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Acknowledgements. We thank the ESRF and SRS Daresbury for data collection facilities; the EMBL outstation, Grenoble, for use of an image plate detector; M.L.D. Page for expert advice; R. Bryan and R. Esnouf for computing; K. Harlos for help with in-house data collection; F. Armstrong and J. Hirst for providing electrochemically reduced methyl viologen. This work was supported by MRC, BBSRC and EU-BIOTECH. The Oxford Centre for Molecular Sciences is funded jointly by BBSRC, EPSRC and MRC. N.E.W.S. was supported by a Wellcome Trust prize studentship. V.F. is a Royal Society university research fellow.

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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 C₁₂₀

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 KC₆₀ and RbC₆₀.

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. KarpI, 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 discovery¹ 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 regimens².

Helicobacter pylori is a micro-aerophilic, Gram-negative, slowgrowing, spiral-shaped and flagellated organism. Its most characteristic enzyme is a potent multisubunit urease³ 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 colonize². H. pylori is probably the most common chronic bacterial infection of humans, present in almost half of the world population². 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 lymphomas². Disease outcome depends on many factors, including bacterial genotype, and host physiology, genotype and dietary habits^{4,5}. *H. pylori* infection has also been associated with persistent diarrhoea and increased susceptibility to other infectious diseases⁶.

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 23S-5S 23S-5S 16S 16S 5S	Coordinates 445,306-448,642 bp 1,473,557-1,473,919 bp 1,209,082-1,207,584 bp 1,511,138-1,512,635 bp 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	Associated genes IS605, 5SRNA and repeat 7; virB4 cag PAI (Fig. 4) IS605, 5SRNA and repeat 7 β and β' RNA polymerase, EF-G (fusA) two restriction/modification systems
Coding sequences 1,590 coding sequences (average 945 bp) 1,091 identified database match 499 no database match)

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

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*¹⁰. Another region is the *cag* pathogenicity island (PAI), which is flanked by 31-bp direct repeats, and appears to be the product of lateral transfer¹¹.

RNA and repeat elements. Thirty-six tRNA species were identified using tRNAscan-SE¹². 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^{11,13} 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 identified¹⁴, we arbitrarily designated basepair one at the start of a 7-mer repeat, (AGTGATT)₂₆, 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 Riley¹⁵ (Table 2). The 1,590 predicted genes had an average size of 945 bp, similar to that observed in other prokaryotes^{7–9}, 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 ~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 complex¹⁶. 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 island¹¹ and the other is the flagellar export pathway which is assembled from orthologues of FliH, FliI, FliP, FlhA, FlhB, FliQ, FliR and FliP¹⁷. 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 structures¹⁸ and assembly of surface structures involved in virulence and DNA transformation¹⁹.

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 recombination²⁰, 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 **p** location of each predicted protein-coding region, RNA gene, and repeat elements in the genome. Symbols are as follows: ++, Co^{2+} , Zn^{2+} , Cd^{2+} ; ?, 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, L-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 TopPred⁴⁷.

endonuclease, *iceA1*, and its associated DNA adenine methyltransferase (M. HypI) genes^{21,22}. 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 volcanii²² and may also operate in H. pylori. Most intriguing, however, is the finding that in *H. pylori* the genes encoding the β 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 cells⁵. One of them, HpaA (HP0797), was previously identified as a lipoprotein in the flagellar sheath and outer membrane^{5,23}. 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^{24–26}, one of which mediates attachment to the Lewis^b 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*²⁷.

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^{28,29}. 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.



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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 alignment⁵⁰. The most likely

e first 20-residue Nto strain variability. The program Signal-P48 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).

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critical interactions with their hosts²⁸. Such 'contingency' genes encode surface structures like pilins, lipoproteins or enzymes that produce lipopolysaccharide molecules²⁸. 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 regions²⁹. 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)⁵. 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^{11,30}. Consistent with its more virulent character, *H. pylori* strain 26695 contains a single contiguous PAI region¹¹ (Fig. 4).

