assembly protein, flagella (flgD) paralysed flagellin (flaG) putative neuraminyllactose-binding haemagglutnin homologue (hpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV)	39,7% 99,8% 99,0% 99,0% 32,9% 40,5% 22,3% 25,5% 22,3% 21,9% 24,2% 772,5% 99,2% 26,8% 21,9% 26,8% 21,9% 24,2% 26,8% 31,7% 31,7% 27,9% 27,9%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemC) protoporphyrinogen oxidase (nemC) protoporphyrinogen oxidase (nemC) HP0604 uroporphyrinogen decarboxylise (nemE) Wenaequinone and ubiquinone	35.1% 50.5% 33.4% e 51.3% 32.7% III 37.9% 42.4% III 37.9% 45.7% 35.9% 46.3%	Murein sact HP0830 HP0738 HP0549 HP0772 HP1565 HP1125 HP0493 HP0743 HP0743 HP1373 HP1372 HP0645 HP1543 HP1544 HP155	toxin-like outer membrane protein  culus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoyl-Lalanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein (merell)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lyfic murein transglycosylase (slt)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis  (murG)	29.5% 30.6% 40.6% 28.5% 36.6% 28.8% 35.7% 35.0% 47.2% 47.2% 47.2% 37.7% 51.9% 33.9% 32.2% 37.2% 31.2% 37.2%	HP0584 HP0601 HP0115 HP0295 HP1576 HP1030 HP0907 HP1030 HP0907 HP1192 HP0410 HP1192 HP0410 HP1192 HP0232 CELLULAR General HP0393 HP0616 HP0039 HP0616	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) fliha protein (flhB) flih protein (flhB) flih protein (flhT) Hook assembly protein (flaG) paralysed flagellia protein (flfA) polar flagellin (flaG) putative neureminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  Chemotaxis protein (cheV)	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 25.5% 23.9% 24.2% 772.5% 99.2% 24.96 772.5% 99.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) oxygen-independent coproporphyrinogen oxidase (hemN) porphobilinogen deaminase (hemC) protoporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen decarboxylase (hemE) uroporphyrinogen decarboxylase (hemE) Menaquinone and ubiquinone HP1380 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA)	35.1% 50.5% 33.4% e 51.3% 32.7% 111 42.4% 111 47.7% 45.7% 46.3% 47.6% 46.3% 47.6% 48.3% 49.4% 48.3% 49.4% 49.4% 49.4% 40	Murein sact HP0830 HP0738 HP0749 HP0772 HP0597 HP1665 HP1125 HP0493 HP0743 HP1373 HP1373 HP1372 HP0645 HP1544 HP1544	toxin-like outer membrane protein  culus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acety/muramoyl-alanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  phospho-N-acety/muramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lytic murein transglycosylase (st)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 33.7% 35.0% 42.6% 42.6% 45.2% 37.7% 51.9% 33.8% 32.2% 31.2% 31.2%	HP0584 HP0601 HP0601 HP0601 HP0907 HP1030 HP0907 HP0907 HP0751 HP0410 HP1192 HP0410 HP1192 CELLULAR General HP0033 HP0616 HP1067 HP1067	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) chemotaxis chemotaxis chemotaxis chemotaxis chemotaxis chemotaxis chemotaxis chemota	39,7% 99,8% 99,0% 99,0% 99,0% 32,9% 40,5% 29,3% 25,5% 22,9% 21,9% 24,2% 772,5% 29,2% 31,7% 29,2% 31,7% 27,9% 99,2% 96,5% 69,5% 69,5%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 hp0604 porphobilinogen deaminase (nemC) protoporphyrinogen oxidase (hemK) HP0804 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen decarboxylase (hemE) Menaquinone and ubiquinone HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA)	35.1% 50.5% 33.4% 6 6 13.3% 32.7% 11 42.4% 11 37.9% 45.7% 35.9% 46.3% 27.6% 26.6%	Murein sack HP0830 HP0548 HP0549 HP0772 HP1665 HP1125 HP0493 HP0743 HP1373 HP1373 HP1543 HP1544 HP1544 HP1544 HP1544	toxin-like outer membrane protein  culus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoyl-Lalanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein (greb)  protein 4 (ppn)  protein (greb)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lyfic murein transglycosylase (slt)  toxR-activated gene (tagE)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase  (murF)	29.5% 30.6% 40.6% 28.5% 30.6% 36.6% 36.6% 35.7% 45.2% 37.7% 51.9% 33.6% 22.2% 37.2% 31.2% 28.2%	HP0584 HP0601 HP0115 HP0205 HP1676 HP120205 HP1274 HP0307 HP0237 HP0410	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla) fliha protein (flhB) flih protein (flhB) flih protein (flhT) Hook assembly protein (flaG) paralysed flagellia protein (flfA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility hammad protein involved in flagellar motility secreted protein involved in flagellar motility chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (ere) haemolysin	39.7% 99.8% 99.0% 32.9% 40.5% 29.3% 225.5% 23.9% 21.9% 24.2% 772.5% 99.2% 24.2% 772.5% 99.2% 99.2% 99.2% 99.2% 99.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 hprophobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0804 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen ill cosynthase (hemD) Menaquinone and ubiquinone HP1300 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0229 geranyltranstransferase (ispA) HF0240 octaprenyl-diphosphate synthase (ispB)	35.1% 50.5% 33.4% e 51.3% 32.7% 111 42.4% 111 47.7% 45.7% 46.3% 47.6% 46.3% 47.6% 48.3% 49.4% 48.3% 49.4% 49.4% 49.4% 40	Murein sact HP0830 HP0738 HP0549 HP0772 HP0569 HP1565 HP1165 HP0493 HP0743 HP1373 HP1373 HP1372 HP0645 HP1643 HP1644 HP1165 HP0740 HP1494	toxin-like outer membrane protein  culus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acelyimuramoyl-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  protein 2 (ppp2)  protein 2 (ppp2)  protein 2 (ppp2)  protein 2 (ppp2)  rod shape-determining protein (mreB)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase  (murF)  UDP-MurNac-tripeptide synthetase (murE)	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 42.6%	HP0584 HP0601 HP0115 HP0295 HP1295 HP1030 HP0397 HP1274 HP0410 HP0410 HP1192 HP1462 HP0462 HP0463 HP0616 HP0393 HP0616 HP1097 HP	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) paralysed flagella protein (pflA) polar flagellin (flaB) putative neuraminyllactose-binding haemagglutinin homologue (flaB) secreted protein involved in flagellar motility secreted protein involved in flagellar motility secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) flagellin fla	39,7% 99,8% 99,0% 99,0% 99,0% 32,9% 40,5% 29,3% 25,5% 22,9% 21,9% 24,2% 772,5% 29,2% 31,7% 29,2% 31,7% 27,9% 99,2% 96,5% 69,5% 69,5%
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) oxygen-independent coproporphyrinogen oxidase (hemN) porphobilinogen deaminase (hemC) protoporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen decarboxylase (hemE) uroporphyrinogen decarboxylase (hemE) Menaquinone and ubiquinone HP1380 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA)	35.1% 50.5% 33.4% e 51.3% 32.7% 111 42.4% 111 47.7% 45.7% 46.3% 47.6% 46.3% 47.6% 48.3% 49.4% 48.3% 49.4% 49.4% 49.4% 40	Murein sack HP0830 HP0548 HP0549 HP0772 HP1665 HP1125 HP0493 HP0743 HP1373 HP1373 HP1543 HP1544 HP1544 HP1544 HP1544	toxin-like outer membrane protein  culus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetyimuramoyit-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  protein 3 penicillin-binding protein 2 (ppp2)  prod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lytic murein transglycosylase (slt)  toxR-activated gene (tagE)  toxR-activated gene (tagE)  toxR-activated gene (tagE)  toxR-activated gene (tagE)  UDP-MurNac-proteiptide presynthetase  (murF)  UDP-MurNac-bripeptide synthetase (murE)  UDP-MurNac-bripeptide synthetase (murE)  UDP-MurNac-bripeptide synthetase  (murE)  UDP-MurNac-bripeptide presynthetase  (murE)  UDP-MurNac-bripeptide   DE - MurNac-bripeptide   DE - MurN	29.5% 30.6% 40.6% 28.5% 30.6% 36.6% 36.6% 35.7% 42.6% 45.2% 37.7% 51.9% 33.6% 22.2% 37.2% 31.2% 28.2% 25.7% 36.0%	HP0584 HP0601 HP0115 HP0205 HP1676 HP120205 HP1274 HP0307 HP0237 HP0410	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) polar flagellin (flaB) polar flagellin (flaG) polar flagellin (flaG) potative neureminyliactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (era) haemolysin Haemolysin (tly) haemolysin (ty) haemolysin secretion protein precursor	39.7% 99.8% 99.0% 32.9% 99.0% 32.9% 40.5% 29.3% 22.55% 22.9% 22.55% 23.9% 22.55% 23.9% 21.9% 24.2% 72.5% 99.2% 29.5% 99.2% 99.
HP0665 oxygen-independent coproporphyrinogen oxidase (hemN) HP1226 oxygen-independent coproporphyrinogen oxidase (hemN) HP0237 oxygen-independent coproporphyrinogen oxidase (hemN) HP02381 porphyrinogen oxidase (hemC) HP0604 uroporphyrinogen oxidase (hemE) HP1224 uroporphyrinogen decarboxylase (hemE) HP1360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0240 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0768 molybdopterin molybdopterin protein A (moaA)	35.1%  50.5% 33.4% e e 51.3% 32.7% iiii 42.4% iiii 37.9% 45.7% 45.7% 46.3% 46.	Murein sact HP0830 HP0788 HP0549 HP0772 HP05897 HP11565 HP0493 HP0743 HP1373 HP1373 HP1373 HP1645 HP1645 HP1645 HP1645 HP1645 HP1645 HP1646 HP1646 HP1647 HP1646 HP1646 HP1647 HP1646 HP1647 HP1646 HP1646 HP1647 HP1646 HP1646 HP1647 HP1646	toxin-like outer membrane protein  culus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acety/muramoyl-alanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  phospho-N-acety/muramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lytic murein transglycosylase (st)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase  (murF)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase (murE)	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 35.7% 42.6% 42.6% 42.6% 42.6% 43.77% 51.9% 33.6% 33.22% 33.2% 33.2% 33.2% 33.2%	HP0584 HP0691 HP0115 HP0295 HP1295 HP10306 HP0397 HP1274 HP0410 HP1192 HP1462 HP0410 HP1192 CELLULAR General HP0019 HP0313 HP0616 HP1067 HP1067 HP10617 HP1068 HP10699	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) putative flagella protein (flaB) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) dhemotaxis protein (cheV) flagelling flagel	39.7% 99.8% 99.0% 32.9% 99.0% 32.9% 40.5% 29.3% 225.5% 22.9% 225.5% 23.9% 21.9% 23.9% 21.9% 31.7% 31.7% 31.7% 31.7% 31.7% 42.79% 96.6% 31.7% 40.2% 45.4% 45.4%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 prophobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0804 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen ill cosynthase (hemD) Menaquinone and ubiquinone HP1380 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0299 geranyltranstransferase (ispA) HP0290 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein A (moaA) HP0788 molybdenum cofactor biosynthesis protein	35.1%  50.5% 33.4% e 651.3% 32.7% IIII 42.4% IIII 42.4% IIII 45.7% 37.9% 46.37% 27.6% 50.9% 46.33% 27.6% 50.9% 60.9% 60.	Murein sact HP0830 HP0738 HP0549 HP0772 HP0569 HP1565 HP1165 HP0493 HP0743 HP1373 HP1373 HP1372 HP0645 HP1643 HP1644 HP1165 HP0740 HP1494	toxin-like outer membrane protein   uulus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (gir)  N-acetylmuramoylalanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)	29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 36.6% 35.7% 42.6% 42.6% 45.2% 37.7% 51.9% 33.6% 32.2% 33.7% 31.2% 31.2% 32.2% 33.7% 33.7%	HP0584 HP0601 HP0115 HP0105 HP1015 HP10295 HP1675 HP10307 HP1274 HP0307 HP1274 HP0410 HP1182 HP0462 HP0232 CELLULAR General HP0482 HP0393 HP0039 HP1067 HP1490 HP1490 HP1490 HP1490 HP1490 HP1490 HP0392	flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) polar flagellin (flaB) polar flagellin (flaB) potative neuraminyliactose-binding haemagglutinin homologue (fipaA) secreted protein involved in flagellar motility PROCESSES chemotaxis protein (cheV) flagellin flagel	39.7% 99.8% 99.0% 32.9% 40.5% 24.2% 72.5% 99.2% 25.5% 27.9% 24.2% 772.5% 99.2% 26.8% 31.7% 31.7% 32.2% 40.2% 40.2% 40.2% 40.2% 40.2% 40.2% 45.4% 41.4%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 oxygen-independent coproporphyrinogen oxidase (hemS) HP0818 prophyrinogen dearminase (hemC) HP0829 uroporphyrinogen dearmoxylase (hemE) HP360 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0929 geranyltranstransferase (ispA) HP0788 molybdenum cofactor biosynthesis protein (HP0788 molybdenum cofactor biosynthesis protein (moaC)	35.1%  50.5% 33.4% e e 51.3% 32.7% iiii 42.4% iiii 37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  31.4% i C	Murein sact HP0330 HP0388 HP0649 HP00788 HP0649 HP0772 HP0697 HP1125 HP0743 HP1373 HP1372 HP0645 HP1543 HP1543 HP1543 HP1544 HP1545 HP1543 HP1545 HP154	toxin-like outer membrane protein  cutulus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoylalanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lytic murein transglycosylase (st)  toxR-activated gene (tagE)  transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-tripeptide synthetase (murE)	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 35.7% 35.0% 47.7% 47.2% 37.7% 47.2% 37.2%	HP0584 HP0691 HP0115 HP0295 HP1575 HP1575 HP1070 HP00907 HP00907 HP0091 HP0410 HP0410 HP1182 HP0410	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) dhemotaxis protein (cheV) flagemolysin (flyB) haemolysin secretion protein precursor (hylB) histdine kinase (cheA) methyl-accepting chemotaxis protein (flpA)	39.7% 99.8% 99.9%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 prophobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0604 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen ill cosynthase (hemD) Menaquinone and ubiquinone HP1380 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0299 geranyltranstransferase (ispA) HP0290 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0788 molybdenum cofactor biosynthesis protein (mosA) HP0780 molybdopterin biosynthesis protein (mosA) HP0172 molybdopterin biosynthesis protein (mosA)	35.1%  50.5% 33.4% e e 51.3% 32.7% iiii 42.4% iiii 42.4% iii 27.9% 46.3% 35.9% 46.3% 53.9% 46.3% 66.6% 39.8% 31.6%  C 97.9% ) 36.3%	Murein sact HP0830 HP0788 HP0549 HP0772 HP05897 HP11565 HP0493 HP0743 HP1373 HP1373 HP1373 HP1645 HP1645 HP1645 HP1645 HP1645 HP1645 HP1646 HP1646 HP1647 HP1646 HP1646 HP1647 HP1646 HP1647 HP1646 HP1646 HP1647 HP1646 HP1646 HP1647 HP1646	toxin-like outer membrane protein   uulus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  gituranter racemase (gir)  N-acetylmuramoyi-L-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  UDP-MurNac-pentapeptide presynthetase  (murG)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-pentapeptide  protein protein (mreB)  rod shape-determining protein (mreB)  rod shape-deter	29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 36.6% 35.7% 42.6% 47.2% 37.7% 51.9% 33.6% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 45.2% 37.2% 31.2% 46.7% 46.7%	HP0584 HP0601 HP0115 HP0105 HP1676 HP1678 HP1678 HP1678 HP0907 HP0907 HP0407 HP0410 HP0410 HP0410 HP0410 HP0410 HP0410 HP0410 HP1082 HP0486 HP0699 HP0686 HP0686 HP0686 HP0686 HP0686 HP0686 HP0689 HP0689 HP0699 HP0699 HP0699	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) flagellin (flaG) poralysed flagellin protein (flaB) potative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein involved in flagellar motility chemotaxis protein (cheV) GTP-binding protein (cheV) GTP-binding protein (rea) haemolysin secretion protein precursor (rylB) histldine kinase (cheA) mettly-accepting chemotaxis protein (flpA) mettly-accepting chemotaxis protein (flpA) mettly-accepting chemotaxis protein (flpA)	39.7% 99.8% 99.9%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (hemN) prophobilinogen dearnionase (hemC) protoporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen oxidase (hemK) HP0604 uroporphyrinogen dearnioxylase (hemE) HP1360 (hempendent) dearnionase and ubiquinone HP1360 (hempendent) dearnionase dearnionase (hempendent) dearnionase (hempendent	35.1% 50.5% 33.4% 6 6 51.3% 32.7% 1111 42.4% 1113.7.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.6% 31.4% C 97.9% 31.4% 31.4% C 31.4%	Murein sact HP0330 HP0388 HP0649 HP0778 HP0649 HP0778 HP0587 HP1125 HP0433 HP1373 HP1372 HP0645 HP1543 HP1543 HP1544 HP1544 HP1544 HP1544 HP1544 HP1544 HP1448 HP0648 HP0648 HP0648	toxin-like outer membrane protein  cutulus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoyl-L-alanine amidase (amiA  penicillin-binding protein 12 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  penicillin-binding protein 2 (pbp2)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  IUDP-Murachylae pentapeptide presynthetase  (murE)  UDP-MurNac-tripeptide synthetase (murNac-tripeptide)  UDP-M	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 35.7% 35.0% 42.6% 45.2% 37.7% 51.9% 33.8% 32.2% 37.3%	HP0584 HP0601 HP0115 HP0105 HP1675 HP1675 HP1676 HP00907 HP00907 HP0091 HP0401 HP0416	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) putative neuraminyllactose-binding hatemagglutinin homologue (hpaA) secreted protein involved in flagellar motility hemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemolysin secretion protein protein precursor (hylB) histdine kinase (cheA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis transducer	39.7% 99.8% 99.9%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 prophobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0604 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen decarboxylase (hemE) HP1280 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0299 geranyltranstransferase (ispA) HP0299 wolybedperin HP0788 molybdenum cofactor biosynthesis protein (mosC) HP0798 molybdopterin biosynthesis protein (mosC) HP0712 molybdopterin biosynthesis protein (mosC) HP0755 molybdopterin biosynthesis protein (mosC) HP0756 molybdopterin biosynthesis protein (mosC) HP07575 molybdopterin biosynthesis protein (mosC) HP0798 molybdopterin biosynthesis protein (mosC)	35.1% 50.5% 33.4% 6 6 51.3% 32.7% 1111 42.4% 1113.7.9% 45.7% 35.9% 46.3% 27.6% 26.6% 39.8% 31.6% 31.4% C 97.9% 31.4% 31.4% C 31.4%	Murein sact HP0330 HP0388 HP0649 HP00788 HP0649 HP0772 HP0697 HP1125 HP0743 HP1373 HP1372 HP0645 HP1543 HP1543 HP1543 HP1544 HP1545 HP1543 HP1545 HP154	toxin-like outer membrane protein   uulus and peptidoglycan  amidase D-alanine-D-alanine ligase A (ddlA)  gituranter racemase (gir)  N-acetyimuramoyi-L-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  protein 2 (ppp2)  pr	29.5% 30.6% 40.6% 28.5% 36.6% 36.6% 36.6% 35.7% 42.6% 45.2% 37.7% 51.9% 33.6% 32.2% 37.2% 31.2% 32.2% 32.2% 37.2% 31.2% 32.2% 37.2% 31.2% 32.2% 37.3%	HP0584 HP0601 HP0115 HP0105 HP1675 HP1675 HP1676 HP00907 HP00907 HP0091 HP0401 HP0416	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) flagellin (flaG) paralysed flagellin protein (flaB) potative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein involved in flagellar motility chemotaxis protein (cheV) chemotaxis prote	39.7% 99.8% 99.9% 99.8% 99.0% 32.9% 40.5% 22.9% 25.5% 22.9% 26.5% 23.9% 24.2% 772.5% 99.2% 24.2% 99.2% 26.5% 99.2% 45.5% 99.2% 45.5% 99.2% 45.5% 99.2% 45.5% 99.2% 45.5% 99.2% 45.5% 99.2% 45.5% 99.2% 45.4% 41.4% 33.2% 45.4% 41.4% 33.2% 50.5% 99.2% 45.4% 41.4% 33.2% 50.5% 99.2% 45.4% 41.4% 33.2% 50.5% 99.2% 45.4% 41.4% 33.2% 50.5% 99.2% 99.2% 50.5% 99.2% 50.5% 99.2% 50.5% 99.2% 50.5% 99.2% 50.5% 99.2% 50.5% 99.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) porphobilinogen deaminase (hemC) protoporphyrinogen oxidase (hemE) HP0604 uroporphyrinogen dearboxylase (hemE) HP1806 oxygen oxyge	35.1%  50.5% 33.4%  6  51.3% 32.7%  111  42.4% 113.7.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.4% C  97.9% 31.6%  31.4% C  30.3% 30.322% 50.8%	Murein sact HP0830 HP0738 HP0778 HP0779 HP0779 HP0637 HP1125 HP0743 HP1373 HP1372 HP0645 HP1643 HP1643 HP1644 HP1646 HP1649 HP1649 HP1649 HP1649 HP1648 HP0648 HP0648 HP0648 HP0648	toxin-like outer membrane protein  utuks and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoyl-alanine amidase (amiA  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein (ppp.)  pepidoglycan associated lipoprotein precu  (omp18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mary)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lyfic murein transglycosylase (slt)  toxR-activated gene (lagE)  toxR-activated gene (lagE)  toxR-activated gene (lagE)  toxR-activated gene (lagE)  UDP-MurNac-pentapeptide presynthetase (murE)  UDP-MurNac-tripeptide synthetase (murNac-tripeptide synthetase (murNac-t	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 35.7% 35.7% 42.6% 47.6% 47.6% 47.7% 47.6% 48.2%	HP0584 HP0601 HP0115 HP0105 HP1575 HP1575 HP1576 HP0907 HP0907 HP0917 HP0416 HP	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B (flaB) flagellin B homologue (fla flagellin B homologue (fla flaB) flagellin B homologue (fla flaB protein (flaB) fliY protein (fliY) Hook assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) putative neuraminyllactose-binding heamagglutinin homologue (hpaA) secreted protein involved in flagellar motility secreted protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemolysin secretion protein precursor (rylB) histidine kinase (cheA) methyl-accepting chemotaxis protein (tlpB) methyl-accepting chemotaxis transducer (tlpC) purine-binding chemotaxis transducer (tlpC)	39.7% 99.8% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 25.5% 21.9% 24.2% 772.5% 99.2% 24.2% 79.5% 29.5%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 HP0237 HP0808 HP0808 HP0808 HP0808 HP0808 HP1224 uroporphyrinogen oxidase (nemC) HP1224 uroporphyrinogen idle carboxylase (hemE) HP124 uroporphyrinogen ill cosynthase (hemD) Menaquinone and ubiquinone HP1800 HP0829 HP0829 HP0829 HP0839 HP084 HP085 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP0789 HP0780 HP0780 HP0780 HP0781 HP0785 HP0785 HP0785 HP0787 HP0786 HP0787 HP0787 HP0787 HP0787 HP0787 HP0787 HP0788 HP0788 HP0788 HP0788 HP0788 HP0788 HP0789 HP0801 HP080	35.1%  50.5% 33.4% e 6 51.3% 32.7% 111 42.4% 111 47.5% 46.3% 47.6%  26.6% 39.8% 31.6%  31.4% C 97.9% 36.3% 31.6%  31.4% 36.3% 31.6%	Murein sact HP0830 HP0733 HP0733 HP0734 HP0772 HP0587 HP1565 HP1156 HP1437 HP0433 HP0373 HP1373 HP1373 HP1543 HP1543 HP1544 HP1554 HP1544 HP1544 HP1544 HP1545 HP0740 HP1448 HP0645 HP0645 HP0645 HP0645 HP0645 HP0645 HP0645 HP0646 HP0648 HP0648 HP0648 HP0648 HP0649 HP0649 HP0649 HP0649 HP0649 HP0649 HP0649 HP0649 HP0648 HP0649 HP06	toxin-like outer membrane protein  culus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  giutamate racemase (gir)  N-acetylmuramoyi-Lalanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mary)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  rod shape-determining protein (mreB)  toxin-activated gene (tagE)  toxin-activated gene  toxi	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 42.6% 43.7% 43.3%	HP0584 HP0601 HP0115 HP0105 HP1075 HP1075 HP1075 HP1075 HP1075 HP0075 HP	flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flix protein (fltY) hock assembly protein, flagella (flgD) paralysed flagella protein (pflA) polar flagellin (flaG) paralysed flagella protein (flaB) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) haemolysin Heamolysin (fly) haemolysin secretion protein precursor (flyfB) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis transducer (flpC) purine-binding chemotaxis protein (cheW) 7	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 22.5% 24.2% 24.2% 24.2% 27.25% 27.25% 27.25% 27.9% 27.
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) porphobilinogen deaminase (hemC) protoporphyrinogen oxidase (hemE) protoporphyrinogen oxidase (hemE) oxygen o	35.1%  50.5% 33.4%  e  51.3% 32.7%  111  42.4%  111  37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  31.4%  C  97.9% 30.36.3% 30.32.2% 50.8%  31.1%	Murein sact HP0830 HP0738 HP0778 HP0779 HP0779 HP0637 HP1125 HP0743 HP1373 HP1372 HP0645 HP1643 HP1643 HP1644 HP1646 HP1649 HP1649 HP1649 HP1649 HP1648 HP0648 HP0648 HP0648 HP0648	toxin-like outer membrane protein  utuks and paptidoglycan  amidase  D-alanine-D-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoyl-alanine amidase (amiA  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein (ppp)  peptidoglycan associated lipoprotein precu  (omp18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  rod shape-determining protein (mreC)  soluble lytic murein transglycosylase (stt)  toxiN-activated gene (lagE)  transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-pentapeptide presynthetase  (murC)  UDP-MurNac-pentapeptide presynthetase  (murC)  UDP-MurNac-pentapeptide synthetase  (murC)  UDP-MurNac-pentapeptide  UDP	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 35.7% 35.7% 45.2% 37.7% 51.9% 33.8% 32.2% 37.2% 37.2% 37.2% 37.2% 37.2% 37.7% 46.7% 37.3% 37.7%	HP0584 HP0601 HP0115 HP0105 HP11575 HP11575 HP1030 HP0907 HP0907 HP0907 HP0916 HP0416	flagellin A (flaA) flagellin B (flaB) paralysed flagella protein (flAB) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility secreted protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) haemolysin (ty) haemolysin secretion protein precursor (ty)B) histidine kinase (cheA) methyl-accepting chemotaxis protein (tlpB) methyl-accepting chemotaxis transducer (tlpC) purine-binding chemotaxis protein (cheW)  cell division inhibitor (minD)	39.7% 99.8% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 25.5% 21.9% 24.2% 772.5% 99.2% 24.2% 79.5% 29.5%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 prophobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0604 uroporphyrinogen decarboxylase (hemE) HP1224 uroporphyrinogen decarboxylase (hemE) HP1280 4-hydroxyberzoate octaprenyltransferase (ubiA) HP0293 geranyltranstransferase (ispA) HP0294 octaprenyl-diphosphate synthase (ispB) Molybdopterin HP0785 molybdenum cofactor biosynthesis protein (moaC) HP0172 molybdopterin biosynthesis protein (moeC) HP0795 molybdopterin biosynthesis protein (moeC) HP0801 molybdopterin biosynthesis protein (moeC) HP0801 molybdopterin converting factor, subunit 1 (moaD) HP0800 molybdopterin converting factor, subunit 2 (moaE)	35.1%  50.5% 33.4% e 6 51.3% 32.7% 111 42.4% 111 43.79% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  31.4% C 97.9% 33.83% 31.6%  31.4% C 97.9% C 97.9	Murein sact HP0830 HP0732 HP0532 HP0543 HP0543 HP0543 HP0543 HP0543 HP0543 HP0545 HP0545 HP0545 HP1564 HP1564 HP0564 HP0564 HP0564 HP0564 HP0564 HP0564 HP0664 HP0665 HP0665 HP0665 HP0666 HP066 HP066 HP066 HP066 HP0666 HP066 HP06	toxin-like outer membrane protein  culus and peptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  gittamate racemase (gir)  N-acetylmuramoyl-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  toxR-activated gene (tagE)  toxR-activated gene  toxR-activated gene  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 42.6% 42.6% 42.6% 42.6% 42.6% 43.7% 42.6% 43.7% 43.3%	HP0584 HP0601 HP0115 HP0105 HP1075 HP1075 HP1075 HP1075 HP1070 HP0907 HP0407 HP0410 HP	flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flix protein (flxB) flix protein (flxB) flix protein (flxB) polar flagellin (flaG) paralysed flagella protein (fplA) polar flagellin (flaG) paralysed flagella protein (flaB) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) haemolysin (fly) haemolysin secretion protein precursor (flyB) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (fleW)  cell division inhibitor (minD) cell division membrane protein (flsX)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 21.9% 22.3% 22.3% 25.5% 21.9% 24.2% 772.5% 23.9% 27.25% 99.2% 26.5% 27.9% 27.9% 27.5% 31.7% 27.9% 40.2% 40.2% 40.2% 45.4% 32.8% 30.7% 45.2% 45.4% 32.8% 30.7% 45.4% 32.8% 30.7% 50.2
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 her oxidase (nemN) HP0247 prothobilinogen deaminase (hemC) HP0381 uroporphyrinogen oxidase (hemE) HP0804 uroporphyrinogen decarboxylase (hemE) HP0804 uroporphyrinogen decarboxylase (hemE) HP0804 uroporphyrinogen decarboxylase (hemE) HP0805 depropriyrinogen decarboxylase (hemE) HP0809 despriyrinogen decarboxylase (hemE) HP0929 despriyrinogen decarboxylase (hemE) HP0708 molybdoperaset (spA) HP0708 despriyrinogen decarboxylase (hemD) Molybdopterin HP0708 molybdopterin biosynthesis protein (moeA) HP0709 molybdopterin biosynthesis protein (moeA) HP0800 molybdopterin biosynthesis protein (moeA) HP0800 molybdopterin biosynthesis protein (moeA) HP0800 molybdopterin oonverting factor, subunit 1 (moaC) Molybdopterin converting factor, subunit 2 (mosE) HP0709 molybdopterin onverting factor, subunit 2 (mosE) MOlybdopterin onverting factor, subunit 2 (mosE) MOlybdopterin-guanine dinucleotide biosymbopterin-guanine dinucleotide biosymbops	35.1%  50.5% 33.4%  6 51.3% 32.7%  1111  42.4%  1111  37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  31.4% C 37.9% 31.9% 50.8% 31.1% 50.28% 31.1% 51.1% 51.1%	Murein sact HP0830 HP0733 HP0733 HP0734 HP0772 HP0587 HP1565 HP1156 HP1437 HP0433 HP0373 HP1373 HP1373 HP1543 HP1543 HP1544 HP1554 HP1544 HP1544 HP1544 HP1545 HP0740 HP1448 HP0645 HP0645 HP0645 HP0645 HP0645 HP0645 HP0645 HP0646 HP0648 HP0648 HP0648 HP0648 HP0649 HP0649 HP0649 HP0649 HP0649 HP0649 HP0649 HP0649 HP0648 HP0649 HP06	toxin-like outer membrane protein  utuks and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamate racemase (glr)  N-acetylmuramoyl-alanine amidase (amiA  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein (ppnicilin-binding protein 1A (ppp-1A)  penicilin-binding protein (ppnicilin-binding protein (ppnicilin-binding protein (ppnicilin-binding protein (ppnicilin-binding protein (ppnicilin-binding)  pospho-N-acetylmuramoyl-pentapeptide- transferase, peptidoglycan synthesis  (murG)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase (murC)  UDP-Murnac-tripeptide synthetase (murnac-tripeptide	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 35.7% 35.7% 42.6% 47.2% 37.7% 51.9% 32.2% 37.2% 37.2% 37.2% 37.2% 37.2% 37.3% 37.7% 46.7% 37.3% 37.7%	HP0584 HP0601 HP0115 HP0105 HP1575 HP1575 HP1576 HP0907 HP0907 HP0916 HP0916 HP0916 HP0916 HP0916 HP0916 HP0916 HP0916 HP0916 HP0917 HP0917 HP0917 HP0917 HP0917 HP0917 HP0917 HP0917 HP0917 HP0918 HP0918 HP0918 HP0918 HP0918	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) protein (flaB) protein (flaB) protein (flaB) protein (flagellin flagellin (flaG) paralysed flagellin protein (flaB) polar flagellin flagellin flagellin flagellin motility secreted protein involved in flagellar motility hermotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (fleA) flagemolysin (flagemolysin (flagemolysin (flagemolysin secretion protein precursor (flyB) heamolysin secretion protein protein (flagemethyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein flpB)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 22.5% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 796.2% 26.5% 29.2% 26.5% 27.9
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) porphobilinogen deaminase (hemC) protoporphyrinogen oxidase (hemS) HP0801 protoporphyrinogen oxidase (hemS) HP0804 protoporphyrinogen oxidase (hemE) HP1824 uroporphyrinogen decarboxylase (hemE) Menaquinone and ubiquinone HP1800 deproporphyrinogen libroxylase (hemD) Menaquinone and ubiquinone HP1800 peranyltranstransferase (ispA) 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0829 geranyltranstransferase (ispA) hP0809 protein A (moaA) molybdopterin molybdopterin biosynthesis protein (moaC) HP0172 molybdopterin biosynthesis protein (moaC) HP0809 molybdopterin biosynthesis protein (moaD) molybdopterin biosynthesis protein (moaD) molybdopterin biosynthesis protein (moaD) molybdopterin converting factor, subunit 1 (moaD) molybdopterin converting factor, subunit 1 (moaD) molybdopterin converting factor, subunit 2 (moaE) molybdopterin deinverting factor, subunit 2 protein (moaE) molybdopterin deinverting factor, subunit 2 protein 4 (moaD)	35.1%  50.5% 33.4% e 6 51.3% 32.7% 111 42.4% 111 43.79% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  31.4% C 97.9% 33.83% 31.6%  31.4% C 97.9% C 97.9	Murein sact HP0830 HP0732 HP0532 HP0543 HP0543 HP0543 HP0543 HP0543 HP0543 HP0545 HP0545 HP0545 HP1564 HP1564 HP0564 HP0564 HP0564 HP0564 HP0564 HP0564 HP0664 HP0665 HP0665 HP0665 HP0666 HP066 HP066 HP066 HP066 HP0666 HP066 HP06	toxin-like outer membrane protein  culus and peptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  gittamate racemase (gir)  N-acetylmuramoyl-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  toxR-activated gene (tagE)  toxR-activated gene  toxR-activated gene  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated  toxR-activated	29.5% 30.6% 40.6% 28.6% 36.6% 36.6% 36.6% 35.7% 35.7% 42.6% 45.2% 37.7% 51.9% 33.8% 32.2% 37.2% 31.2% 37.2% 31.2% 37.3% 31.1% 46.7% 37.3% 31.1%	HP0584 HP0601 HP0115 HP0105 HP1678 HP1678 HP1678 HP1678 HP0479 HP0478	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) polar flagellin (flaG) secreted protein involved in flagellar motility flagellar motility processes  chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (rea) haemolysin (ty) haemolysin (ty) haemolysin secretion protein precursor (hylB) haemolysin secretion protein precursor (tylB) methyl-accepting chemotaxis protein (tlpA) methyl-accepting chemotaxis protein (tlpB) cell division protein (flaS) cell division protein (flaS)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 21.9% 22.9% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 25.5% 23.9% 27.25% 25.5%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) HP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 hp0614 oxygen-independent coproporphyrinogen oxidase (nemN) HP0381 protoporphyrinogen decarboxylase (hemE) HP10804 uroporphyrinogen decarboxylase (hemE) HP10804 uroporphyrinogen ill cosynthase (hemD) Menaquinone and ubiquinone HP1380 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0329 geranyltranstransferase (ispA) Molybdotpterin HP0768 molybdenum cofactor biosynthesis protein (mosC) HP0172 molybdotpterin biosynthesis protein (mosC) HP0172 molybdotpterin biosynthesis protein (mosC) HP0765 molybdotpterin biosynthesis protein (mosC) HP0801 molybdotpterin biosynthesis protein (mosC) HP0801 molybdotpterin onverting factor, subunit 1 (mosL) HP0802 molybdotpterin converting factor, subunit 2 (mosE) HP0769 molybdotpterin plannine dinucleotide biosy protein A (mobA)	35.1%  50.5% 33.4%  6 13.3% 32.7%  11 42.4%  11 37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  31.4% 0 0 0 97.9% 30.38% 31.4% 10 0 37.9% 30.38% 31.4% 10 1 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Murein sact HP0830 HP0732 HP0573 HP0573 HP0573 HP058 HP0743 HP0587 HP1565 HP1127 HP0587 HP1564 HP0743 HP1372 HP1564 HP0623 HP0645 HP065 HP	toxin-like outer membrane protein  cutulus and paptiodgycan  amidase  D-alanineD-alanine ligase A (ddlA)  gittamate racemase (gir)  N-acelyimuramoyl-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  toxR-activated gene (tagE)  transferase peptidoglycan synthesis  (murG)  UDP-MurNac-tripeptide synthetase (murE)  UDP-Macetylquicosamine enoloyruvyl  transferase (murB)  UDP-Macetylquicosamine enoloyruvyl  transferase (murB)  UDP-Nacetylquicosamine enoloyruvyl  transferase (murB)  UDP-Nacetylquicosamine enoloyruvyl  transferase (murB)  UDP-Nacetylmuramoylalanine-D-glutamate  ligase (murD)  Synthetase (kdSA)  3-deoxy-d-manno-octulosonic-acid transferase  (kdA)  ADP-hepitose synthase (rfaE)  APP-hepitose synthase (rfaE)  APP-	29.5% 30.6% 40.6% 48.5% 38.6% 36.6% 33.7% 35.0% 42.6% 42.6% 42.6% 45.2% 37.7% 51.9% 32.2% 32.2% 31.2% 32.2% 31.2% 32.2% 31.2% 31.2% 31.1% 66.7%	HP0584 HP0691 HP0115 HP0115 HP0295 HP1575 HP1575 HP1575 HP1575 HP0907 HP0907 HP0911 HP0180 HP0907 HP0410 HP0191 HP0410 HP	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flagellin B homologue (fla) flagellin B (flaB) flagellin B homologue (flaB) fliAprotein (fliA) fliAprotein (fliA) fliAprotein (fliA) polar flagellin (flaG) putative neuraminyllactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) haemolysin secretion protein precursor (flyB) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) cell division inhibitor (minD) cell division inhibitor (minD) cell division protein (flsA) cell division protein (flsH)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 22.5% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 796.2% 26.5% 23.9% 21.9% 24.2% 796.2% 26.5% 26.5% 27.9% 27.
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) porphobilinogen deaminase (hemC) protoporphyrinogen oxidase (hemR) protoporphyrinogen decarboxylase (hemE) protoporphyrinogen oxidase (hemE) protoporphyrinogen protophysiase (hemE) protoporphyrinogen oxidase (hemE) protoporphyrinogen protophyrinogen protophyrin	35.1%  50.5% 33.4% e e 51.3% 32.7% iiii 42.4% iiii 37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.0% 31.4% i C 97.9% 31.1% 31.1% 50.2% 50.8% 31.1% 51.1	Murein sact HP0830 HP0738 HP0830 HP0738 HP0738 HP0772 HP0837 HP175 HP0772 HP0837 HP175 HP0772 HP0837 HP1772 HP0837 HP1772 HP0837 HP1772 HP0848 HP0848 HP0848 HP0848 HP0848 HP0868 HP0967 HP0868 HP1911	toxin-like outer membrane protein  utuks and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamater racemase (glr)  N-acetylmuramoyl-alanine amidase (amiA  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein (ppoprotein precur  (cmp18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mary)  rod shape-determining protein (mreB)  toxin shape-determining protein (mreB)  toxin-activated gene (tagE)  toxin-activated gene  toxin-activated gene  toxin-activated gene  toxin-activated gene  toxin-activated  toxin-ac	29.5% 30.6% 40.6% 28.6% 36.6% 28.8% 36.6% 28.8% 35.7% 35.7% 51.9% 37.7% 51.9% 33.8% 32.2% 37.2% 31.2% 32.2% 37.7% 46.7% 37.3% 31.1% 67.7% 53.4% 53.8% 53.4% 53.5%	HP0584 HP0601 HP0115 HP0105 HP1575 HP1575 HP1575 HP10301 HP0401 H	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaG) poralysed flagella protein (flaB) polar flagellin (flaG) potative neureminyliactose-binding haemagglutinin homologue (flpaA) secreted protein involved in flagellar motility flagellar mo	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 21.9% 22.3% 22.5% 23.9% 21.9% 24.2% 77.2.5% 23.9% 21.9% 24.2% 77.2.5% 25.5% 23.9% 30.7% 27.9% 30.2% 40
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) NP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 prohobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0804 uroporphyrinogen decarboxylase (hemE) HP1380 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0929 geranyltranstransferase (ispA) HP0398 molybdenum cofactor biosynthesis protein (moaC) HP0765 molybdotperin biosynthesis protein (moaC) HP0775 molybdotperin biosynthesis protein (moaC) HP0780 molybdotperin biosynthesis protein (moaC) HP0780 molybdotperin biosynthesis protein (moaC) HP0801 molybdotperin biosynthesis protein (moaC) HP0801 molybdotperin biosynthesis protein (moaC) HP0801 molybdotperin biosynthesis protein (moaC) HP0802 molybdotperin onverting factor, subunit 1 (moaC) HP0780 molybdotperin converting factor, subunit 2 (moaE) HP0780 molybdotperin converting factor subunit 2 (moaE) HP0780 molybdotperin converting factor subunit 2 (moaE) HP0780 molybdotperin converting factor subunit 2 (moaE)	35.1%  50.5% 33.4%  6 13.3% 32.7%  11 42.4%  11 37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  1.4% 0 C Q7.9% 0 G Q7.9% 31.4% 10 C Q7.9% 10 A3.9% 11 19%	Murein sact HP0830 HP0738 HP0830 HP0738 HP0739 HP0739 HP0772 HP0637 HP1126 HP0772 HP0637 HP1126 HP0773 HP1372 HP0773 HP1372 HP07740 HP	toxin-like outer membrane protein  cutulus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  giutamate racemase (gir)  N-acelyimuramoyl-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  toxR-activated gene (tagE)  transferase peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murNac-tripeptide  (murNac-tripeptide  (murNac-tripeptide  (murNac-tripeptide	29.5% 30.6% 40.6% 48.5% 38.5% 36.6% 33.7% 35.0% 42.6% 42.6% 42.6% 45.2% 37.7% 51.9% 45.2% 32.2% 32.2% 32.2% 32.2% 32.3% 32.3% 32.5% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3%	HP0584 HP0691 HP0115 HP0115 HP0295 HP1575 HP1575 HP1575 HP1575 HP0907 HP0907 HP0907 HP0910 HP0180 HP0910 HP0180 HP0910 HP0910 HP0039	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin B homologue (fla) flagellin B homologue (fla) flagellin B (flaB) flagellin B homologue (fla) fliBp protein (fliP) fliV protein (fliP) fliV protein (fliP) hock assembly protein, flagella (flgD) paralysed flagella protein (flA) polar flagellin (flaG) putative neuraminyflactose-binding haemagglutinin homologue (hpaA) secreted protein involved in flagellar motility PROCESSES  chemotaxis protein (cheV) flagellin kinase (cheA) haemolysin secretion protein precursor (ry)B) histidine kinase (cheA) methyl-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemot	39.7% 99.8% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 772.5% 26.2% 23.9% 21.9% 24.2% 796.2% 26.2% 26.2% 27.9% 27.
HP0665  oxygen-independent coproporphyrinogen oxidase (nemN) oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 HP0237 HP0381 HP02381 HP0604 HP1224 Uroporphyrinogen deaminase (hemC) HP10801 HP1360 HP1360 HP1360 HP1360 HP0929 HP0360 HP0929 HP0240 HP0929 HP0929 HP0940 HP0940 HP0940 HP0958 Molybdopterin HP0768 Molybdopterin biosynthesis protein (mosC) HP0172 Molybdopterin biosynthesis protein (mosC) HP0789 Molybdopterin biosynthesis protein (mosC) HP0800 Molybdopterin biosynthesis protein (mosC) Molybdopterin biosynthesis protein (mosC) Molybdopterin converting factor, subunit 1 (mosC) Molybdopterin converting factor, subunit 1 (mosC) Molybdopterin aconverting factor, subunit 2 (mosE) Molybdopterin aconverting factor, subunit 3 (mosE) Molybdopterin aconverting factor, subunit 4 (mosE) Molybdopterin aconverting factor (mosE) Molybdopterin aconverting factor (mosE)	35.1%  50.5% 33.4% e e 51.3% 32.7% iiii 42.4% iiii 37.9% 45.7% 35.9% 46.3% 27.6%  28.6% 31.9% 31.4% i C 97.9% 31.1% 31.1% insterase 43.7% 50.0%	Murein sact HP0830 HP0738 HP0830 HP0738 HP0738 HP0772 HP0837 HP175 HP0772 HP0837 HP175 HP0772 HP0837 HP1772 HP0837 HP1772 HP0837 HP1772 HP0848 HP0848 HP0848 HP0848 HP0848 HP0868 HP0967 HP0868 HP1911	toxin-like outer membrane protein  utuks and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  glutamater racemase (glr)  N-acetylmuramoyl-alanine amidase (amiA  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein 1A (PBP-1A)  penicilin-binding protein (ppoprotein precur  (cmp18)  phospho-N-acetylmuramoyl-pentapeptide- transferase (mary)  rod shape-determining protein (mreB)  toxin shape-determining protein (mreB)  toxin-activated gene (tagE)  toxin-activated gene  toxin-activated gene  toxin-activated gene  toxin-activated gene  toxin-activated  toxin-ac	29.5% 30.6% 40.6% 28.6% 36.6% 28.8% 36.6% 36.6% 42.8% 33.7% 42.6% 47.7% 51.9% 33.6% 42.6% 45.2% 37.7% 51.9% 33.6% 33.2% 46.7% 33.6% 33.7% 33.7%	HP0584 HP0601 HP0115 HP0105 HP1076 HP1076 HP1076 HP1076 HP00907 HP1076 HP00907 HP00907 HP00907 HP0091 HP0410 HP041	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) polar flagellin (flaG) secreted protein involved in flagellar motility FROCESSES  chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (flaeV) flagellin secretion protein precursor (hylB) haemolysin (ty) haemolysin secretion protein precursor (hylB) haemolysin secretion protein flagellar motily-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpC) purine-binding chemotaxis protein (flsA) cell division protein (flsA) protein (flsA) cell division protein (flsK) cell division protein (flsK) cell division protein (flsK) cell division protein (flsK)	39.7% 99.8% 99.0% 32.9% 40.5% 21.9% 21.9% 22.3% 22.5% 23.9% 21.9% 24.2% 25.5% 23.9% 21.9% 24.2% 26.8% 31.7% 31.7% 25.9% 29.2% 40.2%
HP0665 oxygen-independent coproporphyrinogen oxidase (nemN) NP1226 oxygen-independent coproporphyrinogen oxidase (nemN) HP0237 prohobilinogen deaminase (hemC) HP0381 protoporphyrinogen oxidase (hemS) HP0804 uroporphyrinogen decarboxylase (hemE) HP1380 4-hydroxybenzoate octaprenyltransferase (ubiA) HP0929 geranyltranstransferase (ispA) HP0929 geranyltranstransferase (ispA) HP0398 molybdenum cofactor biosynthesis protein (moaC) HP0765 molybdotperin biosynthesis protein (moaC) HP0775 molybdotperin biosynthesis protein (moaC) HP0780 molybdotperin biosynthesis protein (moaC) HP0780 molybdotperin biosynthesis protein (moaC) HP0801 molybdotperin biosynthesis protein (moaC) HP0801 molybdotperin biosynthesis protein (moaC) HP0801 molybdotperin biosynthesis protein (moaC) HP0802 molybdotperin onverting factor, subunit 1 (moaC) HP0780 molybdotperin converting factor, subunit 2 (moaE) HP0780 molybdotperin converting factor subunit 2 (moaE) HP0780 molybdotperin converting factor subunit 2 (moaE) HP0780 molybdotperin converting factor subunit 2 (moaE)	35.1%  50.5% 33.4%  6 13.3% 32.7%  11 42.4%  11 37.9% 45.7% 35.9% 46.3% 27.6%  26.6% 39.8% 31.6%  1.4% 0 C Q7.9% 0 G Q7.9% 31.4% 10 C Q7.9% 10 A3.9% 11 9%	Murein sact HP0830 HP0738 HP0830 HP0738 HP0738 HP0772 HP0837 HP175 HP0772 HP0837 HP175 HP0772 HP0837 HP1772 HP0837 HP1772 HP0837 HP1772 HP0848 HP0848 HP0848 HP0848 HP0848 HP0868 HP0967 HP0868 HP1911	toxin-like outer membrane protein  cutulus and paptidoglycan  amidase  D-alanineD-alanine ligase A (ddlA)  giutamate racemase (gir)  N-acelyimuramoyl-alanine amidase (amiA  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 1A (PBP-1A)  penicillin-binding protein 2 (pbp2)  prospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)  rod shape-determining protein (mreB)  toxR-activated gene (tagE)  transferase peptidoglycan synthesis  (murG)  UDP-MurNac-pentapeptide presynthetase  (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase (murE)  UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murC)   UDP-MurNac-tripeptide synthetase  (murNac-tripeptide  (murNac-tripeptide  (murNac-tripeptide  (murNac-tripeptide	29.5% 30.6% 40.6% 28.6% 36.6% 28.8% 36.6% 36.6% 42.8% 33.7% 42.6% 47.7% 51.9% 33.6% 42.6% 45.2% 37.7% 51.9% 33.6% 33.2% 46.7% 33.6% 33.7% 33.7%	HP0584 HP0601 HP0115 HP0105 HP1076 HP1076 HP1076 HP1076 HP00907 HP1076 HP00907 HP00907 HP0091 HP040 HP0410	flagellin A (flaA) flagellin A (flaA) flagellin B (flaB) flagellin (flaB) flagellin (flaB) polar flagellin (flaG) secreted protein involved in flagellar motility FROCESSES  chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (flaeV) flagellin secretion protein precursor (hylB) haemolysin (ty) haemolysin secretion protein precursor (hylB) haemolysin secretion protein flagellar motily-accepting chemotaxis protein (flpA) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpB) methyl-accepting chemotaxis protein (flpC) purine-binding chemotaxis protein (flsA) cell division protein (flsA) protein (flsA) cell division protein (flsK) cell division protein (flsK) cell division protein (flsK) cell division protein (flsK)	39.7% 99.8% 99.8% 99.0% 32.9% 40.5% 21.9% 40.5% 22.3% 21.9% 24.2% 772.5% 23.9% 21.9% 24.2% 772.5% 26.2% 23.9% 21.9% 24.2% 796.2% 26.2% 26.2% 27.9% 27.

HP0332	cell division topological specificity factor				-1.0%		(devB)	29.2%
HP0979	(minE) cell divison protein (ftsZ)	33.8% 43.3%	HP1270	NADH-ubiquinone oxidoreductase, NQO11 subunit (NQO11) ({Paracoccus denitrificans}	42 6%		glucose-6-phosphate dehydrogenase (g6pD)	36.7%
HP1159	cell filamentation protein (fic)	63.2%	HP1271	NADH-ubiquinone oxidoreductase, NQO12		HP1495	transaldolase (tal)	33.5%
Cell killing	unqualating autotoxia 04.70/		HP1272	subunit (NQO12) NADH-ubiquinone oxidoreductase, NQO13	43.2%		transketolase A (tktA) transketolase B (tktB)	46.7% 39.7%
HP0887 Chaperones	vacuolating cytotoxin 94.7%			subunit (NQO13)	40.2%	Sugars		
HP0010	chaperone and heat shock protein (groEL)	99.6%	HP1273	NADH-ubiquinone oxidoreductase, NQO14 subunit (NQO14)	31.2%	HP0574 HP0360	galactosidase acetyltransferase (lacA) UDP-glucose 4-epimerase	41.0% 43.1%
HP0109	chaperone and heat shock protein 70 (dnaK)	63.4%	HP1266	NADH-ubiquinone oxidoreductase, NQO3	31.6%	TCA cycle	ODI giacose 4 epimerase	40.170
HP0210	chaperone and heat shock protein C62.5 (htpG)	46.5%	HP1263	NADH-ubiquinone oxidoreductase,		HP0779	aconitase B (acnB) citrate synthase (gltA)	64.0% 47.8%
HP0011	co-chaperone (groES)	99.2%	HP1262	NQO4 subunit (NQO4)(Triticum aestivum) NADH-ubiquinone oxidoreductase, NQO5	44.6%	HP1325	fumarase (fumC)	63.7%
HP1332	co-chaperone and heat-shock protein (dnal)	42.7%		subunit (NQO5)	-1.0%		glycolate oxidase subunit (glcD) isocitrate dehydrogenase (icd)	98.0% 70.7%
HP0110	co-chaperone and heat-shock protein		HP1261	NADH-ubiquinone oxidoreductase, NQO6 subunit (NQO6)	62.2%			70.770
HP1024	(grpE) co-chaperone-curved DNA-binding protein	33.0% A	HP1260	NADH-ubiquinone oxidoreductase, NQO7			AND PHOSPHOLIPID METABOLISM	
		37.7%	HP1267	subunit (NQO7) NADH-ubiquinone oxidoreductase, NQO8	40.7%	General HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein)	
	ne-associated protein plasmid replication-partition related protein	40.496		subunit (NQO8)	42.4%		dehydratase (fabZ) 1-acyl-glycerol-3-phosphate acyltransferase	47.4%
Detoxification 1981		10.17	HP1268	NADH-ubiquinone oxidoreductase, NQO9 subunit (NQO9)	41.2%		(plsC) (Escherichia coli)	32.0%
HP1563	alkyl hydroperoxide reductase (tsaA)	98.5% 99.4%	Amino acid:	s and amines			3-ketoacyl-acyl carrier protein reductase (fabG)	45.7%
HP0875 HP0267	catalase chlorohydrolase	42.6%	HP1398 HP0294		39.6% 75.4%	HP0690	acetyl coenzyme A acetyltransferase	
HP0243	neutrophil activating protein (napA) (bacterioferritin)	95.8%	HP1238	aliphatic amidase (aimE)	37.2%	HP0950	(thiolase) (fadA) acetyl-CoA carboxylase beta subunit	52.0%
HP0389	superoxide dismutase (sodB)	98.6%	HP1399 HP0943		31.070		(accD)	49.4% 52.3%
	thiophene and furan oxidizer (tdhF)	37.6%	HP0056	delta-1-pyrroline-5-carboxylate dehydrogenas	se 32.2%		acetyl-CoA synthetase (acoE) acetyl-coenzyme A carboxylase (accA)	50.3%
HP0355	peptide secretion GTP-binding membrane protein (lepA)	57.3%	HP0723	L-asparaginase II (ansB)	54.1%	HP0559 HP0962	acyl carrier protein (acpP) acyl carrier protein (acpP)	55.3% 56.3%
HP0074 HP0786	lipoprotein signal peptidase (IspA) preprotein translocase subunit (secA)	97.0% 54.0%	HP0132	L-serine deaminase (sdaA)	45.8%	HP0558	beta ketoacyl-acyl carrier protein synthase	II
HP1300	preprotein translocase subunit (secY)	41.2%	Anaerobic HP0666	anaerobic glycerol-3-phosphate dehydrogena	iase,		(fabF) beta-ketoacyl-acyl carrier protein synthase I	50.0% III
HP1255	protein translocation protein, low temperatu (secG)	ire 30.6%	HP0589	subunit C (glpC)	27.2%		(fabH)	44.4%
HP1550	protein-export membrane protein (secD)	38.9%	HP0590	ferredoxin oxidoreductase, beta subunit	43.2%		biotin carboxyl carrier protein (fabE) biotin carboxylase (accC)	30.8% 52.1%
HP1549 HP0576	protein-export membrane protein (secF) signal peptidase I (lepB)	35.1% 40.3%	HP0591 HP0193	ferredoxin oxidoreductase, gamma subunit fumarate reductase, cytochrome b subunit	33.3%	HP0871	CDP-diglyceride hydrolase (cdh)	73.9% 42.4%
HP1152	signal recognition particle protein (ffh)	41.4%		(frdC)	58.8%	HP0215 HP0416	CDP-diglyceride synthetase (cdsA) cyclopropane fatty acid synthase (cfa)	39.7%
HP0795 Transforma	trigger factor (tig)	27.6%	HP0192	fumarate reductase, flavoprotein subunit (frdA)	69.4%	HP0700 HP0195	diacylglycerol kinase (dgkA) enoyl-(acyl-carrier-protein) reductase (NADH	45.8%
HP0520	cag pathogenicity island protein (cag1)	96.5%	HP0191	fumarate reductase, iron-sulfur subunit			(fabl)	45.8%
HP0530 HP0531	cag pathogenicity island protein (cag10) cag pathogenicity island protein (cag11)	98.4% 97.2%	HP1110	(frdB) pyruvate ferredoxin oxidoreductase, alpha	70.8%		fatty acid/phospholipid synthesis protein (plsX)	37.8%
HP0532	cag pathogenicity island protein (cag12)	98.9%		subunit	41.0%	HP0808	Holo-acp synthase (acpS)	29.1%
HP0534 HP0535	cag pathogenicity island protein (cag13) cag pathogenicity island protein (cag14)	98.0% 97.6%	HP1111		43.7%		malonyl coenzyme A-acyl carrier protein transacylase (fabD)	35.4%
HP0536	cag pathogenicity island protein (cag15)	96.4% 98.9%	HP1109	pyruvate ferredoxin oxidoreductase, delta subunit	47.0%	HP1016	phosphatidylglycerophosphate synthase	
HP0537 HP0538	cag pathogenicity island protein (cag16) cag pathogenicity island protein (cag17)	95.3%	HP1108	pyruvate ferredoxin oxidoreductase, gamma	i i		(pgsA) phosphatidylserine decarboxylase proenzyr	35.4% me
HP0539 HP0540	cag pathogenicity island protein (cag18) cag pathogenicity island protein (cag19)	98.7% 99.5%	4TD		37.2%		(psd)	33.2%
HP0521	cag pathogenicity island protein (cag2)	92.5%	HP0828	motive force interconversion ATP synthase FO, subunit a (atpB)	37.7%		phosphatidylserine synthase (pssA) phospholipase A1 precursor	99.6%
HP0541 HP0542	cag pathogenicity island protein (cag20) cag pathogenicity island protein (cag21)	97.8% 97.9%	HP1136 HP1137	ATP synthase FO, subunit b (atpF)	28.3% 32.5%		(DR-phospholipase A)	33.8%
HP0543	cag pathogenicity island protein (cag22)	95.5%	HP1212	ATP synthase FO, subunit c (atpE)	41.2%	PURINES, P	YRIMIDINES, NUCLEOSIDES AND NUCLEO	OTIDES
HP0544 HP0545	cag pathogenicity island protein (cag23) cag pathogenicity island protein (cag24)	99.0% 98.5%	HP1134 HP1132		62.7% 85.6%	General	hata alanina aunthotaga hamalagua	40.0%
HP0546 HP0547	cag pathogenicity island protein (cag25)	95.7% 92.9%	HP1135	ATP synthase F1, subunit delta (atpH)	24.6%		beta-alanine synthetase homologue onucleotide metabolism	40.0%
HP0522	cag pathogenicity island protein (cag26) cag pathogenicity island protein (cag3)	98.1%	HP1131 HP1133		32.7% 37.8%	HP0372	deoxycytidine triphosphate deaminase	00.00/
HP0523 HP0524	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5)	95.7% 99.1%	Electron train	nsport			(dcd) deoxyuridine 5Õ-triphosphate nucleotidohydr	28.2% frolase
HP0526	cag pathogenicity island protein (cag6)	97.5%	HP0146	cbb3-type cytochrome c oxidase subunit Q (CcoQ)	44.2%		(dut)	41.4%
HP0527 HP0528	cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8)	94.6% 99.0%	HP0265	cytochrome c biogenesis protein (ccdA)	35.4%		ribonucleoside diphosphate reductase, beta subunit (nrdB)	а 39.0%
HP0529	cag pathogenicity island protein (cag9)	98.9%	HP0378 HP0147	cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit,	37.5%		ribonucleoside-diphosphate reductase 1 alp subunit (nrdA)	pha 28.4%
HP1378 HP1361	competence lipoprotein (comL) competence locus E (comE3)	25.5% 26.7%		membrane-bound (fixP)	33.0%	HP0825	thioredoxin reductase (trxB)	45.9%
HP1006	conjugal transfer protein (traG)	27.3%	HP0144	cytochrome c oxidase, heme b and copper- binding subunit, membrane-bound (fixN)	43.9%		nucleotide biosynthesis	44.8%
HP1421 HP0333	conjugative transfer regulon protein (trbB) DNA processing chain A (dprA)	30.7% 32.9%	HP0145	cytochrome c oxidase, monoheme subunit,	45.7%	HP0618	50-guanylate kinase (gmk) adenylate kinase (adk)	33.3%
HP0042 HP0525	trbl protein virB11 homologue	31.4% 100.0%	HP1461	cytochrome c551 peroxidase	48.5%	HP1112 HP0255	adenylosuccinate lyase (purB) adenylosuccinate synthetase (purA)	49.5% 44.6%
HP0441	VirB4 homologue	23.5%	HP1227 HP0277		38.4% 52.5%	HP1434	formyltetrahydrofolate hydrolase (purU)	49.1%
HP0017 HP0459	virB4 homologue (virB4) virB4 homologue (virB4)	25.2% 25.3%	HP0588	ferrodoxin-like protein	42.6%		glycinamide ribonucleotide synthetase (purD)	31.8%
		20.070	HP1508 HP1161		29.4% 47.0%	HP0854	GMP reductase (guaC)	31.8%
CENTRAL II General	NTERMEDIARY METABOLISM		HP0642	NAD(P)H-flavin oxidoreductase	46.1%		GMP synthase (guaA) inosine-5Ō-monophosphate dehydrogenase	56.1%
HP1014		33.2%	HP0954 HP0634	oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (hydD)	32.7%	HP0829		
HP1186 HP0004	carbonic anhydrase carbonic anhydrase (icfA)	37.0%			54.7%		(guaB)	58.5%
HP0869			HP0633	quinone-reactive Ni/Fe hydrogenase, cytoch	154.7% nrome	HP0198	(guaB) nucleoside diphosphate kinase (ndk)	58.5% 67.7%
	hydrogenase expression/formation protein	33.3%	HP0633 HP0632	quinone-reactive Ni/Fe hydrogenase, cytoch	154.7% nrome 51.4%	HP0198 HP0742	(guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA)	58.5% 67.7% 56.5%
HP0900	hydrogenase expression/formation protein (hypA)		HP0632	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB)	154.7% nrome 51.4%	HP0198 HP0742 HP1530	(guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB)	58.5% 67.7%
HP0900	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB)	33.3%	HP0632 HP0631	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA)	154.7% nrome 51.4% 68.5% 68.9%	HP0198 HP0742 HP1530 Pyrimidine ri HP1084	(guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB)	58.5% 67.7% 56.5% 20.7% 38.7%
HP0900 HP0899	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein	33.3% 28.1%	HP0632	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase,	154.7% frome 51.4% 68.5%	HP0198 HP0742 HP1530 Pyrimidine ri HP1084 HP0919	(guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine-hydrolysing) (pyrAb)	58.5% 67.7% 56.5% 20.7% 38.7%
	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein hydrogenase expression/formation protein	33.3% 28.1% 41.4% 38.5%	HP0632 HP0631	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (flbcH) ubiquinol cytochrome c oxidoreductase, bubqiquinol cytochrome c oxidoreductase, subiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, subiquinol cytochrome c oxidoreductase, cytochrome c oxido	154.7% 151.4% 68.5% 68.9% 39.3%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237	(guaB) nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7%
HP0899	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD)	33.3% 28.1% 41.4% 38.5% 47.8%	HP0632 HP0631 HP1539	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (flbcH) ubiquinol cytochrome c oxidoreductase, bubqiquinol cytochrome c oxidoreductase, subiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, subiquinol cytochrome c oxidoreductase, cytochrome c oxido	154.7% frome 51.4% 68.5%	HP0198 HP0742 HP1530 Pyrimidine ri HP1084 HP0919 HP1237 HP0349 HP0266	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrG) carbamoyl-phosphate synthetase (pyrG) dihydroortase (pyrC)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0%
HP0899 HP0898 HP0047	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7%	HP0632 HP0631 HP1539 HP1538 HP1540	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (flocH) ubiquinol cytochrome c oxidoreductase, cytochrome c sudorefluctase, cytochrome c sudorefluctase, cytochrome c sudorefluctase, cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (flocF)	154.7% 151.4% 68.5% 68.9% 39.3%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0349 HP0266 HP0581	(guaB) uncleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutarnine-hydrokysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 31.5%
HP0899 HP0898 HP0047 HP0197	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) a bioquinol cytochrome c oxidoreductase, cytochrome b subunit (hydH) ubiquinol cytochrome c subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 27e-28 subunit (fbcF) doroff	164.7% hrome 51.4% 68.5% 68.9% 39.3% 28.8% 39.2%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1011 HP1257	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutarnine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotate dehydrogenase (pyrD) orotate phosphoribosyltransferase (pyrE)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 41.5% 41.5% 35.5%
HP0899 HP0898 HP0047	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-ademosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) abiquinol cytochrome c oxidoreductase, cytochrome b subunit (hyd-I) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbeH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbeH) ubiquinol cytochrome coxidoreductase, rileske 27e-25 subunit (fbcF) dororif 2-keto-3-deoxy-6-phosphogluconate aldolase (eda)	164.7% hrome 51.4% 68.5% 68.9% 39.3% 28.8% 39.2% e e 50.3%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1257 HP0056	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrAa) CTF synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 41.5% 55.5% F)39.0%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1532	Inydrogenase expression/formation protein (trypA) hydrogenase expression/formation protein (trypB) hydrogenase expression/formation protein (trypB) hydrogenase expression/formation protein (trypD) hydrogenase expression/formation protein (trypD) hydrogenase expression/formation protein (trypB) S-adenosylmethionine synthetase 2 (metX) 373 glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Doug HP1099	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 1 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) denorff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda)	154.7% nrome 51.4% 68.5% 68.9% 39.3% 28.8% 39.2%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0349 HP0266 HP0581 HP1011 HP1011 HP1257 HP0005 HP1474 HP0777	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrCa) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate dehydrogenase (pyrD) orotate phosphoribosyltransferase (pyrE) orotdine SO-phosphate decarboxylase (pyrF thymidylate kinase (trnk) uridine SO-monophosphate (UMP) kinase	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 41.5% 35.5% F)39.0% 33.9%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) seamond for the first of	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c sudoreductase, cytochrome c sudoreductase, cytochrome c sudoreductase, legister See-28 subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-28 subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 70 3-xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	164.7% nrome 51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 50.3% 50.7%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP0349 HP0286 HP0581 HP1011 HP1257 HP0005 HP1474 HP0777	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrB) dihydroorotase (pyrC) diffydroorotase (pyrC) diffydroorotase (pyrC) diffydroorotase (pyrC) diffydroorotase (pyrC) vordate phosphorbosyltransferase (pyrE) orotdine SO-phosphate decarboxylase (pyrF) urldine SO-monophosphate (UMP) kinase (pyrH)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 41.5% 55.5% F)39.0%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Doug HP1099 HP1100 Fermentatio HP0691	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydG)/ quinone-reactive Ni/Fe hydrogenase, small subunit (hydA)/ ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (hydA)/ ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fboH)/ ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-28 subunit (fboF)/ doroff 2-keto-3-deoxy-6-phosphogluconate aidolase (eda) 6-phosphogluconate dehydratase 7-3-0-3-0-3-0-3-0-3-0-3-0-3-0-3-0-3-0-3-	164.7% hrome 51.4% 68.5% 68.9% 39.3% 28.8% 39.2% e e 50.3%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP1091 HP1237 HP0349 HP0268 HP0268 HP1011 HP1011 HP1257 HP0005 HP1474 HP0777 Salvage of n HP07104	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) irbonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) yorotale phosphorbosyltransferase (pyrE) orotidine 5O-phosphate decarboxylase (pyrF) urdine 5O-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 2O-phosphate (DMP) kinase (20X0-yclic-nucleotide 2O-phosphodiesterase	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% F)39.0% 50.4%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine I	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) are glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-mettyhydantoinase polyphosphate kinase (ppk) biosynthesis	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 29.9% 38.5%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Doug HP1099 HP1100 Fermentatio HP0691 HP0692	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydA)/ guinone-reactive Ni/Fe hydrogenase, large subunit (hydA)/ ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (hydA)/ ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fboH)/ ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fboF)/ doroff/ 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 7-3-xoxadigate coA-transferase subunit A (xyXI) 3-xoxadigate coA-transferase subunit B (xXII) 3-xoxadigate coA-transferase subunit B (xXIII)	164.7% hromore for the following for the followi	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0349 HP0268 HP0581 HP1257 HP00581 HP1257 HP00777 Salvage of n HP10777	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrCa) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) urdime 5C-phosphate decarboxylase (pyrF) urdime 5C-monophosphate (UMP) kinase (pyrH) urdime 5C-phosphote (UMP) kinase (pyrH) urdime 5C-phosphote (UMP) kinase (pyrH) oroticinucleotide 2C-phosphodiesterase (pydB)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 50.4% 50.4%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine II HP0422	Inydrogenase expression/formation protein (typsA) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsD) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoliase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9%	HP0632 HP0631 HP1639 HP1538 HP1540 Entner-Douc HP109 HP1100 Fermentatio HP0692 HP0903	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome oxidoreductase, cytochrome oxidoreductase, cytochrome oxidoreductase, cytochrome oxidoreductase, restead oxidoreductase, cytochrome oxidoreductase, restead oxidoreductase, resteadoreductase, reste	164.7% 170me 51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 65.0.7% 65.5% 65.5%	HP0198 HP0742 HP1530 Pyrimidine n HP1094 HP1237 HP0349 HP1237 HP0368 HP0581 HP1011 HP1257 HP0005 HP1257 HP00077 Salvage of n HP1014 HP1014 HP0104 HP0104	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) iibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrB) carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotate dehydrogenase (pyrD) orotate phosphoribosyltransferase (pyrE) orotidine 5O-phosphate decarboxylase (pyrF) urdine 5O-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 250-oyclic-nucleotide 2O-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (decB)	58.5% 67.7% 56.5% 20.7% 38.7% - 48.6% 39.7% 50.10% 31.5% 41.5% 41.5% 35.5% F)39.0% 33.9% 50.4%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1632 Phosphorus HP0620 HP0696 HP0696 HP0696 HP0402 HP0422 HP0422 HP0020	Inydrogenase expression/formation protein (typsA) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsB) S-ademosylmethionine synthetase 2 (metX) 378 glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rspcA) (rspcB)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9% 38.5% 33.3% 45.6%	HP0632 HP0631 HP1539 HP1540 Enther-Dout HP1090 HP1100 HP0691 HP0692 HP0903 HP0904 HP0904	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, snall subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome c oxidoreductase, restex 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 73-oxoadipate coA-transferase subunit A (xxiD) 3-oxoadipate coA-transferase subunit B (xxiE) sacetate kinase (ackA) [Escherichia coli) phosphate acetylaransferase (pta)	164.7% 170me 51.4% 68.5% 68.5% 68.9% 39.3% 28.8% 39.2% 20.3% 65.5% 73.2% 42.3% 61.0% 28.9%	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0266 HP0266 HP1011 HP1011 HP1011 HP1011 HP1017 HP0077 HP0072 HP0072 HP0072 HP0072 HP0072 HP0072 HP0072	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) tibonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrG) dihydrorotiase (pyrC) dihydrorotiase (pyrC) dihydrorotiase (pyrC) dihydrorotiate devarbonylase (pyrD) orotiale phosphoribosyltransferase (pyrE) orotidine 5O-phosphate decarboxylase (pyrF) tymidylate kinase (tmk) uridine 5O-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides (pdB) 200-oyclic-nucleotide 2O-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB)	58.5% 67.7% 56.5% 20.7% 38.7% 50.7% 10.0% 31.5% 50.7% 35.5% 50.4% 35.5% 50.4% 56.5% 55.5% 55.5% 55.5% 55.5% 55.5%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1532 Phosphorus HP0620 HP0630 HP1010 Polyamine I HP0422 HP0020 HP0020 HP0032	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) scaeposylmethionine synthetase 2 (metX) 3rs glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pryophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidline decarboxylase	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.9% 38.5% 33.3%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Double HP109 Fermentatio HP0691 HP0892 HP0903 HP0904 HP0905	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydro)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydro)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydro)/ quinone-reactive Ni/Fe hydrogenase, small subunit (hydro)/ ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, respective of the subunit (both) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doroff 2-xeto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 71 3-oxoadipate co-A-transferase subunit A (xyID) 3-oxoadipate co-A-transferase subunit B (xyID) 3-oxoadipate co-A-transferase subunit B (pxiE) phosphotransacelylase (pta) phosphotransacelylase (pta) short-chain alcohol dehydrogenase	164.7% hromore for the following for the followi	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0237 HP0268 HP0268 HP1011 HP1011 HP1027 HP1267 HP1474 HP0005 HP1474 HP0774 HP0104 HP0774 HP0104 HP0572 HP1178 HP0178 HP0735	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (gyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (gyrAb) carbamoyl-phosphate synthase (pyrC) dihydrorotase (pyrC) dihydrorotase (pyrC) dihydrorotate dehydrogenase (pyrD) orotate phosphoribosyltransferase (pyrE) orotidine 50-phosphate decarboxylase (pyrF) tymidylate kinase (tmk) urdine 50-monophosphate (UMP) kinase (pyrH) urdine 50-monophosphate (UMP) kinase (pyrH) purine-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas	58.5% 67.7% 56.5% 20.7% 38.7% 50.7% 10.0% 31.5% 50.7% 35.5% 50.4% 35.5% 50.4% 56.5% 55.5% 55.5% 55.5% 55.5% 55.5%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0696 HP1010 Polyamine I HP0422 HP0020 HP0832 Other HP0070	Indrogenase expression/formation protein (typsA) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsD) seadenosylmethionine synthetase 2 (metX) as 3c adenosylmethionine synthetase 2 (metX) as 3c compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rspC) spermidine synthase (speE) urease accessory protein (ureE)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.9% 38.5% 33.3% 45.6% 97.1%	HP0632 HP1639 HP1538 HP1540 Entner-Douc HP109 HP1100 Fermentatio HP0691 HP0903 HP0904 HP0904 HP0905 Gluconeof	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome oxidoreductase, cytochrome oxidoreductase, cytochrome oxidoreductase, cytochrome c oxidoreductase, labiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcH) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 3-axoxadipate coA-transferase subunit A (xxiD) 3-axoxadipate coA-transferase subunit B (xxiE) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) short-chain alcohol dehydrogenase snesisi nesisi	164.7% hromore for the following for the following for fol	HP0198 HP0742 HP1530 HP1094 HP0989 HP1237 HP0249 HP0256 HP0256 HP0011 HP1058 HP1011 HP1058 HP1017 HP00777 Salvage of r HP0107 HP1179 HP	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrAa) cTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotate (pyrC) dihydroorotate (pyrC) orotdine 5O-phosphate decarboxylase (pyrF) orotdine 5O-phosphate decarboxylase (pyrF) nucleosides and nucleotides 20-00-phosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-00-phosphotidestrase(apti) adenine phosphoribosyltransferase (apti) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (gpt) sunthine guannie phosphoribosyl transferase (gpt) (gpt)	58.5% 67.7% 56.5% 20.7% 38.7% -1.0% 31.5% 41.5% 35.5% 50.4% 50.3% 50.4% 50.3% 50.4% 50.3% 50.4% 50.3% 50.5%
HP0899 HP0898 HP0047 HP0197 Amino suge HP0620 HP0696 HP0696 HP0696 HP0620 HP0832 Other HP00709 HP0081	Inydrogenase expression/formation protein (typsA) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typsB) hydrogenase expression/formation protein (typcD) hydrogenase expression/formation protein (typsD) hydrogenase expression/formation protein (typsD) scalenosylmethionine synthetase 2 (metX) as glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glimS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.5% 33.3% 45.6% 26.5% 97.1% 97.1%	HP0632 HP1639 HP1539 HP1540 Entner-Douc HP1090 HP1100 Fermentatio HP0691 HP0903 HP0904 HP0905 HP0905 HP1385 Gluconeoge HP1385	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c labunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aidolase (eda) 6-phosphogluconate dehydratase 3-axoadipate coA-transferase subunit A (hydD) 3-axoadipate coA-transferase subunit B (hydE) acetate kinase (ackA) (Escherichia coli) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) short-chain alcohol dehydrogenase incisis fructose-1-6-lisphosphatase phosphosphorolpyruvate synthase (ppsA)	164.7% hromore for fine for fi	HP0198 HP0742 HP1530 HP1084 HP0919 HP1237 HP0246 HP0246 HP0256 HP0011 HP1011 HP1011 HP1011 HP1025 HP1025 HP1025 HP1017 HP1077 HP1077 HP1077 HP1078 HP1179 HP	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosyleyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis sapartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotdine 5O-phosphate decarboxylase (pyrF) orotdine 5O-phosphate decarboxylase (pyrF) hymidylate kinase (myk) uridine 5O-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 2030-yclic-nucleotide 2O-phosphodiesterase (pdB) purine-nucleoside phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (gpt) santhine guanine phosphoribosyl transferase (gpt) order biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA)	58.5% 67.7% 56.5% 20.7% 38.7% -48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% F)39.0% 33.9% 50.4% 50.3% 55.5% 55.5% 55.5% 82 27.1% 42.8%
HP0899 HP0898 HP0047 HP097 Amino suge HP1632 Phosphorus HP0620 HP0696 HP0696 HP0832 Other HP0042 HP0070 HP0089 HP0069 HP0068	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) ara glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methyhlydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (rispC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureG) urease accessory protein (ureG) urease accessory protein (ureG) urease accessory protein (ureH)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 26.5% 33.3% 45.6% 26.5% 97.1% 94.5% 95.0%	HP0632 HP1639 HP1538 HP1540 Entner-Douc HP109 HP1100 Fermentatio HP0691 HP0905 HP0904 HP0905 HP0905 HP0357 Gluconeoge HP1385 HP1121 HP1385 HP0121 HP1385	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC)   quinone-reactive Ni/Fe hydrogenase, large subunit (hydA)   subu	164.7% hromorome 51.4% 68.5% 68.5% 68.5% 68.9% 39.2% 28.8% 39.2% 26.5% 650.7% 6	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0237 HP0266 HP1237 HP0266 HP1474 HP0111 HP0777  Salvage of n HP0174 HP0177 HP0104 HP0572 HP1178 HP0178 HP1178 HP0178 HP0478 HP0478 HP0478 HP0478 HP0478 HP0478 HP0478	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) bibonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) CTP synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotidine 50-monophosphate (UMP) kinase (pyrT) tymindylate kinase (tmk) uridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-Optophosphodiesterase (cpdB) 20-Optophosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA)	58.5% 67.7% 56.5% 20.7% 38.7% -48.6% 39.7% 50.7% -1.0% 31.5% 41.5% 35.5% 50.4% 33.9% 50.4% 31.8% 50.3% 50.3% 50.3% 42.8% 44.3%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0896 HP1010 Polyamine I HP0422 HP0020 HP0832 Other HP0070 HP0089 HP0068 HP0068	"hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) seadenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydrantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureE) urease accessory protein (ureG) urease accessory protein (ureH) urease accessory protein (ureI)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 56.9% 38.5% 97.1% 94.5% 94.5%	HP0632 HP1639 HP1538 HP1540 Entiner-Douc HP1090 HP1100 HP0691 HP0692 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP1345 Glycopics Glycopics HP1345 HP1345 HP1345 HP1345 HP1345 HP1345 HP1345	quinone-reactive NI/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive NI/Fe hydrogenase, large subunit (hydB) quinone-reactive NI/Fe hydrogenase, large subunit (hydB) quinone-reactive NI/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome c oxidoreductase, reske 2Fe-2S subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase n 3-oxoadipate coA-transferase subunit A (xyID) 3-oxoadipate coA-transferase subunit B (xyiE) acetate kinase (ackA) [Escherichia coli) phosphate acetyltransferase (pta) phosphorasectylase (pta) short-chain alcohol dehydrogenase areasis fructose-16-bisphosphatase phosphoglucorate kinase enolase (eno)	164.7% horrorme 51.4% 68.5% 68.9% 39.3% 28.8% 39.2% 65.5% 65.5% 65.5% 50.7% 50.7% 50.5% 50.7% 50.5% 50.7% 50.5% 50.5% 50.7% 50.5% 50	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0234 HP0268 HP0268 HP1027 HP0267 HP0077 Salvage of n HP0177 Salvage of n HP0177 HP0178 HP1178 HP1178 HP0777 HP0043 HP0045 HP0045 HP0045 HP0045 HP0045	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) iibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (ptp) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (ptp) dide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylas	58.5% 67.7%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0820 HP1010 Polyamine I HP0422 HP0020 HP0832 Other HP0070 HP0088 HP0068 HP0068 HP0067 HP0073	"hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypB) seadenosylmethionine synthetase 2 (metX) are glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydrattoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureG) urease accessory protein (ureH) urease alpha subunit (ureA) (urea midolydrolase)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 56.9% 38.5% 97.1% 94.5% 94.5% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0%	HP0632 HP1639 HP1538 HP1540 HP109 HP1009 HP100 HP0892 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP1385 Glycopyies HP1385 HP0154 HP10164 HP0176 HP0176 HP0176	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, reseks 2-Fe-2S subunit (fbcH) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase n 3-oxoadipate coA-transferase subunit A (xyID) 3-oxoadipate coA-transferase subunit B (xyiE) 3-oxoadipate coA-transferase subunit B (xyiE) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphorasectylase (pta) short-chain alcohol dehydrogenase areasis fructose-16-bisphosphatase phosphoenolpyruvate synthase (ppsA) phosphorplycerate kinase enolase (eno) fructose-bisphosphate aldolase (tsr) glucokinase (glk)	164.7% hromore for the following for the following for fol	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0237 HP0268 HP1037 HP0268 HP1077 Salvage of n HP0177 HP0179 HP1178 HP0179 HP1178 HP0045 HP0045 HP0045 HP0045 HP0045 HP00683	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (ppt) oide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (glmU)	58.596 67.796 56.596 20.796 48.696 48.696 30.796 50.796 41.596 31.596 50.396 50
HP0899 HP0898 HP0047 HP0197 Amino suge HP1632 Phosphorus HP0620 HP0696 HP0696 HP0681 HP0422 HP04081 HP0422 HP0482 HP04832 Other HP04834 HP0484 HP04	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) ara glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureA) urease accessory protein (ureA) urease accessory protein (ureA)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 56.9% 38.5% 97.1% 94.5% 94.5% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc HP109 Fermentatio HP0691 HP0903 HP0903 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0154 HP0165 HP0165 HP0106 HP0176 HP0107 HP0176 HP1108	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC)   quinone-reactive Ni/Fe hydrogenase, large subunit (hydA)   subu	164.7% hromore for the following for the following for fol	HP0198 HP0742 HP1530 HP1530 HP1630 HP1084 HP0981 HP0237 HP0237 HP02349 HP0268 HP0268 HP0104 HP0104 HP0104 HP017 HP037 HP037 HP0075 Suyas-nucle HP017 HP0045 HP0045 HP0048 HP0048 HP0048 HP0048 HP0048 REGULATOF	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) iibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (ptp) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (ptp) dide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylase (galU) UDP-glucose pyrophosphorylas	58.5% 67.7%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0820 HP1010 Polyamine I HP0422 HP0020 HP0832 Other HP0070 HP0088 HP0068 HP0068 HP0067 HP0073	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypE) S-adenosylmethionine synthetase 2 (metX) ara glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biologynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureA) (urea amidohydrolase) urease between the subunit (ureA) (urea amidohydrolase)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 28.9% 38.5% 33.3% 46.6% 26.5% 97.1% 98.5% 90.0% 91.0% 91.0% 91.0% 91.0%	HP0632 HP1639 HP1538 HP1540 Entner-Douc HP109 HP1100 Fermentatio HP0691 HP0903 HP0903 HP0905 HP0905 HP0917 HP0917 HP0917 HP0918 HP0176 HP1108	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fboH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-28 subunit (fboF) doroff 2-keto-3-deoxy-6-phosphogluconate aidolase (eda) 3-oxoadipate coA-transferase subunit A (hyiD) 3-oxoadipate coA-transferase subunit B (vixIE) acetate kinase (ackA) [Escherichia coil) phosphotransacelylase (pta) short-chain alcohol dehydrogenase snesis fructose-16-bisphosphatase phosphoglycerate kinase enolase (eno) fructose-bisphosphate aidolase (pts) glucose-6-phosphate isomerase (pgi) glycerateknase (eps)	164.7% hromore for the first form for for for form for	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1237 HP0236 HP0236 HP0237 HP0237 HP0237 HP0246 HP0041 HP014 HP0571 HP0051 HP0164 HP0164 HP0164 HP0777 Salvage of n HP0164 HP01652 HP0164 HP01672 HP0164 HP0168 HP0683 HP0083 REGULATOF General	(guaB)  (guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutarnine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) orotate phosphoribosyltransferase (pyrE) uridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides Ø20-oyclic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyl transferas (pdf) santhine guanine phosphoribosyl transferase (pdf) nodulation protein (nolK) UDP-quoose pyrophosphorylase (galU) UDP-N-acety(glucosamine pyrophosphorylas (glmU)	58.5% 58.5%
HP0899 HP0898 HP0047 HP0197 Amino suga HP1632 Phosphorus HP0620 HP0686 HP0042 HP0040 HP0040 HP0040 HP0040 HP0040 HP0070 HP0069 HP0067 HP0073 HP0072 HP0075	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) seadenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureA) (urease archive) archive accessory accessory archive accessory acc	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.9% 33.3% 45.6% 97.1% 94.5% 94.5% 96.2% 96.5% 100.0%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc HP109 Fermentatio HP0691 HP0903 HP0903 HP0905 HP0905 HP0905 HP0905 HP0905 HP0905 HP0154 HP0165 HP0165 HP0106 HP0176 HP0107 HP0176 HP1108	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (hyd-I) ubiquinol cytochrome c oxidoreductase, cytochrome or subunit (hyd-I) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (hyd-I) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (hyd-I) ubiquinol cytochrome c oxidoreductase, relieske 2Fe-2S subunit (hydF) 2-ketio-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 10 3-oxoadipate coA-transferase subunit A ((yxID) 3-oxoadipate coA-transferase subunit B (yxIE) 3-oxoadipate coA-transferase subunit B (yxIE) 3-oxoadipate coA-transferase subunit B (yxIE) 3-phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphoralse-16-bisphosphatase phosphoenoloyruvate synthase (ppsA) phosphorgophosphosphate aldolase (tsr) glucokinase (gik) glucose-6-phosphate dehydrogenase (app) glyceraldehyde-3-phosphate dehydrogenase (app)	164.7% hromore for the first form for for for form for	HP0198 HP0742 HP1530 Pyrimidine n HP1084 HP0919 HP1084 HP0919 HP0286 HP0286 HP0286 HP0286 HP0349 HP0286 HP011 HP034 HP014 HP0777 Salvage of n HP0104 HP0177 HP0104 HP0178 HP0188 HP088 HP088 HP0883 REGULATOF General HP1032	(guaB)  (guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutarnine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (pyrCa) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) phosphore decarboxylase (pyrE) uridine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides Ø20-cyclic-nucleotide 20-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyl transferas (pdp) urine-nucleoside phosphoribosyl transferase (pdp) urine-nucleoside phosphoribosyltransferase (pd) urine-nucleoside phosphoribosyltransfe	58.5% 58.5%
HP0899 HP0898 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0896 HP0030 HP0832 Other HP0030 HP00834 HP00070 HP00089 HP00070 HP00070 HP00070 HP00070 HP00070 HP00070 HP00070 HP0070	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) search of the construction of the cons	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.9% 33.3% 45.6% 94.5% 94.5% 92.9% 94.5% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0%	HP0632 HP1639 HP1638 HP1640 Entner-Douc HP109 HP100 HP0892 HP0903 HP0904 HP0905 HP0357 Gluconeoge HP1345 Glycopyes HP1345 HP0154 HP0154 HP0164 HP0176 HP1106	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydG) quinone-reactive Ni/Fe hydrogenase, large subunit (hydG) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome or subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome coxidoreductase, cieda chorial cytochrome ci subunit (fbcH) 3-oxidipate coA-transferase subunit A (yxiD) 3-oxidipate coA-transferase subunit B (yxiD) 3-oxidipate coA-transferase subunit B (yxiD) 3-oxidipate coA-transferase subunit B (yxiD) 3-oxidipate coA-transferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphophatea cytochrome ci subunit B (yxiD) phosphophycerate kinase enolase (eno) fructose-lisphosphate aldolase (tsr) glucokinase (glk) glucose-G-phosphate dehydrogenase (app) glyceraldehyde-3-phosphate dehydrogenase (app)	164.7% horrorme 151.4% 68.5% 68.9% 68.9% 39.3% 28.8% 39.2% 65.5% 65.5% 65.5% 65.5% 65.5% 67.32% 67.32% 67.32% 67.32% 67.33% 67.3	HP0198 HP0742 HP1530 Pyrimidine n HP1034 HP0399 HP1237 HP0237 HP0237 HP0237 HP0266 HP0266 HP0681 HP1011 HP0581 HP1017 HP00777 Salvage of n HP0104 HP0777 Sulvage of n HP0104 HP0777 Sulvage of n HP0104 HP0683 REGULATOF General HP1032 HP1032 HP1032 HP1032	(guaB)  (guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutarnine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutarnine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotate phosphoribosyltransferase (pyrE) phosphopentomutase (deoB) purine-nucleosides and nucleotides DiOcyclic-nucleotide 20-phosphodiesterase (ppt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (apt) phosphopentomutase (deoB) purine-nucleoside phosphoribosyltransferase (ppt) dube-synthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nodulation protein (noIK) UDP-N-acetylglucosamine pyrophosphorylas (glmU) UP-N-acetylglucosamine pyrophosphorylas (glmU) atternative transcription initiation factor, sign (fliA) carbon starvation protein (cstA)	58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 58.5% 59.5%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0630 HP0630 HP0630 HP0630 HP0632 Other HP0070 HP0070 HP0071 HP0077 HP0077 HP0077 HP0077 HP0077 HP0077 HP0077 HP0077	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) s-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) s compounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureR) urease plans subunit (urea) urease plans subunit (urea) urease protein (ureC)	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.9% 33.3% 45.6% 97.1% 94.5% 94.5% 96.2% 96.5% 100.0%	HP0632 HP1639 HP1538 HP1540 Entiner-Douch HP1099 HP1100 Fermentatio HP0692 HP0903 HP0905 HP0905 HP0905 HP0905 HP1086 HP0905 HP1086 HP0905 HP1108 HP1084 HP0184	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydr)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydr)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydr)/ quinone-reactive Ni/Fe hydrogenase, small subunit (hydr), ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fboH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fboF) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fboF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate aldolase (eda) 8-phosphogluconate dehydratase (vi)/ 3-oxoadipate co-A-transferase subunit A (vi)/Di 3-oxoadipate co-A-transferase subunit B (vi)/Di 3-oxoadipate co-A-transferase subunit B (vi)/Di 3-oxoadipate co-A-transferase (pta) phosphotransacetylase (pta) short-chain alcohol dehydrogenase enesis phosphoenolpyruvate synthase (ppsA) phosphoenolpyruvate synthase (ppsA) phosphoenolpyruvate synthase (ppsA) phosphoenolpyruvate kinase enolase (eno) fructose-bisphosphate isomerase (pgi) glucose-6-phosphate isomerase (pgi) glyceraldehyd-3-phosphate dehydrogenase (gap) phosphoglycerate mutase (pgm)	164.7% horrores 164.9% horrores 164.9% horrores 168.5% horrore	HP0198 HP0742 HP1530 HP1530 HP1630 HP1084 HP0081 HP0237 HP0234 HP0281 HP0281 HP0281 HP0281 HP0281 HP0281 HP0381 HP0484 HP0488 HP0488 REGULATOF	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrC) difflydrorottase (pyrC) difflydrorottase (pyrC) difflydrorottase (pyrC) difflydrorottase (pyrC) difflydrorottase (pyrC) orotidine 5O-phosphate decarboxylase (pyrF) orotidine 5O-phosphate decarboxylase (pyrF) nucleosides and nucleotides (pxR) (pxR) (pxR) nucleosides and nucleotides (pxR) (pxR) (pxR) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferase (pxR) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (algA) nucleoside phosphorylase (gaIU) UDP-N-acety(glucosamine pyrophosphorylas (gimU) XY FUNCTIONS alternative transcription initiation factor, sign (IIIA) carbon storage regulator (csrA) (carbon storage regulator (csrA) carbon storage regulation protein (fur)	58.5% 58.5%
HP0899 HP0898 HP0047 HP0197 Amino suge HP1632 HP0620 HP0680 HP0680 HP0680 HP0680 HP0081 HP0081 HP00832 Other HP00832 Other HP0070 HP0089 HP0075 HP0075 HP0075 HP0075 HP0075 HP0075 HP0075 HP0076 HP0076 HP0076 HP0077	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminomanic protein furctose-6-phosphate aminomanic protein protein (pgmS) scompounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biolosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureA) (urease armidohydrogenase (MAD(PH)-MAD(PH	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.9% 38.5% 33.3% 45.6% 97.1% 94.5% 97.1% 94.5% 96.0% 98.5% 100.0% 100.0% 98.0%	HP0632 HP1639 HP1538 HP1540 Entner-Douc HP1099 HP1100 Fermentatio HP0692 HP0903 HP0904 HP0905 HP0905 HP0912 HP0905 HP1346 HP0184	quinone-reactive Ni/Fe hydrogenase, cytoch b subunit (hydr)/ quinone-reactive Ni/Fe hydrogenase, large subunit (hydr)/ quinone-reactive Ni/Fe hydrogenase, small subunit (hydr)/ quinone-reactive Ni/Fe hydrogenase, small subunit (hydr), ubiquinol cytochrome c oxidoreductase, cytochrome b subunit (fboH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fboF) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fboF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate aldolase (eda) 8-phosphogluconate dehydratase (vi)/ 3-oxoadipate co-A-transferase subunit A (vi)/Di 3-oxoadipate co-A-transferase subunit B (vi)/Di 3-oxoadipate co-A-transferase subunit B (vi)/Di 3-oxoadipate co-A-transferase (pta) phosphognase acetyltransferase (pta) phosphognase acetyltransferase (pta) phosphognase acetyltransferase (pta) short-chain alcohol dehydrogenase enesis encolse (eno) fructose-bisphosphate aldolase (tsr) glucose-6-phosphate somerase (pgi) glucose-6-phosphate somerase (pgi) glucose-6-phosphate somerase (pgi) glyceraldehyde-3-phosphate dehydrogenase (gap) phosphoglycerate mutase (pgm) phosphoglycerate somerase (pgi) osphate somerase (pgi) osph	164.7% horrorme 151.4% 68.5% 68.9% 68.9% 39.3% 28.8% 39.2% 65.5% 65.5% 65.5% 65.5% 65.5% 67.32% 67.32% 67.32% 67.32% 67.33% 67.3	HP0198 HP0742 HP1530 HP1530 HP1630 HP1084 HP0081 HP0287 HP0281 HP0281 HP0281 HP0281 HP0281 HP0381 HP0484 HP0484 HP0683 REGULATOF General HP0384 HP1684 HP1688 HP1482 HP1688 HP1482 HP1688	(guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) irbonucleotide biosynthesis asparate transcarbamoylase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrB) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotale phosphorbosyltransferase (pyrE) orotale phosphorbosyltransferase (pyrE) orotale phosphorbosyltransferase (pyrE) urdine 50-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-ophosphate (epyrE) phosphopentomutase (deoB) purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas (gpt) otide biosynthesis and conversions mannose-6-phosphate isomerase (pmi) or (alpA) mannose-6-phosphate isomerase (pmi) or (alpA) UDP-P-glucose pyrophosphorylase (gaIU) UDP-N-acety(glucosamine pyrophosphorylas (gimU) XY FUNCTIONS alternative transcription initiation factor, sign (filiA) carbon starvation protein (cstA) carbon storage regulator (csrA) ferric uptake regulation protein (furly guanosine pentaphosphate phosphorylorly	58.5% (67.7%) 56.6% (67.7%) 56
HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus HP0620 HP0680 HP0680 HP0680 HP0081 HP0081 HP0082 HP0083 HP0070 HP0070 HP0075 HP0075 ENERGY MI Aerobic HP1222	hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypB) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypD) hydrogenase expression/formation protein (hypB) S-adenosylmethionine synthetase 2 (metX) ars glucosamine fructose-6-phosphate aminomanic protein furctose-6-phosphate aminomanic protein protein (pgmS) scompounds inorganic pyrophosphatase (ppa) N-methylhydantoinase polyphosphate kinase (ppk) biolosynthesis arginine decarboxylase (speA) carboxynorspermidine decarboxylase (nspC) spermidine synthase (speE) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureF) urease accessory protein (ureH) urease accessory protein (ureA) (urease armidohydrogenase (MAD(PH)-MAD(PH	33.3% 28.1% 41.4% 38.5% 47.8% 39.7% 62.1% 41.7% 50.0% 50.0% 50.9% 33.3% 45.6% 94.5% 94.5% 92.9% 94.5% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0% 96.0%	HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc HP1099 HP1100 Fermentatio HP0692 HP0903 HP0904 HP0905 HP0357 Glyconysis HP0904 HP1015 HP1015 HP1015 HP1015 HP1015 HP1015 HP1016 HP0176 HP0176 HP1016 HP0176 HP10176 HP1	quinone-reactive NI/Fe hydrogenase, cytoch b subunit (hydC) quinone-reactive NI/Fe hydrogenase, large subunit (hydA) quinone-reactive NI/Fe hydrogenase, large subunit (hydA) quinone-reactive NI/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome to oxidoreductase, cytochrome to subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome ci subunit (fbcH) ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) control cytochrome c subunit (fbcF) doroff 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase 3-axoadipate coA-transferase subunit A (hydD) 3-axoadipate coA-transferase subunit B (hydE) accetate kinase (ackA) (Escherichia coli) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphate acetyltransferase (pta) phosphogluconacetylase (pta) short-chain alcohol dehydrogenase senseis fructose-1,6-bisphosphatase phosphonolyyruvate synthase (ppsA) phosphoglycerate kinase enolase (eno) fructose-bisphosphate dehydrogenase (app) glyceraldehyde-3-phosphate dehydrogenase (app) phosphoglycerate mutase (ppm) triosephosphate isomerase (tpi) osphate achiavy	164.7% horrorme 51.4% 668.5% 668.9% 639.3% 688.9% 639.9% 639.2% 69.5% 65	HP0198 HP0742 HP1530 HP1530 HP1630 HP1084 HP0081 HP0287 HP0281 HP0281 HP0281 HP0281 HP0281 HP0381 HP0484 HP0484 HP0683 REGULATOF General HP0384 HP1684 HP1688 HP1482 HP1688 HP1482 HP1688	(guaB)  (guaB)  nucleoside diphosphate kinase (ndk) phosphoribosylpyrophosphate synthetase (prsA) purine nucleoside phosphorylase (punB) ibonucleotide biosynthesis aspartate transcarbamoylase (pyrB) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthase (glutamine- hydrolysing) (pyrAb) carbamoyl-phosphate synthetase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) dihydroorotase (pyrC) orotdine 5O-phosphate decarboxylase (pyrF) orotdine 5O-phosphate decarboxylase (pyrF) urdine 5O-monophosphate (UMP) kinase (pyrH) nucleosides and nucleotides 20-0x-qiclien-ucleotide 2O-phosphodiesterase (pdB) adenine phosphoribosyltransferase (apt) purine-nucleoside phosphoribosyltransferase (pdB) purine-nucleoside phosphoribosyltransferase (ppl) purine-nucleoside phosphoribosyltransferase (ppl) purine-nucleoside phosphoribosyltransferase (ppl) urine-nucleoside phosphoribosyltransferase (ppl) urine-nucleoside prophosphoribosyltransferase (ppl) urine-nucleoside prophosphori	58.5% 58.5%

H		~							
		penta-phosphate guanosine-3Õ-pyrophospho	)- 36.7%	HP1471	type IIS restriction enzyme R protein				30.5%
		hydrolase (spoT) peptide methionine sulphoxide reductase	30.770	HP1366	(BCGIB) type IIS restriction enzyme R protein				58.2% 56.2%
		(msrA)	66.8%	111 1000		37.1%	HP1197		79.0%
			46.2%	HP1208	ulcer associated adenine specific DNA				55.8%
	HP1572 HP0703		31.9% 44.2%	HP1209					68.3% 57.8%
			28.7%	HP1209	ulcer-associated gene restriction endonucle (iceA)				46.8%
			26.8%	HP1347		43.1%		ribosomal protein S17 (rps17)	55.4%
	HP1365	response regulator	32.4%				HP1244	ribosomal protein S18 (rps18)	55.2%
	HP0166		51.0%	TRANSCRIP					61.1%
			37.1% 43.5%	Degradation	of RNA				49.6% 41.4%
			97.7%	HP1213	polynucleotide phosphorylase (pnp) DNA-dependent RNA polymerase				42.4%
H	HP0164	signal-transducing protein, histidine kinase	27.1%	HP1293	DNA-directed RNA polymerase, alpha subu	ınit	HP1313	ribosomal protein S3 (rps3)	56.7%
	HP1364	signal-transducing protein, histidine kinase	24.9%		(rpoA)	35.3%			51.2%
H		signal-transducing protein, histidine kinase (atoS)	30.0%	HP1198	DNA-directed RNA polymerase, beta subun				65.5% 32.1%
H			34.5%						62.2%
	HP1287	transcriptional regulator (tenA)	34.7%	Transcription HP0866	n factors transcription elongation factor GreA (greA)				45.0%
H			33.3%	HP1514	transcription termination factor NusA				50.4%
-	REPLICATIO	N				39.1%			26.3%
	Degradation			HP0001	transcription termination factor NusB (nusB)		tRNA modific HP1141	ication methionyl-tRNA formyltransferase (fmt)	37.5%
		ATP-dependent nuclease (addB)	27.2%	HP1203	transcription termination factor NusG (nusG)				46.6%
			37.6%	HP0550		56.6%	HP0361	pseudouridylate synthase I (hisT)	32.2%
	DNA replica	tion, restriction, modification, recombination							29.3%
			38.2%	RNA proces				S-adenosylmethionine:tRNA ribosyltransferase-isomerase (queA)	39.3%
H		adenine specific DNA methyltransferase (dpnA)	37.4%	HP0640 HP0662		37.4% 37.3%			36.2%
H		adenine specific DNA methyltransferase	01.410	111 0002	riboridoledae III (Irie)	07.070	HP1148	tRNA (guanine-N1)-methyltransferase (trmD)	39.1%
		(HINDIIM)	33.4%	TRANSLATIO	ON			tRNA delta(2)-isopentenylpyrophosphate	00.70/
H		adenine specific DNA methyltransferase	00.50	General					30.7% 45.6%
		(HINFIM) adenine specific DNA methyltransferase	62.5%				Translation 1		40.070
			33.9%	Aminoacyl t	RNA synthetases			ATP-dependent RNA helicase, DEAD-box	
H		adenine specific DNA methyltransferase		HP1241 HP0319		44.9% 25.0%		family (deaD)	37.7%
			29.3%			E0.10/-		peptide chain release factor RF-1 (prfA)	52.6%
F		adenine specific DNA methyltransferase (mod)	33.9%	HP0886	cysteinyl-tRNA synthetase (cysS)	97.3%			49.6% 43.7%
H	HP0593	adenine specific DNA methyltransferase	00.070	HP0476		43.1%	HP1195	translation elongation factor EF-G (fusA)	67.5%
			38.5%	HP0643		39.8%	HP0177	translation elongation factor EF-P (efp)	45.1%
H		adenine specific DNA methyltransferase		HP0960	glycyl-tRNA synthetase, alpha subunit (glyQ)				43.1%
		(mod) adenine specific DNA methyltransferase	42.2%	HP0972		22 606			89.5% 65.3%
-		(VSPIM)	42.1%	HP1190		32.4%			45.4%
F			32.1%	HP1422 HP1547				translation initiation factor IF-3 (infC)	43.4%
			42.9%	HP0182		E0.001			
H		chromosomal replication initiator protein (dnaA)	34.9%	HP0417		42 4%		T AND BINDING PROTEINS	
		cytosine specific DNA methyltransferase	34.970	HP0403	phenylalanyl-tRNA synthetase, alpha subun	III	General HP0179	ADC transporter ATD hinding protein	66.7%
		(BSP6IM)	37.0%	1100400	(pheS)	TO.7 70			31.1%
H	HP0051	cytosine specific DNA methyltransferase		HP0402	phenylalanyl-tRNA synthetase, beta subunit (pheT)				52.3%
			39.0%	HP0238		39.8%	HP1576	ABC transporter, ATP-binding protein (abc)	48.2%
-		cytosine specific DNA methyltransferase (HPHIMC)	38.7%	HP1480	seryl-tRNA synthetase (serS)	48.3%	HP1465	ABC transporter, ATP-binding protein	0700
H			97.4%			42.1%		(HI1087) ABC transporter, ATP-binding protein (yhcG)	37.8%
H	HP0501	DNA gyrase, sub B (gyrB)	46.0%	HP1253 HP0774		52.6% 54.7%		ABC transporter, ATP-binding protein (yheS)	)36.3%
			35.3%	HP1153		43.7%	HP1577	ABC transporter, permease protein (yaeE)	43.1%
		DNA helicase, putative DNA ligase (lig)	38.8% 40.1%		of proteins, peptides and glycopeptides				29.7%
			32.6%	HP0570	aminopeptidase a/i (pepA)	30.0%		histidine and glutamine-rich protein histidine-rich, metal binding polypeptide	50.0%
	HP1470	DNA polymerase I (polA)	40.0%			40.3%		(hpn)	100.0%
	HP1460		42.0%	HP0794	ATP-dependent clp protease proteolytic		HP1206	multidrug-resistance protein (hetA)	26.2%
			26.0%	HP1379		42.00%			32.4%
-		DNA polymerase III delta prime subunit (holB)	48.6%	HP0223	ATP-dependent protease (sms)	44.00%	HP0600 HP1181		29.7% 29.1%
H		DNA polymerase III epsilon subunit (dnaQ)		HP1374	ATP-dependent protease ATPase subunit			sodium- and chloride-dependent transporter	
H	HP0717	DNA polymerase III gamma and tau subuni		LIDOGEA				sodium- and chloride-dependent trans-	101.770
			39.0% 36.6%	HP0264	ATP-dependent protease binding subunit (clpB)	97.7%			30.8%
			32.7%	HP0169		40.1%			36.6%
i			28.3%	HP0516	heat-shock protein (hslU) ORF1	98.4%		s, peptides and amines	
H	HP0116	DNA topoisomerase I (topA)	45.1%	HP0515		07.170		amino acid ABC transporter, periplasmic binding protein (yckK)	41.5%
	HP0440	DNA topoisomerase I (topA) endonuclease III	31.7%	HP0470 HP0657		97.9% 24.2%	HP0939	amino acid ABC transporter, permease	41.070
			36.6% 40.1%	HP1485		35.2%			46.9%
H	HP0705	excinuclease ABC subunit A (uvrA)	53.4%	HP1350		10.070			41.7% 44.5%
H			53.1%	HP1012 HP1435				dipeptide ABC transporter, ATP-binding	44.0%
			31.5%	HP0404	protein kinase C inhibitor (SP:P16436)	40.2%		protein (dppD)	59.5%
			58.9% 48.5%	HP1019		52.9%		dipeptide ABC transporter, ATP-binding	
			32.9%	HP1584 HP0382		35.7%		protein (dppF) dipeptide ABC transporter, periplasmic	54.8%
H		helicase	33.0%	111 000L	zinc-metalloprotease (YJR117W)			dipoptide 700 transporter, peripidantie	
	HP0883 HP1059	Holliday junction DNA helicase (ruvA)			and the second s	36.2%		dipeptide-binding protein (dppA)	39.8%
		Holliday junction DNA halicage (ruyR)	39.0%	Nucleoprote		50.2 10		dipeptide ABC transporter, permease	39.8%
F			54.6%	HP0835	histone-like DNA-binding protein HU (hup)	44.6%	HP0299	dipeptide ABC transporter, permease protein (dppB)	49.3%
F		Holliday junction endodeoxyribonuclease (ruvC)	54.6% 34.7%	HP0835 Protein mod	histone-like DNA-binding protein HU (hup) dification	44.6%	HP0299 HP0300	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein	49.3% in
F F	HP0675	Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC)	54.6% 34.7% 31.8%	HP0835 Protein mod HP0363	histone-like DNA-binding protein HU (hup) diffication L-isoaspartyl-protein carboxyl methyltransfer (pcm)	44.6% erase 43.0%	HP0299 HP0300	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC)	49.3% in 52.5%
H H	HP0675 HP0995	Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerD)	54.6% 34.7% 31.8% 27.8%	HP0835 Protein mod HP0363 HP1299	histone-like DNA-binding protein HU (hup) diffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map)	44.6% erase 43.0%	HP0299 HP0300 HP1506 HP1171	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gltS) glutamine ABC transporter, ATP-binding	49.3% in 52.5% 56.9%
	HP0675 HP0995 HP0323 HP0676	Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine	54.6% 34.7% 31.8% 27.8% 31.1%	HP0835 Protein mod HP0363	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfel (pcm) methionine amino peptidase (map) peptidyl-protyl <i>cis-trans</i> isomerase B,	44.6% erase 43.0% 43.0%	HP0299 HP0300 HP1506 HP1171	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gltS) glutamate permease (gltS) glutamine ABC transporter, ATP-binding protein (glnG)	49.3% in 52.5%
H H H H	HP0675 HP0995 HP0323 HP0676	Holliday junction endodeoxyribonuclease (nuxC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNAÑprotein-cysteine methyltransferase (dat1)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0%	HP0835 Protein mod HP0363 HP1299	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfel (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B,	44.6% erase 43.0% 43.0%	HP0299 HP0300 HP1506 HP1171 HP1172	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gltS) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic	49.3% in 52.5% 56.9%
H H H H	HP0675 HP0995 HP0323 HP0676	Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNANprotein-cysteine methylated-DNANproteine methylated-DNANprotei	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rottamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-tyr rottamase (syb)	44.6% erase 43.0% 43.0% 58.1% pe	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gtlS) glutamate permease (gtlS) glutamine ABC transporter, ATP-binding protein (glnQ) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH)	49.3% in 52.5% 56.9% 51.9% 32.2%
H H H H H	HP0675 HP0995 HP0323 HP0676 HP0387 HP0153	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) membrane bound endonuclease (nuc) membranese (abtri) primasomal protein replication factor (priA) recombinase (recA)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793	histone-like DNA-binding protein HU (hup) sifikation L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-tyr rotamase (slyD) polypeptide deformylase (def)	44.6% erase 43.0% 43.0% 58.1% pe 40.4% 41.8%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (gltS) glutamite ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6%
+ + + + + +	HP0675 HP0995 HP0323 HP0676 HP0387 HP0153 HP0925	Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNANprotein-cysteine methylated-DNANproteine methylated-DNANprotei	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 36.5%	HP0835  Protein mod HP0363  HP1299 HP1441  HP1123  HP0793  Ribosomal p	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cis-trans isomerase, FKBP-tyr rotamase (siy5t) polypeptide delormylase (def) proteins: synthesis and modification	44.6% 44.6% 43.0% 43.0% 43.0% 68.1% pe 40.4% 41.8%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gltS) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, Periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnH) glutamine-ABC transporter, permease protein (glnH) glutamine-ABC transporter, permease protein (glnH)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein
	HP0675 HP0995 HP0323 HP0676 HP0387 HP0153 HP0925 HP0911	Holliday junction endodeoxyribonuclease (tuv.C) (tuv.C) integrase/recombinase (xer.C) integrase/recombinase (xer.C) integrase/recombinase (xer.C) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltrans/erase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep.)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 36.5% nt 33.8%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201	histone-like DNA-binding protein HU (hup) iffication Lisoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-tyr rotamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (pril)	44.6%  44.6%  43.0%  43.0%  43.0%  43.0%  43.0%  58.1%  59.0%  50.0%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite permease (gllS) glutamite ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnH)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6%
+ + + + + + +	HP0675 HP0995 HP0323 HP0676 HP0387 HP0153 HP0925 HP0911 HP1362	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNAMprotein-cysteine methylatransterase (datt) primosomal protein replication factor (priA) recombinase (reca) recombinase (reca) recombinase (reca) replication factor (priA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 11.5% 36.5% mt 33.8% 39.4%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201 HP1200	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfei (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cie-trans isomerase, FKBP-tyr rotamase (slyb) polypeptide delormylase (def) proteins: synthesis and modification ribosomal protein L10 (rpl10)	44.6%  44.6%  43.0%  43.0%  43.0%  58.1%  pe  40.4%  41.8%  52.0%  30.4%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250	dipeptide ABC transporter, permease protein (dppBl) dipeptide ABC transporter, permease protein (dppBl) dipeptide ABC transporter, permease protein (dppC) glutamate permease (gitS) glutamine ABC transporter, ATP-binding protein (glinC) glutamine ABC transporter, periplasmic glutamine-binding protein (glinH) glutamine ABC transporter, permease protein (glinP) glutamine ABC transporter, ATP-binding	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein
	HP0675 HP0995 HP0323 HP0676 HP0387 HP0153 HP0925 HP0911 HP1362 HP1383	Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methyltrans/ferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) repair protein (recR) rep helicase, single-stranded DNA-depende AT Pase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit	54.6% 34.7% 31.8% 27.8% 31.19 41.09 36.3% 99.19 36.5% it 33.8% 39.4% 33.4%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201 HP1200 HP1202	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cie-trans isomerase, FKBP-tyr rotamase (slyb) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (rpf11) ribosomal protein L10 (rpf10) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11)	44.6% 44.6% 43.0% 43.0% 43.0% 58.1% pe 40.4% 41.8% 52.0% 53.4% 63.8%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252	dipeptide ABC transporter, permease protein (dppBl) dipeptide ABC transporter, permease protein (dppBl) dipeptide ABC transporter, permease protein (dppC) glutamiate permease (gitS) glutamiate ABC transporter, ATP-binding protein (ginC) glutamiane ABC transporter, periplasmic glutamine-binding protein (ginH) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, periplasmic	49.3% in 52.5% 56.9% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1%
	HP0675 HP0995 HP0323 HP0676 HP0387 HP0153 HP0925 HP0911 HP1362 HP1383 HP0661 HP1323	Holliday junction endodeoxyribonuclease (ruv.C) integrase/recombinase (xer.C) integrase/recombinase (xer.C) integrase/recombinase (xer.D) membrane bound endonuclease (nuc) methylated-DNA/kprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (rmhA) ribonuclease HII (rmhB)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 93.1% 36.5% nt 33.8% 33.8% 33.4% 33.4% 33.4% 33.4%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201 HP1200 HP1202 HP1068	histone-like DNA-binding protein HU (hup) iffication Lisoaspartyl-protein carboxyl methyltransfel (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cis-trans isomerase, FKBP-tyr potamase (sly) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (pri10) ribosomal protein L11 (pri11) ribosomal protein L11 (mpi11) ribosomal protein L11 (mpi111) ribosomal protein L11 (mpi1111) ribosomal protein L11 (mpi1111) ribosomal protein L11 (mpi1111) ribosomal protein L11 (mpi11111) ribosomal protein L11 (mpi111111) ribosomal protein L11 (mpi111111111111111111111111111111111111	44.6% 43.0% 43.0% 43.0% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 58.3% 58.3% 58.3% 58.3% 58.3% 58.3% 58.3% 58.3% 58.3% 58.3% 58.3%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiae ABC transporter, ATP-binding protein (ghO) glutamine ABC transporter, periplasmic glutamine-ABC transporter, periplasmic glutamine-binding protein (ginH) glutamine-ABC transporter, permease protein (ginH) glutamine-ABC transporter, permease protein (ginH) oligopeptide-ABC transporter, ATP-binding protein (oppD) oligopeptide-ABC transporter, periplasmic oligopeptide-ABC	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9%
	HP0675 HP0995 HP0995 HP0676 HP0387 HP0153 HP0925 HP0911 HP1362 HP1383 HP0661 HP1323 HP1245	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/Bjortein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) restriction modification system S subunit ribonuclease H (rnhA) ribonuclease H (rnhB) single-strande DNA-brinding protein (ssb)	54.6% 54.6%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201 HP1200 HP1202 HP1068 HP1068	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cie-trans isomerase, FKBP-tyr rotamase (slyb) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf10) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11)	44.6% 43.0% 43.0% 43.0% 58.1% ppe 40.4% 51.5% 52.0% 53.4% 63.8% 53.8% 38.4% 50.0%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnP) glutamine-ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, ATP-binding protein (oppD) glutamine ABC transporter, perplasmic oligopeptide ABC transporter, perplasmic oligopeptide-binding protein (oppA) glutamine ABC transporter, permease	49.3% in 52.5% 56.9% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1%
	HP0675 HP0995 HP0995 HP0676 HP0387 HP0153 HP0925 HP0911 HP1362 HP1383 HP0661 HP1323 HP1245 HP1245	Holliday junction endodeoxyribonuclease (ruv.C) integrase/recombinase (xer.C) integrase/recombinase (xer.C) integrase/recombinase (xer.D) membrane bound endonuclease (nuc) methylated-DNA/kprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (rmhA) ribonuclease HII (rmhB)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 93.1% 36.5% nt 33.8% 33.8% 33.4% 33.4% 33.4% 33.4%	HP0835 Protein mod HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201 HP1200 HP1200 HP1088 HP0084 HP1309 HP1309	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cie-trans isomerase, FKBP-tyr rotamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L10 (rpf10) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11) ribosomal protein L13 (rpf13) ribosomal protein L13 (rpf13) ribosomal protein L14 (rpf14) ribosomal protein L15 (rpf15)	44.6% 43.0% 43.0% 43.0% 58.1% ppe 40.4% 41.8% 52.0% 30.4% 63.8% 38.4% 50.0% 65.9% 42.5% 65.9%	HP0299 HP0300 HP1506 HP171 HP1172 HP1169 HP1170 HP0250 HP1251 HP1251	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) glutamiate permease (gltS) glutamiate permease (gltS) glutamiae ABC transporter, ATP-binding protein (glnG) glutamiae ABC transporter, periplasmic glutamiae-binding protein (glnH) glutamiae ABC transporter, permease protein (glnP) glutamiae ABC transporter, permease protein (glnP) glutamiae ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppB) oligopeptide ABC transporter, permease	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% in 30.9% 39.1% 59.6%
	HP0675 HP0996 HP0996 HP0323 HP0676 HP0153 HP0915 HP0911 HP1362 HP1383 HP0661 HP1323 HP1245 HP1009	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerD) membrane bound endonuclease (nuc) methylated-DNANprotein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinate (recA) recombinate (recA) repair potein (recR) rephiciase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease HI (mhB) single-strand DNA-binding protein (ssb) single-strand DNA-binding protein (ssb) single-stranded-DNA-specific exonuclease (recJ) site-specific recombinase	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 36.5% nt 33.8% 33.4% 33.4% 33.4% 33.4% 33.1% 56.4% 56.5% 56.4% 56.5% 56.	HP0885 Protein mod HP1299 HP1441 HP1123 HP0793 HP1201 HP1200 HP1200 HP1200 HP1068 HP0084 HP1309 HP1301 HP1309 HP1311	histone-like DNA-binding protein HU (hup) fification Lisoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rottamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-tyr rottamase (sly) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 ((prl1) ribosomal protein L10 (prl10) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl13) ribosomal protein L13 (rpl13) ribosomal protein L14 (rpl14) ribosomal protein L14 (rpl14) ribosomal protein L15 (rpl15) ribosomal protein L15 (rpl15) ribosomal protein L16 (rpl16)	44.6% 44.6% 43.0% 43.0% 43.0% 58.1% 58.1% 58.2% 58.2% 58.2% 58.9% 58.4% 58.9% 58.4% 50.0% 65.9% 65.9%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiae ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-ABC transporter, periplasmic glutamine-ABC transporter, permease protein (glnP) glutamine-ABC transporter, permease protein (glnP) glutamine-ABC transporter, ATP-binding protein (oppD) oligopeptide-ABC transporter, periplasmic oligopeptide-ABC transporter, permease protein (oppD) oligopeptide-ABC transporter, permease protein (oppP) oligopeptide-ABC transporter, permease protein (oppC) oligopeptide-ABC transporter, permease protein (oppC)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% iin 30.9% 39.1% 28.7% 59.6% 31.4%
	HP0676 HP0395 HP0323 HP0676 HP0387 HP0153 HP0925 HP0387 HP1382 HP1383 HP0661 HP1323 HP1245 HP1245 HP10348	Holliday junction endodeoxyribonuclease (ruxC) integrass/recombinase (xerC) integrass/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methylaterase (data) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende AT Pase (rep) restriction modification system S subunit ribonuclease H (rmhA) ribonuclease H (rmhA) ribonuclease H (rmhA) single-stranded-DNA-pinding protein (ssb) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF)	54.6% 34.7% 31.8% 27.8% 41.0% 53.3% 99.1% 65.5% nt 33.4% 33.4% 33.4% 33.6% 33.6% 33.6% 21.3% 33.7%	HP0835 Protein mod HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1201 HP1202 HP1202 HP1088 HP0084 HP1309 HP1301 HP1312 HP1301	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppi) peptidyl-protyl cie-trans isomerase, FKBP-tyr rotamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L10 (rpf10) ribosomal protein L10 (rpf10) ribosomal protein L11 (rpf11) ribosomal protein L13 (rpf13) ribosomal protein L14 (rpf14) ribosomal protein L15 (rpf15) ribosomal protein L15 (rpf15) ribosomal protein L16 (rpf16) ribosomal protein L16 (rpf16) ribosomal protein L17 (rpf15) ribosomal protein L17 (rpf15)	44.6% 43.0% 43.0% 43.0% 58.1% ppe 40.4% 41.8% 52.0% 30.4% 63.8% 38.4% 50.0% 65.9% 62.4% 48.3% 62.4%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0261 HP0819	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) glutamite ABC transporter, ATP-binding protein (glind) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine-binding protein (glinH) glutamine ABC transporter, permease protein (glinP) glutamine ABC transporter, permease protein (glinP) glutamine ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, permease protein (pppB) dilgopeptide ABC transporter, permease protein (pppB) dilgopeptide ABC transporter, permease protein (pppB) coligopeptide ABC transporter, permease protein (pppB) coligopeptide ABC transporter, permease protein (pppC) cosmportection protein (pppC) cosmportection protein (prov)	49.3% in 52.5% 56.9% 56.9% 32.2% 27.6% iin 30.9% 39.1% 59.6% 31.4% 38.3%
	HP0676 HP0323 HP0323 HP0676 HP0387 HP0183 HP0921 HP0381 HP0921 HP1383 HP0661 HP1383 HP1245 HP1245 HP1245 HP10462	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) membrane bound endonuclease (nuc) membranese (datt) primosomal protein replication factor (priA) recombinase (reca)) recombinase (reca) recombinade (reca) recombinade (reca) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mNA) ribonuclease H (mNA) single-strand DNA-binding protein (ssb) single-strand DNA-binding protein (ssb) single-strand protein (sub) single-stranded-DNA-specific exonuclease (recl) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fsdS)	54.6% 54.7% 31.8% 27.8% 31.8% 27.8% 31.1% 41.0% 36.3% 39.1% 39.1% 36.5% 11.8% 39.4% 36.5% 11.8% 39.4% 36.1% 36.3% 39.4% 36.3% 32.6% 33.8% 33.8% 33.8% 37.7% 37.7% 37.70%	HP0885 Protein mac HP1299 HP1441 HP1123 HP0793 Ribasomal p HP1201 HP1201 HP1202 HP1202 HP1309 HP1309 HP1301 HP1311 HP1312 HP1312 HP1312 HP1312 HP1312 HP1312 HP1312 HP1312 HP1313 HP13	histone-like DNA-binding protein HU (hup) fification Lisosapartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rottamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-tyr ordamase (slyl) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L1 (prl1) ribosomal protein L11 (prl1) ribosomal protein L11 (rpl10) ribosomal protein L11 (rpl11) ribosomal protein L13 (rpl13) ribosomal protein L14 (rpl14) ribosomal protein L14 (rpl14) ribosomal protein L15 (rpl15) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L17 (rpl17) ribosomal protein L18 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L18 (rpl18)	44.6% 43.0% 43.0% 43.0% 43.0% 58.1% ppe 40.4% 41.8% 52.0% 53.4% 63.8% 65.9% 42.5% 62.4% 44.5% 62.4% 44.5% 62	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1251 HP0251 HP0819 HP0819 HP0818	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamite ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, permease protein (oppB) oligopeptide ABC transporter, permease protein (oppB) oligopeptide ABC transporter, permease protein (oppB) oligopeptide ABC transporter, permease protein (oppC) osmoprotection protein (proVI)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% iin 30.9% 39.1% 59.6% 31.4% 38.3% 30.4% 51.4% 51.4%
	HP0675 HP0923 HP0923 HP0676 HP0387 HP0163 HP0921 HP1362 HP1362 HP1363 HP1363 HP1223 HP1223 HP1223 HP1245 HP1048 HP1049 HP1641 HP10462	Holliday junction endodeoxyribonuclease (ruxC) integrass/recombinase (xerC) integrass/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methylaterase (datt) treombinase (recA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende AT Pase (rep) restriction modification system S subunit ribonuclease H (rnhA) ribonuclease H (rnhA) ribonuclease HI (rnhB) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fisdS) type I restriction enzyme M protein (fisdS)	54.6% 34.7% 34.7% 31.8% 27.8% 31.1% 41.0% 56.3% 99.1% 10.5%	HP0885 Protein mao HP1299 HP1441 HP1123 HP0793 Ribosomal p HP1200 HP1200 HP1200 HP1200 HP1200 HP1200 HP1301 HP1310 HP13112 HP1312 HP1303 HP1417 HP1303	histone-like DNA-binding protein HU (hup) fification L-isoaspartyl-protein carboxyl methyltransfei (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rottamase (ppi) peptidyl-protyl cis-trans isomerase, FKBP-tyr rottamase (slyt) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (prl1) ribosomal protein L11 (prl10) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl13) ribosomal protein L13 (rpl13) ribosomal protein L14 (rpl14) ribosomal protein L15 (rpl15) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L17 (rpl17) ribosomal protein L18 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19)	44.6% 44.6% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 50.0% 63.8% 43.9% 65.9% 42.5% 66.4% 43.9% 65.9% 65.9% 65.9% 65.9%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1250 HP1251 HP1251 HP0251 HP0251 HP0819 HP0818 HP0936	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiae ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (pppP) dipeptide ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) camoprotection protein (proV) camoprotection protein (proV) comportection protein (proV) proline /betalen transporter (porP)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1% 59.6% 51.4% 30.4% 51.4% 29.1%
	HP0675 HP0923 HP0923 HP0676 HP0323 HP0676 HP0325 HP0911 HP1383 HP0861 HP1323 HP1624 HP10348 HP10463 HP10463 HP0463 HP0463 HP0463	Holliday junction endodeoxyribonuclease (ruxC) integrass/recombinase (xerC) integrass/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methylaterase (datu) protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende AT Pase (rep) restriction system S subunit ribonuclease H (rmhA) ribonuclease H (rmhA) ribonuclease H (rmhA) single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fisdS) type I restriction enzyme R protein (fisdR)	54.6% 34.7% 34.7% 31.8% 27.8% 31.1% 41.0% 56.3% 99.1% 10.5%	HP0835 Protein mod HP0363 HP1299 HP1441 HP1123 HP0723 Ribosomal p HP1200 HP1200 HP1200 HP1200 HP1200 HP1200 HP1301 HP1301 HP1301 HP1301 HP1301 HP1301 HP1301 HP1301 HP1303 HP1303 HP1303 HP1303 HP1303 HP1306 HP1306 HP1307 HP1307 HP1307 HP1308 HP1308 HP1309 HP1301 HP	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppl) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppl) polypeptide delormylase (def) proteins: synthesis and modification ribosomal protein L10 (rpf10) ribosomal protein L10 (rpf10) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11) ribosomal protein L13 (rpf13) ribosomal protein L14 (rpf14) ribosomal protein L15 (rpf15) ribosomal protein L16 (rpf16) ribosomal protein L17 (rpf15) ribosomal protein L17 (rpf17) ribosomal protein L17 (rpf18) ribosomal protein L17 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L20 (rpf20)	44.6% 44.6% 43.0% 43.0% 43.0% 58.1% pe 40.4% 41.8% 52.0% 53.4% 653.8% 653.8% 653.8% 652.4% 445.5% 65.9	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1251 HP0251 HP0261 HP0819 HP0819 HP0816 HP0816	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiae ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (pppP) dipeptide ABC transporter, ATP-binding protein (oppD) oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppC) camoprotection protein (proV) camoprotection protein (proV) comportection protein (proV) proline /betalen transporter (porP)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% iin 30.9% 39.1% 59.6% 31.4% 38.3% 30.4% 51.4% 51.4%
	HP0676 HP0923 HP0676 HP0887 HP0887 HP0887 HP0981 HP0981 HP1883 HP0861 HP1245 HP1245 HP1094 HP1009 HP1009 HP1009 HP10464 HP0464 HP0464 HP0464	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNANprotein-cysteine methylatransterase (datt) primosomal protein replication factor (priA) recombinase (reca) recombinase (reca) recombinase (reca) recombinade (reca) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mNA) ribonuclease H (mNB) single-stranded-DNA-specific exonuclease (rec) single-stranded-DNA-specific exonuclease transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fisdM) type I restriction enzyme M protein (fisdM) type I restriction enzyme M protein (fisdM) type I restriction enzyme R protein (fisdR)	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 36.5% 11 33.9% 99.1% 36.5% 11 33.9% 99.4% 36.1% 56.4% 56.3% 52.6% 32.6% 32.6% 32.7% 37.7% 37.7% 48.0%	HP0885 Protein mod HP0363 HP1299 HP1441 HP1123 HP1441 HP10783 Ribosomal F HP1200 HP1202 HP1202 HP1202 HP1309 HP1301	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfei (pcm) methionine amino peptidase (map) peptidyl-protyl ciz-frans isomerase B, cyclosporin-type rotamase (ppB) peptidyl-protyl cis-frans isomerase, FKBP-tyr rotamase (slyl) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (prl1) ribosomal protein L11 (prl10) ribosomal protein L11 (rpl11) ribosomal protein L11 (rpl11) ribosomal protein L13 (rpl13) ribosomal protein L14 (rpl14) ribosomal protein L15 (rpl15) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L20 (rpl20) ribosomal protein L20 (rpl20)	44.6% 43.0% 43.0% 43.0% 58.1% Pepe 44.4% 43.6% 52.0% 63.8% 63.8% 42.5% 42.5% 65.9% 42.5% 50.9% 50.9% 50.9% 50.9% 50.9% 50.9% 50.9% 50.9% 54.5%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1262 HP1261 HP0261 HP0818 HP00818 HP00806 HP0333 Anions	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-binding protein (glnH) glutamine-binding protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (oppD) oligopeptide ABC transporter, permease protein (oppD) camoprotection protein (proV) camoprotection protein (proV) camoprotection protein (proV) proline /betaine transporter (proP) serine transporter (sdaC)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% ein 30.9% 39.1% 59.6% 51.4% 30.4% 51.4% 29.1%
+ + + + + + + + + + + + + + + + + + +	HP0675 HP0323 HP0323 HP0676 HP0133 HP0138 HP0138 HP0138 HP01383 HP038 HP1245 HP1245 HP1245 HP1454 HP1463 HP1464 HP0463 HP0463 HP0464 HP0463 HP0464 HP0463 HP0464 HP0464 HP0464	Holliday junction endodeoxyribonuclease (ruxC) integrass/recombinase (xerC) integrass/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNA/protein-cysteine methylaterase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) report in the protein replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (rnhA) ribonuclease H (rnhA) ribonuclease H (rnhA) single-stranded-DNA-specific exonuclease (rec) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (fisdS) type I restriction enzyme R protein (fisdR) type I restriction enzyme S protein (fisdR) type I restriction enzyme S protein (fisdR) type I restriction enzyme R protein (fisdR) type I restriction enzyme R protein (fisdR) type I restriction enzyme R protein (fisdR) type I restriction enzyme S protein (fisdR) type I restriction enzyme R protein (fisdR)	54.6% 34.7% 31.8% 27.8% 31.19% 31.19% 31.19% 31.19% 31.19% 30.5% nt 33.8% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.77% 37.77% 37.77% 37.77% 37.77% 37.77% 37.77% 37.77%	HP0885  Protein mod HP0363  HP1299 HP1441  HP1123  HP0783  Ribosomal p HP1200 HP1200 HP1200 HP1200 HP1200 HP1200 HP1201 HP1202 HP1088  HP0084 HP1301 HP1301 HP1301 HP1302 HP1303 HP1301 HP1303 HP1301 HP1303 HP1303 HP1303 HP1304 HP1305 HP1306 HP1307 HP1306 HP1307 HP1307 HP1316 HP0126 HP0266 HP0266	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppl) peptidyl-protyl cie-trans isomerase B, cyclosporin-type rotamase (ppl) peptidyl-protyl cie-trans isomerase, FKBP-tyr (rotamase (slyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L10 (rpf10) ribosomal protein L10 (rpf10) ribosomal protein L11 (rpf11) ribosomal protein L11 (rpf11) ribosomal protein L13 (rpf13) ribosomal protein L14 (rpf14) ribosomal protein L15 (rpf16) ribosomal protein L16 (rpf16) ribosomal protein L17 (rpf17) ribosomal protein L19 (rpf18) ribosomal protein L19 (rpf19) ribosomal protein L19 (rpf19) ribosomal protein L20 (rpf20)	3.04.6% 44.6% 43.0% 43.0% 43.0% 58.1% 58.1% 52.0% 30.4% 63.8% 63.8% 65.9% 62.4% 44.5% 62.4% 44.5% 65.9% 62.4% 45.5% 65.9% 62.4% 46.9%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1261 HP0251 HP0319 HP0055 HP0055 HP00363 Anions	dipeptide ABC transporter, permease protein (dpps) dipeptide ABC transporter, permease protein (dpps) dipeptide ABC transporter, permease protein (dpps) glutamite permease (gltS) glutamite ABC transporter, ATP-binding protein (glnC) glutamite-binding protein (glnC) glutamite-binding protein (glnH) glutamite-binding protein (glnH) glutamite-binding protein (glnH) glutamite-ABC transporter, permease protein (glnP) glutamite-ABC transporter, ATP-binding protein (pppD) oligopeptide-ABC transporter, periplasmic oligopeptide-binding protein (pppA) oligopeptide-ABC transporter, permease protein (pppB) oligopeptide-ABC transporter, permease protein (pppB) oligopeptide-ABC transporter, permease protein (pppC) osmoprotection protein (ppoM) osmoprotection protein (proW) proline permease (putP) proline-betaine transporter (proP) serine transporter (glaC)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% 61.30.9% 39.1% 59.6% 31.4% 39.3% 44.6% 44.6%
+ + + + + + + + + + + + + + + + + + +	HP0675 HP0323 HP0687 HP0387 HP0153 HP0153 HP0387 HP0387 HP0381 HP0383 HP1383 HP1383 HP1383 HP1383 HP1384 HP1384 HP1384 HP1384 HP1384 HP1384 HP1384 HP1384 HP1384 HP1384 HP0486 HP0486 HP0488 HP0488 HP0488 HP0488	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNAMprotein-cysteine methylatransterase (datt) primosomal protein replication factor (priA) recombinase (reca) recombinase (reca) recombinase (reca) recombinase (reca) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) restriction modification system S subunit ribonuclease H (mhB) single-stranded-DNA-specific exonuclease single-stranded-DNA-specific exonuclease (recl) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (hsdM) type I restriction enzyme M protein (hsdM) type I restriction enzyme R protein (hsdM) type I restriction enzyme M protein (hsdM) type I restriction enzyme R protein (hsdM)	54.6% 34.7% 34.7% 31.8% 27.8% 41.0% 36.3% 99.19% 36.5% tt 33.8% 39.4% 36.1% 55.4% 36.3% 32.6% 32.6% 32.6% 32.7% 37.7% 37.7% 48.0% 49.0% 54.4% 55.4% 56.4% 56.5% 56.4% 56.5% 56	HP0885  Protein mod HP0383  HP1299 HP1441  HP1123  HP0793  Ribosomal p HP1201 HP1200 HP1200 HP1200 HP1301 HP1200 HP1301 HP1200 HP1301	histone-like DNA-binding protein HU (hup) iffication L-Isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rottamase (ppi) peptidyl-prolyl cis-trans isomerase, FKBP-tyr potratamase (siyD) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L11 (pri10) ribosomal protein L11 (pri10) ribosomal protein L11 (pri11) ribosomal protein L14 (pri13) ribosomal protein L14 (pri14) ribosomal protein L14 (pri14) ribosomal protein L15 (pri15) ribosomal protein L16 (pri16) ribosomal protein L19 (pri19) ribosomal protein L19 (pri19) ribosomal protein L19 (pri19) ribosomal protein L20 (pri20) ribosomal protein L30	33.4% 44.6% 43.0% 43.0% 43.0% 58.1% pe 40.4% 41.8% 52.0% 53.6% 53.8% 653.8% 653.8% 653.8% 653.9% 65.9% 62.4% 44.5% 65.9% 62.4% 44.5% 65.9% 65.9% 45.5% 65.9% 54.5% 65.9% 54.5% 65.9% 54.5% 65.9% 54.5% 65.9% 54.5% 65.9% 54.5% 65.9% 54.5% 65.9% 54.5% 65.9% 56.9% 54.5% 65.9% 56.9%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0251 HP0319 HP0319 HP033 Anions HP0473	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding protein (ginC) glutamine ABC transporter, periplasmic glutamine-binding protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, permease protein (ginP) glutamine ABC transporter, ATP-binding protein (ppD) oligopeptide ABC transporter, periplasmic oligopeptide ABC transporter, permease protein (ppD) oligopeptide ABC transporter, permease protein (ppDP) oligopeptide ABC transporter, permease protein (ppDP) oligopeptide ABC transporter, permease protein (ppDP) osmoprotection protein (ppDP) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betaine transporter (proP) serine transporter (sdaC)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% iii 30.9% 39.1% 28.7% 59.6% 31.4% 30.4% 51.4% 38.3% 44.6% 38.4% 38.4%
+ + + + + + + + + + + + + + + + + + +	HP0676 HP02323 HP02323 HP0676 HP0153 HP0153 HP0387 HP0387 HP0381 HP1362 HP1383 HP1684 HP1684 HP16948 HP16948 HP16948 HP16948 HP16948 HP0464 HP	Holliday junction endodeoxyribonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylated-DNANprotein-cysteine methylatransterase (datt) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) restriction modification system S subunit ribonuclease H (mhA) ribonuclease H (mhB) single-stranded-DNA-specific exonuclease single-stranded-DNA-specific exonuclease (recI) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme M protein (hsdM) type I restriction enzyme R protein (nsdR) type I restriction enzyme R protein (nsdR) type I restriction enzyme M protein (hsdM)	54.6% 34.7% 34.7% 31.8% 27.8% 41.0% 36.3% 99.19% 36.5% tt 33.8% 34.9% 38.19% 58.3% 5	HP0835 Protein mod HP10963 HP1441 HP1129 HP1441 HP10783 Ribosomal p HP1200 HP1202 HP1202 HP1202 HP1004 HP1309 HP1311 HP1312 HP1312 HP1314 HP1314 HP1314 HP1314 HP1314 HP1314 HP1314 HP1316 HP1317 HP1317 HP1318 HP1317 HP1318	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfei (pcm) methionine amino peptidase (map) peptidy-protyl oiz-frans isomerase B, cyclosporfir-type rotamase (ppl) peptidyl-protyl oiz-frans isomerase, FKBP-tyr rotamase (sly) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L10 (rpl10) ribosomal protein L10 (rpl10) ribosomal protein L11 (rpl11) ribosomal protein L15 (rpl15) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L18 (rpl16) ribosomal protein L19 (rpl17) ribosomal protein L19 (rpl18) ribosomal protein L19 (rpl18) ribosomal protein L20 (rpl20) ribosomal protein L21 (rpl21) ribosomal protein L21 (rpl21) ribosomal protein L21 (rpl21) ribosomal protein L22 (rpl22) ribosomal protein L23 (rpl23) ribosomal protein L23 (rpl23) ribosomal protein L23 (rpl23) ribosomal protein L27 (rpl27)	44.6% 43.0% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 58.1% 52.0% 63.8% 63.8% 65.9% 65.9% 65.9% 62.4% 48.3% 65.9% 65.9% 62.4% 48.3% 50.9% 65.9% 62.4% 48.3% 63.8% 63.8% 63.8% 65.9% 66.9% 66.9% 66.9% 66.9%	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1251 HP0251 HP0261 HP0318 HP0336 HP0336 HP0375 HP0475	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamine ABC transporter, ATP-binding protein (glnQ) glutamine ABC transporter, periplasmic glutamine-binding protein (glnH) glutamine-bBC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glpD) digopeptide ABC transporter, permease protein (ppBD) digopeptide ABC transporter, permease protein (ppBD) digopeptide ABC transporter, permease protein (ppBC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline /betaine transporter (proP) serine transporter (sdCC) molybdenum ABC transporter, ATP-binding protein (modD) molybdenum ABC transporter, periplasmic molybdate-binding protein (modA)	49.3% in 52.5% 56.9% 51.9% 32.2% 27.6% 61.30.9% 39.1% 59.6% 31.4% 39.3% 44.6% 44.6%
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+ + + + + + + + + + + + + + + + + + +	HP0676 HP00387 HP00387 HP01638 HP01638 HP0981 HP1682 HP1882 HP1245 HP1245 HP1245 HP1245 HP1464 HP0464 HP0464 HP0464 HP0464 HP0463 HP1404 HP0464 HP0464 HP1403 HP1404 HP1403 HP1404 HP1403 HP1404 HP1403 HP1404 HP1403 HP1404 HP1403 HP1404 HP1403 HP1404 HP1403 HP1404 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP1404 HP1405 HP140	Holliday junction endodeoxyribonuclease (ruxc) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylatec-DANA[protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) repelicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (rmhA) single-stranded-DNA-specific exonuclease (recA) repelicative DNA-binding protein (ssb) single-stranded-DNA-specific exonuclease (recA) repelication of the protein (recR) site specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme B protein (hsdN) type I restriction enzyme M protein (hsdN) type I restriction enzyme R protein (hsdN) type II re	54.6% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 36.5% nt 33.8% 39.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.4% 33.1% 56.3% 52.6% 33.4% 33.6% 33.6% 33.1% 56.3% 57.7% 37.7% 37.7% 37.7% 37.7% 57.0% 59.3% 50.6% 53.3% 50.6% 53.3% 50.6% 53.3% 50.6% 53.3% 50.6% 53.3% 50.6% 50.7% 50.	HP0885  Protein mod HP0383  HP1299 HP1441 HP1123 HP1441 HP10783  Ribasomal p HP1201 HP1202 HP1202 HP1084 HP1309 HP1301 HP1202 HP1309 HP1301 HP1309 HP1319	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rottamase (pyl) peptidyl-protyl cis-trans isomerase, FKBP-tyr ordamase (syl) polypeptid deformylase (def) proteins: synthesis and modification ribosomal protein L11 (rph1) ribosomal protein L11 (rph1) ribosomal protein L11 (rph1) ribosomal protein L11 (rph1) ribosomal protein L13 (rph3) ribosomal protein L14 (rph14) ribosomal protein L15 (rph15) ribosomal protein L16 (rph16) ribosomal protein L16 (rph16) ribosomal protein L16 (rph16) ribosomal protein L17 (rph17) ribosomal protein L18 (rph18) ribosomal protein L19 (rph19) ribosomal protein L19 (rph19) ribosomal protein L19 (rph19) ribosomal protein L20 (rpl20) ribosomal protein L21 (rpl21) ribosomal protein L22 (rpl22) ribosomal protein L23 (rpl23) ribosomal protein L24 (rpl24) ribosomal protein L27 (rpl27) ribosomal protein L28 (rpl28) ribosomal protein L29 (rpl29) ribosomal protein L29 (rpl29) ribosomal protein L29 (rpl29) ribosomal protein L34 (rpl34) ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribo	44.6% 43.0% 43.0% 43.0% 43.0% 43.0% 43.0% 58.1% 58.1% 52.0% 53.0.4% 63.8% 52.0% 63.8% 63.8% 63.8% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 42.5% 65.9% 43.9% 65.9	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0313 HP0035 HP0473 HP0474 HP0473 HP0474 HP	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiae ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnT) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (pppD) oligopeptide ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betaine transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, periplasmic molybdate-binding grotein (modD) molybdenum ABC transporter, periplasmic molybdate-binding grotein (modA) molybdenum ABC transporter, periplasmic molybdate-binding grotein (modA) molybdenum ABC transporter, periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (gluP) L-lactate permease (gluP) L-lactate permease (gluP) L-lactate permease (gluP) L-lactate permease (gluP)	49.3% in 52.5% 56.5%
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+ + + + + + + + + + + + + + + + + + +	HP0676 HP00387 HP00387 HP00387 HP00387 HP00153 HP00281 HP00281 HP00281 HP00281 HP00381 HP00381 HP00381 HP00381 HP10382 HP10384 HP10384 HP10384 HP10384 HP10384 HP10483 HP00484 HP00484 HP00484 HP00484 HP00484 HP10487 HP10589 HP1377 HP10582 HP14072 HP1368	Holliday junction endodeoxyribonuclease (ruxc) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylatec-DANA[protein-cysteine methyltransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) recombinase (recA) repelicase, single-stranded DNA-depende ATPase (rep) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (rmhA) single-stranded-DNA-specific exonuclease (recA) repelicative DNA-binding protein (ssb) single-stranded-DNA-specific exonuclease (recA) repelication of the protein (recR) site specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme B protein (hsdN) type I restriction enzyme M protein (hsdN) type I restriction enzyme R protein (hsdN) type II re	54.6% 34.7% 34.7% 31.8% 27.8% 31.1% 41.0% 36.3% 99.1% 36.5% 11 33.8% 36.5% 11 33.8% 38.1% 38.1% 58.4% 58.3% 58.4% 58.3% 58.6% 31.7% 31.7% 37.7%	HP0885  Protein mod HP0363  HP1299 HP1441  HP1123 HP1297 HP1202 HP1202 HP1202 HP1202 HP1202 HP1301 HP1309 HP1301 HP1316 HP1309 HP1301 HP1317 HP1316 HP1309 HP1301 HP1317 HP1316 HP1309 HP1301 HP1317 HP1316 HP1309 HP1317 HP1316 HP12020 HP1317 HP1316 HP12029 HP1301 HP1317 HP1316 HP12029 HP1317 HP1317 HP1318 HP1317	histone-like DNA-binding protein HU (hup) iffication L-isoaspartyl-protein carboxyl methyltransfer (pcm) methionine amino peptidase (map) peptidyl-protyl cis-trans isomerase B, cyclosporin-type rottamase (pyl) peptidyl-protyl cis-trans isomerase, FKBP-tyr ordamase (syl) polypeptide deformylase (def) proteins: synthesis and modification ribosomal protein L10 (rpl10) ribosomal protein L11 (rpl10) ribosomal protein L11 (rpl10) ribosomal protein L11 (rpl11) ribosomal protein L13 (rpl13) ribosomal protein L14 (rpl14) ribosomal protein L15 (rpl15) ribosomal protein L16 (rpl16) ribosomal protein L16 (rpl16) ribosomal protein L17 (rpl17) ribosomal protein L18 (rpl18) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L19 (rpl19) ribosomal protein L29 (rpl29) ribosomal protein L29 (rpl20) ribosomal protein L29 (rpl23) ribosomal protein L30 (rpl33) ribosomal protein L31 (rpl31) ribosomal protein L32 (rpl33) ribosomal protein L32 (rpl33) ribosomal protein L32 (rpl34) ribosomal protein L32 (rpl34) ribosomal protein L32 (rpl35) ribosomal protein L34 (rpl34) ribosomal protein L36 (rpl36) ribosomal protein L37 (rpl37) ribosomal protein L36 (rpl36) ribosomal protein L37 (rpl37) ribosomal protein L36 (rpl36) ribosomal protein L37 (rpl37) ribosomal protein L37 (rpl37) ribosomal protein L36 (rpl36) ribosomal protein L37 (rpl37) ribosomal protein L37 (rpl37	33.4% 59% 41.8% 52.2% 54.7% 41.7% 55.1% 55	HP0299 HP0300 HP1506 HP1171 HP1172 HP1169 HP1170 HP0250 HP1252 HP1251 HP0251 HP0313 HP0035 HP0473 HP0474 HP0473 HP0474 HP	dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppB) dipeptide ABC transporter, permease protein (dppC) glutamiae ABC transporter, ATP-binding protein (glnC) glutamine ABC transporter, periplasmic glutamine ABC transporter, periplasmic glutamine ABC transporter, permease protein (glnT) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (glnP) glutamine ABC transporter, permease protein (pppD) oligopeptide ABC transporter, ATP-binding protein (pppD) oligopeptide ABC transporter, permease protein (pppD) oligopeptide ABC transporter, permease protein (pppC) osmoprotection protein (proV) osmoprotection protein (proV) osmoprotection protein (proV) proline/betaine transporter (proP) serine transporter (sdaC) molybdenum ABC transporter, periplasmic molybdate-binding grotein (modD) molybdenum ABC transporter, periplasmic molybdate-binding grotein (modA) molybdenum ABC transporter, periplasmic molybdate-binding grotein (modA) molybdenum ABC transporter, periplasmic molybdate-binding protein (modA) molybdenum ABC transporter (gluP) L-lactate permease (gluP) L-lactate permease (gluP) L-lactate permease (gluP) L-lactate permease (gluP)	49.3% in 52.5% 56.5%

Cations HP0791								
	cadmium-transporting ATPase, P-type		HP0258	conserved hypothetical integral membrane protein			conserved hypothetical protein conserved hypothetical protein	29.3% 31.0%
	(cadA)	97.5%	HP0284	conserved hypothetical integral membrane		HP0741	conserved hypothetical protein	30.2%
HP0969		37.3%	LIDOGGO	protein			conserved hypothetical protein	33.7%
HP1328 HP1329		28.9% 31.3%	HP0362	conserved hypothetical integral membrane protein			conserved hypothetical protein conserved hypothetical protein	32.4% 36.1%
HP1503		30.3%	HP0415	conserved hypothetical integral membrane			conserved hypothetical protein	31.0%
HP1073		92.4%	1100400	protein		HP0813	conserved hypothetical protein	32.5%
HP1072 HP0471	copper-transporting ATPase, P-type (copA) glutathione-regulated potassium-efflux syste		HP0467	conserved hypothetical integral membrane protein			conserved hypothetical protein conserved hypothetical protein	27.8% 52.1%
	protein (kefB)	99.3%	HP0571	conserved hypothetical integral membrane			conserved hypothetical protein	32.2%
HP0687		33.6%	LIDOCAA	protein			conserved hypothetical protein	33.8%
HP1561	iron(III) ABC transporter, periplasmic iron- binding protein (ceuE)	27.5%	HP0644	conserved hypothetical integral membrane protein		HP0892 HP0894	conserved hypothetical protein conserved hypothetical protein	39.1% 39.8%
HP1562	iron(III) ABC transporter, periplasmic iron-		HP0677	conserved hypothetical integral membrane			conserved hypothetical protein	30.7%
LIDAGO	binding protein (ceuE)	28.2%		protein			conserved hypothetical protein	33.6%
HP0888	iron(III) dicitrate ABC transporter, ATP-bindir protein (fecF)	ng 34.4%	HP0693	conserved hypothetical integral membrane protein			conserved hypothetical protein conserved hypothetical protein	36.2% 31.1%
HP0889	iron(III) dicitrate ABC transporter, permease	34.470	HP0718	conserved hypothetical integral membrane			conserved hypothetical protein	29.1%
	protein (fecD)	38.3%		protein		HP0975	conserved hypothetical protein	25.0%
HP0686 HP0807		29.7% 28.5%	HP0737	conserved hypothetical integral membrane protein	33.3%		conserved hypothetical protein	31.5% 95.9%
HP1400		26.3%	HP0758	conserved hypothetical integral membrane		HP1046	conserved hypothetical protein conserved hypothetical protein	32.6%
HP1344	magnesium and cobalt transport protein			protein		HP1049	conserved hypothetical protein	39.7%
HP1183	(corA) NA+/H+ antiporter (napA)	26.3% 26.6%	HP0759	conserved hypothetical integral membrane protein			conserved hypothetical protein	41.3% 24.7%
HP1552	Na+/H+ antiporter (nhaA)	49.2%	HP0787	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	34.7%
HP1077	nickel transport protein (nixA)	98.7%		protein	25.2%	HP1182	conserved hypothetical protein	34.6%
HP0490	putative potassium channel protein, putative	25.7%	HP0851	conserved hypothetical integral membrane protein			conserved hypothetical protein	21.5% 42.4%
Nucleoside	s, purines and pyrimidines	23.770	HP0920	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	22.5%
HP1290	nicotinamide mononucleotide transporter			protein	36.3%	HP1242	conserved hypothetical protein	42.3%
LIBAGO		28.0%	HP0946	conserved hypothetical integral membrane protein			conserved hypothetical protein	44.6% 36.8%
HP1180	pyrimidine nucleoside transport protein (nupC)	32.9%	HP0952	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	26.3%
Other	(паро)	UE.U 10		protein	38.5%	HP1335	conserved hypothetical protein	33.9%
HP0876	iron-regulated outer membrane protein		HP0983	conserved hypothetical integral membrane protein	32.8%		conserved hypothetical protein	27.2%
		27.6%	HP1044	conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	36.2% 33.6%
HP0915	iron-regulated outer membrane protein (frpB)	28.1%		protein		HP1401	conserved hypothetical protein	27.5%
HP0916	iron-regulated outer membrane protein	20.170	HP1061	conserved hypothetical integral membrane	05.00		conserved hypothetical protein	41.6%
	(frpB)	28.8%	HP1080	protein conserved hypothetical integral membrane			conserved hypothetical protein conserved hypothetical protein	27.4% 23.7%
HP1129		29.7%	111 1000	protein			conserved hypothetical protein	40.3%
HP1130 HP1339		33.5% 46.8%	HP1162	conserved hypothetical integral membrane		HP1426	conserved hypothetical protein	40.0%
HP1340	biopolymer transport protein (exbD)	35.8%	HP1175	protein conserved hypothetical integral membrane	27.6%		conserved hypothetical protein conserved hypothetical protein	37.8% 37.9%
HP1445		45.5%	111/11/5	protein	40.6%		conserved hypothetical protein	39.0%
HP1446 HP1512	biopolymer transport protein (exbD) iron-regulated outer membrane protein	36.2%	HP1184	conserved hypothetical integral membrane		HP1453	conserved hypothetical protein	26.8%
111 1012	(frpB)	26.6%	HP1185	protein conserved hypothetical integral membrane	23.5%	HP1459 HP1504	conserved hypothetical protein conserved hypothetical protein	30.1% 23.9%
HP0653		99.4%	111 1100	protein	55.5%		conserved hypothetical protein	30.6%
HP1341	siderophore-mediated iron transport protein (tonB)	37.2%	HP1225	conserved hypothetical integral membrane		HP1533	conserved hypothetical protein	25.4%
		01.E 10	LIDAGGA	protein	31.6%		conserved hypothetical protein	40.5%
OTHER CA	TEGORIES		HP1234	conserved hypothetical integral membrane protein	29.0%		conserved hypothetical protein conserved hypothetical protein	42.2% 39.0%
General		0770	HP1235	conserved hypothetical integral membrane			conserved hypothetical protein	32.0%
HP0924 HP1034		37.7% 36.3%	LIDAGGG	protein	30.9%	HP1589	conserved hypothetical protein	35.1%
HP1000		29.7%	HP1330	conserved hypothetical integral membrane protein	41.7%		conserved hypothetical protein (plasmid pHPM180)	41.8%
HP1139		47.4%	HP1331	conserved hypothetical integral membrane	11.770	HP0028	conserved hypothetical secreted protein	42.1%
HP0827		46.8%		protein	33.6%	HP0139	conserved hypothetical secreted protein	37.1%
Adaptation: HP1496	s and atypical conditions general stress protein (ctc)	26.5%	HP1343	conserved hypothetical integral membrane protein	49.1%		conserved hypothetical secreted protein conserved hypothetical secreted protein	30.6% 31.4%
HP1483		33.3%	HP1363	conserved hypothetical integral membrane	40.170		conserved hypothetical secreted protein	24.3%
HP0927	heat shock protein (htpX)	32.8%	LIBLIAND	protein	33.1%	HP0235	conserved hypothetical secreted protein	31.5%
HP0280 HP1228	heat shock protein B (ibpB) invasion protein (invA)	27.2% 38.2%	HP1407	conserved hypothetical integral membrane protein	22.4%		conserved hypothetical secreted protein conserved hypothetical secreted protein	29.2% 36.4%
HP0970	nickel-cobalt-cadmium resistance protein	36.270	HP1466	conserved hypothetical integral membrane			conserved hypothetical secreted protein	29.8%
	(nccB)	21.1%		protein	30.9%	HP0518	conserved hypothetical secreted protein	96.9%
HP1444 HP0930		42.1%	HP1484	conserved hypothetical integral membrane		HP0785	conserved hypothetical secreted protein	26.6%
HPU930								
HP0315		37.7% 70.2%	HP1486	protein conserved hypothetical integral membrane	41.2%	HP0949	conserved hypothetical secreted protein	39.7% 29.4%
HP0315 HP0967	virulence associated protein D (vapD) virulence associated protein D (vapD)	37.7% 70.2% 28.9%	HP1486	protein conserved hypothetical integral membrane protein	23.8%	HP0949 HP0977 HP0980	conserved hypothetical secreted protein conserved hypothetical secreted protein	39.7% 29.4% 57.4%
	virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog	70.2% 28.9%	HP1486 HP1487	conserved hypothetical integral membrane protein conserved hypothetical integral membrane	23.8%	HP0949 HP0977 HP0980 HP1075	conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein	29.4% 57.4% 42.9%
HP0967 HP1248	virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB)	70.2% 28.9% 36.0%	HP1487	conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein	23.8%	HP0949 HP0977 HP0980 HP1075 HP1098	conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0%
HP0967 HP1248 HP0885	virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN)	70.2% 28.9%	HP1487 HP1509	conserved hypothetical integral membrane protein conserved hypothetical integral membrane	23.8%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117	conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein	29.4% 57.4% 42.9%
HP0967 HP1248 HP0885	virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ted functions	70.2% 28.9% 36.0%	HP1487	conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane conserved hypothetical integral membrane	23.8% 30.7% 34.3%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285	conserved hypothetical secreted protein conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0%
HP0967 HP1248 HP0885 Colicin-rela	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein bomolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellurite resistance cluster	70.2% 28.9% 36.0% 33.5% 25.7%	HP1487 HP1509 HP1548	conserved hypothetical integral membrane protein protein conserved hypothetical integral membrane protein conserved hypothetical integral membrane protein	23.8% 30.7% 34.3% 30.6%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285 HP1286	conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN profein (mviN) ted functions collicin tolierance-like profein (tolB) phage/collicin/tellurite resistance cluster tery profein	70.2% 28.9% 36.0% 33.5%	HP1487 HP1509	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical iron-sulfur protein	23.8% 30.7% 34.3%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285 HP1286 HP1464	conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and &	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) virulence factor mviN protein (mviN) ted functions collicin tolerance-like protein (tolB) phage/collicin/tellurite resistance cluster terY protein malog sensitivity	70.2% 28.9% 36.0% 33.5% 25.7%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein	23.8% 30.7% 34.3% 30.6% 41.2% 32.0% 21.8%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285 HP1286 HP1464	conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (toIB) phage/colicin/fellurife resistance cluster tery protein inalog sensitivity 185 rRNA (adenosine-N6,N6)-dimethyl-	70.2% 28.9% 36.0% 33.5% 25.7%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0575	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein	23.8% 30.7% 34.3% 30.6% 41.2% 32.0% 21.8% 38.8%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551	conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/felluntle resistance cluster tery' protein (TSS rRNA (adenosine-N6,N6)-dimethyl-transferase (ksqA) membrane (usion protein (mtrC)	70.2% 28.9% 36.0% 36.0% 25.7% 25.6%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein	23.8% 30.7% 34.3% 30.6% 41.2% 21.8% 38.8%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285 HP1286 HP1464 HP1488 HP1551 UNKNOWN	conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein (mriOg sensitivity 16S rRNA (adenosine-N6,N6-) dimethyltransferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66)	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 35.5% 24.2%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492	conserved hypothetical integral membrane protein conserved hypothetical ipoprotein conserved hypothetical immembrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical michondrial protein 4 conserved hypothetical michondrial protein 4	23.8% 30.7% 30.6% 41.2% 32.0% 32.0% 38.8% 23.2% 48.2%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1286 HP1286 HP1488 HP1488 HP1551 UNKNOWN General	conserved hypothetical secreted protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein b (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery' protein virulence sensitivity 168 rfNA( adenosine-N6,N6-)-dimethyl-transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P),	70.2% 28.3% 36.0% 33.5% 25.7% 26.6% 35.5% 24.2% 62.3% 39.7%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitto-chondrial protein 4 conserved hypothetical protein intuitive protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein conserved hypothetical protein	23.8% 30.7% 34.3% 34.3% 34.6% 412% 32.0% 32.0% 32.9% 48.2% 48.2%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1285 HP1484 HP1484 HP1488 HP1551 UNKNOWN General HP0390 HP1193	conserved hypothetical secreted protein definition of the protein secreted protei	29.4% 57.4% 42.9% 32.3% 31.9% 38.0% 37.5% 29.8% 42.7%
HP0967 HP1248 HP0885 <i>Colicin-rela</i> HP1126 HP0428 <i>Drug and &amp;</i> HP1431 HP0606 HP0630 HP1476 HP1165	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) virulence factor mviN protein (mviN) ted functions collicin tolerance-like profein (tolB) phage/collicin/tellurifier resistance cluster terY protein resistance cluster terY protein (mrichy factorial) virulence (skspA) membrane fusion protein (mrtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 35.5% 24.2%	HP1487 HP1509 HP1548 HP0138 HP0151 HP0575 HP1258 HP1492 HP0032 HP0035	conserved hypothetical integral membrane protein conserved hypothetical ipoprotein conserved hypothetical immembrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical michondrial protein 4 conserved hypothetical michondrial protein 4	23.8% 30.7% 34.3% 30.6% 41.2% 32.0% 38.8% 48.2% 48.2% 37.0% 34.1%	HP0949 HP0977 HP0980 HP1075 HP1078 HP1117 HP1216 HP1285 HP1484 HP1484 HP1484 HP1551 UNKNOWN General HP0390 HP0193 HP0872	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkyphosphonate uptake protein (phnA)	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4% 42.7% 38.3% 46.6% 611.9%
HP0967 HP1248 HP0885 <i>Colicin-rela</i> HP1126 HP0428 <i>Drug and &amp;</i> HP1431 HP0606 HP0630 HP1476 HP1165	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions collein tolerance-like protein (tolB) phage/collicin/tellurite resistance cluster tery' protein (misc) gensitivity (misc) gensitivity (misc) gensitivity (misc) gensitivity (misc) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative protein tetA(P), putative	70.2% 28.9% 33.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0%	HP1487 HP1509 HP1548 HP0138 HP0151 HP0575 HP1258 HP1492 HP0032 HP0035 HP0086 HP0094	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protein	23.8% 30.7% 34.3% 30.6% 41.2% 32.0% 32.0% 38.8% 38.8% 37.7% 28.2% 37.7% 28.7% 28.7% 28.7% 28.7% 28.7%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1171 HP1216 HP1286 HP1286 HP1464 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP10390 HP1193 HP10390 HP1193 HP10390	conserved hypothetical secreted protein definition of the protein secreted protei	29.4% 57.4% 42.9% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 61.1% 38.9% 35.5%
HP0967 HP1248 HP0885 <i>Collicin-rela</i> HP1126 HP0428 <i>Drug and &amp;</i> HP1431 HP0606 HP0630 HP1476 HP1165 <i>Transposo.</i> HP1008	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein terY protein virulence (kspA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative protein protein colicin tetracycline resistance protein tetA(P), putative 15200 insertion sequence from SARA17	70.2% 28.3% 36.0% 33.5% 25.7% 26.6% 35.5% 24.2% 62.3% 39.7%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0032 HP0032 HP0036 HP0094 HP0100	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein	23.8% 30.7% 34.3% 34.3% 32.0% 412% 32.0% 32.9% 48.2% 33.8% 23.2% 48.2% 37.0% 34.1% 28.7% 28.8%	HP0949 HP0970 HP1075 HP1075 HP11076 HP1117 HP1216 HP12186 HP1286 HP1484 HP1488 HP1551 UNKNOWN General HP0390 HP1193 HP0390 HP193 HP0390 HP0390 HP0390 HP0390	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacterioferritin comigratory protein (bcp) catalase-like protein	29.4% 57.4% 42.9% 42.9% 32.3% 31.9% 38.0% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9%
HP0967 HP1248 HP0885 Collicin-rela HP1126 HP0428 Drug and & HP1431 HP0606 HP0630 HP1476 HP1165 Transposo. HP1008 HP0414 HP0988	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery 'protein inalog sensitivity 16S rRNA (adenosine-N6,N6-) dimethyl-transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 15200 insertion sequence from SARA17 IS200 insertion sequence from SARA17 IS000 insertion sequence from SARA17	70.2% 28.9% 28.9% 35.5% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 39.9% 972.9%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP1492 HP0035 HP0035 HP0086 HP00086 HP0009 HP0100 HP0102	conserved hypothetical integral membrane protein conserved hypothetical inconserved hypothetical inconserved hypothetical inconserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein 4 conserved hypothetical protein conserved hypothet	23.8% 30.7% 34.3% 34.3% 34.5% 41.2% 32.0% 32.0% 38.8% 38.8% 38.8% 37.0% 34.1% 28.7% 29.8% 32.0% 29.3% 39.9%	HP0949 HP0977 HP0980 HP1075 HP1075 HP1117 HP1216 HP1286 HP1484 HP1488 HP1461 UNKNOWN General HP0390 HP1193 HP0872 HP0207 HP0136 HP1048	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkyphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacteriofertini comigratory protein (bcp) catalase-like protein	29.4% 57.4% 42.9% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 61.1% 38.9% 35.5%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and a HP1431 HP0606 HP0630 HP1476 HP1165 Transposo. HP1008 HP0988 HP09414 HP0988 HP0998	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein b (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions collicin tolierance-like protein (tolB) phage/collicin/tellulrite resistance cluster tery' protein (msiC) gensitivity (msiC) gensitivity (msiC) gensitivity (msiC) gensitivity (msiC) protein (mtrC) modulator of drug activity (mds66) phenylacylic acid decarboxylase tetracycline resistance protein tetA(P), putative msicro gensitivity (msiC) insertion sequence from SARA17 IS200 insertion sequenc	70.2% 28.9% 28.9% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0575 HP1258 HP0032 HP0032 HP0036 HP0094 HP0100 HP0102 HP01016	conserved hypothetical integral membrane protein conserved hypothetical inconsulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical pro	23.8% 30.7% 34.3% 30.6% 41.2% 32.0% 32.0% 38.8% 38.8% 38.8% 38.8% 38.9% 38.9% 38.9% 38.9% 38.9% 38.9% 39.7% 39.7% 39.7% 39.7%	HP0949 HP0977 HP0980 HP1075 HP10980 HP1075 HP11285 HP11285 HP1286 HP1286 HP1286 HP1484 HP1488 HP1551 UNKNOWN General HP0390 HP193 HP0390 HP193 HP0485 HP0485 HP0485 HP01485	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacterioferritin comigratory protein (bcp) catalase-like protein	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 37.5% 27.4% 42.7% 38.3% 42.7% 38.3% 46.6% 61.1% 38.9% 35.5% 30.8%
HP0967 HP10885 Collicin-related HP1126 HP1126 HP0431 HP0606 HP0630 HP1476 HP1058 HP1008 HP1008 HP008 HP00988 HP00988 HP09988 HP09988 HP09988	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery 'protein unalog sensitivity 16S r/tNA (adenosine-N6,N6)-dimethyl-transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 1S200 insertion sequence from SARA17 IS00 insertion sequence from SARA17 IS00 insertion sequence from SARA17 IS00 transposase (tnpA) IS00 transposase (tnpA) IS00 transposase (tnpA)	70.2% 28.9% 28.9% 35.6% 25.7% 25.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 97.2% 97.2% 97.2%	HP1487 HP1509 HP1548 HP0138 HP0138 HP0438 HP0451 HP0675 HP1258 HP1492 HP0032 HP0035 HP0008 HP0009 HP0100 HP0100 HP0100 HP0100 HP0100 HP0100 HP0105	conserved hypothetical integral membrane protein conserved hypothetical iron-sulfur protein conserved hypothetical ipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitU-like protein conserved hypothetical	23.8% 30.7% 34.3% 34.3% 34.5% 32.0% 32.0% 32.0% 23.2% 48.2% 38.8% 37.0% 38.9% 23.2% 43.2% 37.9% 38.9% 37.9% 38.9% 37.9% 38.9% 37.9% 38.9% 37.9% 38.9%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1286 HP1285 HP1484 HP1551 UNKNOWN General HP0390 HP193 HP0485 HP0485 HP0485 HP0485 HP10486 HP0485 HP10981 HP0981	conserved hypothetical secreted protein secreted protein hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein secreted hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein (activation of the hypothetical secreted protein (hypothetical secreted hypothetical sec	29,4% 57,4% 42,9% 27,0% 32,3% 31,9% 38,5% 38,5% 42,7% 38,3% 42,7% 38,3% 46,6% 61,1% 38,9% 35,5% 30,8% 44,0% 42,5% 42,5%
HP0967 HP1248 HP0885 Collicin-rela HP1426 HP0428 Drug and e HP1431 HP0606 HP1476 HP1476 HP1088 HP0414 HP0988 HP0988 HP0998 HP0998 HP0998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998 HP1998	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery' protein virulence sensitivity 168 rfNA( adenosine-N6,N6-)-dimethyl-transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 15200 insertion sequence from SARA17 15200 15200 15200 15200 15200 15200 15200 15200 15200 15200 15200 15200 15200 15200 15200	70.2% 28.9% 28.9% 36.0% 33.5% 25.7% 25.6% 36.0% 37.7% 27.0% 37.2% 39.7% 37.2% 97.2% 97.2% 97.2% 97.2%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0151 HP0258 HP1492 HP0032 HP0032 HP0032 HP00032 HP0006	conserved hypothetical integral membrane protein conserved hypothetical inconsulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical pro	23.8% 30.7% 34.3% 34.3% 32.0% 32.0% 32.0% 38.8% 23.2% 48.2% 37.0% 34.1% 28.7% 28.8% 37.9% 39.9% 39.9% 30.9% 30.9% 30.9%	HP0949 HP0977 HP0980 HP1075 HP1088 HP1117 HP1268 HP1268 HP1464 HP1488 HP1464 HP1488 HP1481 HP0390 HP1193 HP0372 HP0372 HP0390 HP1193 HP0485 HP1484 HP0486 HP1484 HP0486 HP1044 HP1048 HP1048 HP1048 HP1048 HP1048 HP1048 HP1048	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkyphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacteriofertini comigratory protein (bcp) catalase-like protein (sceA) GTP-binding protein (tgb1) GTP-binding protein (tgb1) GTP-binding protein (tog)	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 42.5% 44.0% 42.5%
HP0967 HP1248 HP0885 Colicin-rela HP0428 Drug and & HP0431 HP0680 HP1476 HP1068 HP165 Transposo. HP1008 HP0414 HP0988 HP014 HP0988 HP1096 HP1056 HP10	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions collicin tolierance-like protein (tolB) phage/collicin/tellurife resistance cluster tery 'protein (TSB; RTNA (adenosine-N6,N6-)-dimethyl-transferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions (15200 insertion sequence from SARA17 (1500 fransposase (tnpA) (1500 fransposase (tnpB)	70.2% 28.9% 36.0% 36.0% 33.5% 25.7% 25.6% 36.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4%	HP1487 HP1509 HP1548 HP0138 HP01438 HP0151 HP0258 HP1492 HP0035 HP0035 HP0040 HP0004 HP0100 HP01016 HP01016 HP01016 HP01016 HP01016 HP010233 HP0233	conserved hypothetical integral membrane protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protein con	23.896 30.796 34.396 30.696 41.296 32.096 21.896 38.896 23.296 48.296 34.196 34.196 32.096 33.996 33.996 33.996 30.796	HP0949 HP0977 HP0980 HP1075 HP1088 HP1117 HP1216 HP1286 HP1484 HP1488 HP1486 HP1484 HP1488 HP1561 UNKNOWN General HP0390 HP0390 HP0390 HP0490	conserved hypothetical secreted protein hypothetical secreted protein hypothetical secreted protein hypothetical secreted protein aldyphosphonate uptake protein (phnA) ATP-binding protein comigratory protein (bcp) catalase-like protein comigratory protein comigratory protein comigratory protein comigratory protein comigratory protein comigratory pr	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8% 42.7% 38.3% 46.6% 61.1% 38.9% 33.5% 44.0% 42.5% 44.0% 42.5% 44.0% 42.5% 44.0% 42.5% 44.0% 42.5% 44.0% 42.5% 44.0%
HP0967 HP1248 HP0885 Collicin-rela HP1426 HP0428 Drug and e HP1431 HP0606 HP1476 HP1476 HP1087 HP0414 HP0988 HP0988 HP0998 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098 HP1098	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery' protein (malog sensitivity) 185 rtNA (adenosine-N6,N6-)-dimethyl-transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative nortein sequence from SARA17 18200 insertion sequence from SARA17 18200 insertion sequence from SARA17 18200 transposase (tnpA) 18305 transposase (tnpB)	70.2% 28.9% 28.9% 36.0% 33.5% 25.7% 26.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 37.2% 97.2% 97.2% 97.2% 97.2% 93.4%	HP1487 HP1509 HP1548 HP0138 HP01438 HP0151 HP0256 HP1258 HP1032 HP0032 HP0032 HP0006 HP0094 HP0100 HP0100 HP0102 HP0105 HP0105 HP0105 HP0105 HP0105 HP0106 HP0107 HP0106 HP0107 HP0108	conserved hypothetical integral membrane protein conserved hypothetical intermediate inconserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical	23.8% 30.7% 34.3% 34.3% 34.3% 32.0% 32.0% 32.0% 38.8% 38.8% 23.2% 48.2% 37.0% 34.1% 528.7% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 33.9% 30.7% 33.9%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1286 HP1286 HP1286 HP1484 HP1484 HP1484 HP1487 HP0390 HP	conserved hypothetical secreted protein safekping protein conserved hypothetical secreted protein safekping protein (mpr) sacterioferritin comigratory protein (bcp) catalase-like protein (mpr) sacterioferritin comigratory protein (bcp) catalase-like protein (mpr) sacterioferritin comigratory protein (xseA) GTP-binding protein (tpt) GTP-binding protein hypothetical secreted protein (gtp1) GTP-binding protein hypothetical secreted gtp2) GTP-binding protein hypothetical secreted gtp2) GTP-binding protein hypothetical secreted gtp2) GTP-binding gtp3	29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 42.7% 42.7% 38.3% 42.7% 38.3% 42.7% 38.9% 42.5% 44.0% 35.5% 30.8% 44.1% 44.1% 42.5% 48.1% 48.2% 54.1% 54.1%
HP0967 HP1248 HP0885 Colicin-rela HP1426 HP0428 Drug and e HP1451 HP0606 HP1476 HP1476 HP1087 HP0988 HP0414 HP0988 HP0988 HP0988 HP1098 HP1098 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10987 HP10988	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery' protein (msic) gensitivity 16S rRNA (adenosine-N6,N6-)-dimethyl-transferase (ksgA) membriane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative protein sequence from SARA17 ISB05 transposase (mpA) ISB05 transposase (mpB)	70.2% 28.9% 28.9% 36.0% 33.5% 25.7% 26.6% 35.5% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 33.9% 37.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0161 HP0575 HP1258 HP0032 HP0032 HP0036 HP00094 HP0100 HP0100 HP01017 HP0106 HP0107 HP0108 HP0216 HP0216 HP0216 HP0228 HP0238 HP0238	conserved hypothetical integral membrane protein conserved hypothetical lipoprotein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protein con	23.8% 30.7% 34.3% 34.3% 34.3% 32.0% 32.0% 32.0% 38.8% 38.8% 23.2% 48.2% 37.0% 34.1% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 32.9% 33.9% 30.5% 30.5% 30.5% 30.5% 30.5%	HP0949 HP0977 HP0980 HP1075 HP1088 HP1107 HP1216 HP1296 HP1296 HP1296 HP1488 HP1488 HP1551 UNKNOWN General HP0390 HP1093 HP0372 HP0390 HP0490	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkyphosphonate uptake protein (phnA) ATP-binding protein comigratory protein (bcp) catalase-like protein comigratory protein (bcp) catalase-like protein comigratory protein (bcp) catalase-like protein (gtp1) GTP-binding protein homologue (yphC) GTP-binding protein, fusA-homolog (yihK) lipase-like protein	29,4% 57,4% 42,9% 42,9% 27,0% 32,3% 31,9% 31,9% 32,3% 42,7% 42,7% 38,3% 46,6% 611% 38,9% 42,5% 30,8% 44,5% 44,5% 44,5% 44,5% 44,5% 44,5% 54,1% 5
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and 6 HP0431 HP0606 HP1431 HP0606 HP1635 HP108 HP014 HP0948 HP0944 HP0948 HP0949 HP1635 HP1635 HP1635 HP1635 HP1635 HP1636 H	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions collicin tolerance-like protein (tolB) phage/collicin/tellulrife resistance cluster tery protein ratio gensitivily ransferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 1500 fransposase (tnpA) 15005 transposase (tnpB)	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 25.6% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 93.4% 93.4% 93.4% 93.4%	HP1487 HP1509 HP1548 HP1438 HP1438 HP0151 HP0258 HP1492 HP0035 HP0035 HP0094 HP0102 HP0102 HP0102 HP0104 HP0104 HP0105 HP0105 HP0105 HP0105 HP0107 HP0106 HP0107 HP0106 HP0107 HP0106 HP0107 HP0107 HP0107 HP0108 HP0107 HP0108 HP0107 HP0108 HP0109 HP0210	conserved hypothetical integral membrane protein conserved hypothetical inconsulfur protein conserved hypothetical inconsulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protein c	23,8% 30,7% 30,7% 31,3% 31,3% 33,7% 31,3% 33,7% 34,5% 31,5%	HP0949 HP0977 HP0980 HP1075 HP1088 HP1075 HP1216 HP1286 HP1286 HP1488 HP1488 HP1488 HP1561 WINKNOWN General HP0390 HP1093 HP0872 HP0486 HP1044 HP0303 HP0881 HP0881 HP0883 HP0884 HP088 HP0884	conserved hypothetical secreted protein Adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkyphosphonate uptake protein (phnA) ATP-binding protein comigratory protein (bcp) catalase-like protein comigratory protein (bcp) catalase-like protein comigratory protein (bcp) catalase-like protein (phnA) ATP-binding protein homologue (yphC) GTP-binding protein homologue (yphC) GTP-binding protein, fusA-homolog (yihK) lipase-like protein ilfU-like protein ilfU-like protein ilfU-like protein infU-like protein ilfU-like protein	29.4% 57.4% 42.9% 42.9% 32.3% 31.9% 31.9% 31.9% 32.5% 42.7% 42.7% 46.6% 46.6% 40.8%
HP0967 HP1248 HP0885 Collain-rela HP1426 HP0428 Drug and a HP1431 HP0606 HP1476 HP1050 HP1476 HP1050 HP1098 HP0414 HP0988 HP0988 HP0988 HP1098	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster tery' protein railog sensitivity 165 rRNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative resistance protein retA(P), putative 15200 insertion sequence from SARA17	70.2% 28.9% 28.9% 36.0% 33.5% 25.7% 26.6% 35.5% 36.2% 39.7% 37.7% 33.9% 33.9% 33.9% 97.2%	HP1487 HP1509 HP1548 HP0138 HP1438 HP0131 HP0575 HP1258 HP0022 HP0032 HP0032 HP0004 HP0100 HP01007 HP0107 HP0107 HP0107 HP0108 HP0107 HP0108 HP0108 HP0109	conserved hypothetical integral membrane protein conserved hypothetical interprotein conserved hypothetical membrane protein conserved hypothetical mitchondrial protein 4 conserved hypothetical protein conserved hypothet	23.8% 30.7% 34.3% 34.3% 34.3% 32.9% 32.9% 32.9% 38.8% 38.8% 32.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216 HP1286 HP1286 HP1286 HP1286 HP1286 HP1488 HP1488 HP1488 HP1488 HP1488 HP0807 HP0303 HP0807 HP0186 HP	conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacterioferatin comigratory protein (bcp) catalase-like protein (champy-lacicon) dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (dbg) GTP-binding protein hypothetical secreted protein (yink) lipsae-like protein nilf-sike protein nilf-sike protein pts protein (pls)	29, 4% bd. 42, 9% 27,0% bd. 29, 9% bd. 29, 9% bd. 27,0% bd. 29, 9% bd. 27,0%
HP0967 HP1248 HP0885 Colicin-rela HP1126 HP0428 Drug and 6 HP0431 HP0606 HP1431 HP0606 HP1635 HP108 HP014 HP0948 HP0944 HP0948 HP0949 HP1635 HP1635 HP1635 HP1635 HP1635 HP1636 H	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions collicin tolerance-like protein (tolB) phage/collicin/tellulrife resistance cluster tery protein ratio gensitivily ransferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-related functions 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 1500 fransposase (tnpA) 15005 transposase (tnpB)	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 25.6% 24.2% 62.3% 39.7% 27.0% 33.9% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 93.4% 93.4% 93.4% 93.4%	HP1487 HP1509 HP1548 HP1438 HP1438 HP0151 HP0258 HP1492 HP0035 HP0035 HP0094 HP0102 HP0102 HP0102 HP0104 HP0104 HP0105 HP0105 HP0105 HP0105 HP0107 HP0106 HP0107 HP0106 HP0107 HP0106 HP0107 HP0107 HP0107 HP0108 HP0107 HP0108 HP0107 HP0108 HP0109 HP0210	conserved hypothetical integral membrane protein conserved hypothetical inconsulfur protein conserved hypothetical inconsulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protein c	23,8% 30,7% 32,8% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 32,9% 33,9% 30,5% 30,5% 30,5% 30,5% 30,5% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3% 31,3%	HP0949 HP0977 HP0980 HP1075 HP1088 HP1177 HP1216 HP1286 HP1288 HP1286 HP1288 HP1484 HP1488 HP1561 WINKNOWN HP1488 HP1561 HP1030 HP0303 HP0372 HP0303 HP0372 HP0303 HP0487 HP0486 HP1048 HP0486 HP1048 HP0486 HP1048 HP0486 HP1048 HP0486	conserved hypothetical secreted protein Adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkyphosphonate uptake protein (phnA) ATP-binding protein comigratory protein (bcp) catalisae-like protein comigratory protein (bcp) catalisae-like protein dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein hormologue (yphC) GTP-binding protein, fusA-homolog (yihK) lipase-like protein hymothic protein (phs protein (phs pottein (phs phs pottein (phs pottein (phs pottein (phs pottein (phs pottein (phs phs pottein (phs phs pottein (phs phs pottein (phs phs pottein (phs pottein (phs phs phs pottein (phs phs phs pottein (phs phs phs phs phs phs phs phs phs phs	29.4% 42.9% 42.9% 42.9% 42.9% 42.9% 42.9% 42.9% 31.9% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 42.7% 43.2% 42.7% 43.2%
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HP0967 HP1248 HP0885 Collcin-rela HP1126 HP0428 Drug and & HP1431 HP0606 HP1476 HP1476 HP1476 HP1088 HP0414 HP0988 HP0998 HP0998 HP0998 HP1096 HP1535 HP0417 HP0988 HP088	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein bromolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellunfe resistance cluster tery' protein (Tellunfe resistance protein (mtrC) modulator of drug activity (mda66) phenylacylic acid decarboxylase tetracycline resistance protein tetA[P), putative mrelated functions (S200 insertion sequence from SARA17 (S205 transposase (tnpA) (S805 transposase (tnpA) (S805 transposase (tnpA) (S805 transposase (tnpA) (S805 transposase (tnpB) (S805 t	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 24.2% 62.3% 39.7% 27.0% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.5% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.4% 97.5%	HP1487 HP1509 HP1548 HP1438 HP1438 HP0151 HP1258 HP1492 HP0035 HP0035 HP0036 HP0094 HP0102 HP0102 HP0104 HP0104 HP0104 HP0105 HP0107 HP0107 HP0108 HP0108 HP0108 HP01094 HP0216 HP0216 HP0216 HP0238 HP0238 HP0238 HP0338 HP0338 HP0338 HP0338	conserved hypothetical integral membrane protein conserved hypothetical inconsulfur protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical pro	23,896 30,796 34,396 30,696 41,296 32,096 31,396 38,896 21,896 32,296 48,296 37,796 34,196 28,876 29,876 30,976 30	HP0949 HP0977 HP0980 HP1075 HP1088 HP1177 HP1216 HP1286 HP1286 HP1288 HP1484 HP1488 HP1481 HP1488 HP1581 HP0390 HP0390 HP0390 HP0390 HP0390 HP0391 HP0391 HP0490 HP	conserved hypothetical secreted protein adheping hypothetical secreted protein conserved hypothetical secreted protein altiviphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacteriofertini comigratory protein (bcp) catalisae-like protein comigratory protein (bcp) catalisae-like protein (gtp1) GTP-binding protein hypothetin (yseA) GTP-binding protein hypothetin (yseA) GTP-binding protein hypothetin hypothetin hypothetin (yseA) GTP-binding protein hypothetin hypotheti	29.4% 42.9% 42.9% 42.9% 42.9% 42.9% 42.9% 42.9% 42.9% 31.9% 42.9% 31.9% 42.7% 42.9% 42.7%
HP0987 HP1248 HP0885 Collicin-rela HP1428 HP0428 Drug and a HP1431 HP0606 HP1476 HP1030 HP1476 HP1008 HP100	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein bromolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellunfe resistance cluster tery' protein (Tellunfe resistance protein (mtrC) modulator of drug activity (mda66) phenylacylic acid decarboxylase tetracycline resistance protein tetA[P), putative mrelated functions (S200 insertion sequence from SARA17 (S205 transposase (tnpA) (S805 transposase (tnpA) (S805 transposase (tnpA) (S805 transposase (tnpA) (S805 transposase (tnpB) (S805 t	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 24.2% 62.3% 39.7% 27.0% 33.9% 97.2%	HP1487 HP1509 HP1548 HP1438 HP1438 HP1438 HP16575 HP1258 HP1492 HP0035 HP0035 HP0036 HP0010 HP0102 HP0102 HP01017 HP0102 HP0104 HP0107 HP0107 HP0108 HP0107 HP0108 HP0107 HP0108 HP0107 HP0108 HP0107 HP0108 HP0108 HP0108 HP0109	conserved hypothetical integral membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical protei	23,8% 30,7% 31,3% 32,0% 33,0% 31,3% 31,3% 33,0% 31,3% 31,3% 31,3% 33,0% 31,3% 31,3% 33,0% 31,3% 31,3% 33,0% 31,3%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1175 HP1098 HP1181 HP1216 HP1286 HP1286 HP1286 HP1288 HP1288 HP1288 HP1488 HP1488 HP1481 HP0481 HP0307 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0080	conserved hypothetical secreted protein development of the hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacteriofertini comigratory protein (bcp) catalase-like protein (mpr) bacteriofertini comigratory protein (bcp) catalase-like protein (gbt) GTP-binding protein (gbt) GTP-binding protein homologue (yphC) GTP-binding protein homologue (yphC) GTP-binding protein homologue (yphC) HiU-like protein protein (gbs) protein (pfs) protein phosphatase 2C homolog (ptc1) solute-binding signature and mitochondrial	29.4% 44.29% 42.9% 31.9% 31.9% 31.9% 31.9% 31.9% 31.9% 31.9% 42.7% 32.274% 42.9% 42.7% 42.7% 42.7% 32.7% 35.5% 30.7% 35.5% 30.7% 35.5% 30.7% 36.7% 36.7% 36.7% 36.7% 36.7% 36.7% 36.7% 36.7% 37.3% 36.7% 37.3% 36.7% 37.3% 37.3% 37.3% 36.7% 37.3% 37.
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HP0967 HP1248 HP0885 Colicin-rela HP1128 HP0428 HP1431 HP06050 HP1431 HP06050 HP1476 HP1605 HP1605 HP1608 HP0184 HP0988 HP0184 HP0988 HP0186 HP1635 HP0437 HP0989 HP0998 HP0999 HP1634 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0437 HP0438 HP0437 HP0438 H	virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein D (vapD) virulence associated profein homolog (vacB) virulence factor mviN protein (mviN) ted functions collicin tolierance-like protein (tolB) phage/collicin/tellulrife resistance cluster tery' protein ratiog sensitivity ransferase (ksqA) membrane fusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative r-related functions 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15200 fransposase (tnpA) 15605 transposase (tnpB)	70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 36.5% 24.2% 62.3% 39.7% 62.3% 39.7% 33.9% 97.2% 97.2% 97.2% 97.2% 97.2% 97.4% 93.5% 93.4%	HP1487 HP1509 HP1548 HP1438 HP1438 HP1438 HP1057 HP1258 HP1492 HP0035 HP0035 HP0036 HP0010 HP0100 HP0100 HP0100 HP0100 HP0100 HP0100 HP0100 HP0100 HP0107 HP0107 HP0108 HP0107 HP0108 HP0107 HP0108 HP0108 HP0109	conserved hypothetical integral membrane protein conserved hypothetical membrane protein conserved hypothetical membrane protein conserved hypothetical mitochondrial protein conserved hypothetical protein conserved hypot	23,8% 30,7% 32,0%	HP0949 HP0977 HP0980 HP1075 HP1098 HP1175 HP1098 HP1181 HP1216 HP1286 HP1286 HP1286 HP1288 HP1288 HP1288 HP1488 HP1488 HP1481 HP0481 HP0307 HP0190 HP0190 HP0190 HP0190 HP0190 HP0190 HP0080	conserved hypothetical secreted protein protein hypothetical secreted protein conserved hypothetical secreted protein conserved hypothetical secreted protein adhesin-thiol peroxidase (tagD) aldo-keto reductase, putative alkylphosphonate uptake protein (phnA) ATP-binding protein (mpr) bacteriofertini comigratory protein (bcp) catalase-like protein cinamyi-alcohol dehydrogenase ELI3-2 (cad) exonuclease VII-like protein (xseA) GTP-binding protein (dpt) GTP-binding protein homologue (yphC) GTP-binding protein (usA-homolog (yihk) lipase-like protein nitU-like protein protein (sps) protein (pfs) protein phosphatase 2C homolog (ptc1) solute-binding signature and mitochondrial signature protein (dsbC), individual difficial redenage protein (dsbC),	29.4% 44.29% 42.97% 42.97% 42.97% 42.97% 42.97% 42.97% 42.97% 42.97% 42.97% 42.97% 42.97% 43.97% 46.69% 46.
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