VacA induces the formation of acidic vacuoles in host epithelial cells, and its presence is associated epidemiologically with tissue damage and disease³¹. 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*⁵. Sequence differences at the amino terminus and central sections are noted among VacA proteins derived from Tox⁺ and Tox⁻ strains³¹. This Tox⁺ *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, cag/ and cag/l. 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 suggestion¹¹. 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)⁴⁷. 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.

cytotoxin ($\sim 26-31\%$) (Fig. 5). However, they lack the pairedcysteine residues and the cleavage site required for release of the VacA toxin from the bacterial membrane³¹ (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* pathogenesis³². The LPS of *H. pylori* is several orders of magnitude less immunogenic than that of enteric bacteria³³ and the O antigen of many *H. pylori* isolates is known to mimic the human Lewis^x and Lewis^y blood group antigen³². Genes for synthesis of the lipid A molecule, the core region, and the O antigen were identified. Two genes with low similarity to fucosyl-transferases (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 host⁵. 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. coli³⁴, 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 bacterioferritin³⁴, and Pfr, a non-haem cytoplasmic iron-containing ferritin used for storage of iron³⁵. 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 colonization³⁶. 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 regulon⁵.

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 potential³⁷ and subsequently to modify its microenvironment through the action of urease and the release of factors that inhibit acid production by parietal cells⁵. A switch in membrane polarity provides an electrical barrier that prevents the entry of protons (H⁺). 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 cytoplasm³⁸, this idea is not supported by the identified transporter

Table 3 Hon	nopolymeric tracts and d	inucleotide r	epeats in <i>H. pylori</i>					
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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^{2+} supply, an essential component of urease activity³⁹. 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 response⁴⁰. 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 characteristc of Gramnegative bacteria. Colours correspond to transport role categories defined by Riley¹⁵: 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 HPO₄²⁻ (HI1604), NO₃²⁻ (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 (gInHMPQ), 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 (Ni²⁺ for urease activation), corA (Mg²⁺ for phosphohydrolases, phosphotransferases, ATPases) and feoB (Fe²⁺

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 Ni²⁺-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, D-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.

proteins, sensor-regulator pairs and other proteins may be acid-induced.

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*⁷. 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 organisms⁴¹. 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 α 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^{41,42}.

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) homologues.

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^{5,21,31}. The extent of molecular mimicry between *H. pylori* and its human host, an underappreciated topic, can now be fully explored⁴³. 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*⁷, *Mycoplasma genitalium*⁸, and *Methanococcus jannaschii*⁹. Ninety-two per cent of the genome was covered by at least one λ 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 GeneMark⁴⁵ 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 described⁹. ORFs were also analysed using 175 hidden Markov models constructed for a number of conserved protein families (pfam v1.0) using hmmer⁴³. In addition, all ORFs were searched against the prosite motif database using MacPattern⁴⁶. 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 TopPred⁴⁷ was used to identify membranespanning 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 bacteria⁴⁸. 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 EcoCyc⁴⁹.

Received 16 May; accepted 1 July 1997.

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Acknowledgements. D.E.B., M.B. and W.H. are supported by grants from the NIH; P.K. is supported by a grant from the National Center for Research Resources. We thank N. S. Akopyants for preparing high quality chromosomal DNA from *H. pylori* strain 26695; M. Heaney, J. Scott, A. Saeed and R. Shirley for software and database support; and V. Sapiro, B. Vincent, J. Mechan and D. Mass for computer system support.

Correspondence and requests for materials should be addressed to J.-F.T. (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.

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 identifies.

AMINO-ACI	D BIOSYNTHESIS	
General	hydentoin utilization protein A (hyuA)	28.6%
Aromatic an	nino-acid family	20.0 /0
HP1038	3-dehydroquinase type II (aroQ)	99.4%
HP0283 HP0134	3-dehydroquinate synthase (aroB) 3-deoxy-D-arabino-heptulosonate	38.1%
	7-phosphate synthase (dhs1)	54.6%
HP0401	3-phosphoshikimate	E2 60%
HP1279	anthranilate isomerase (trpC)	47.0%
HP1282	anthranilate synthase component I (trpE)	47.9%
HP1280 HP1281	anthranilate synthase component II (trpD) anthranilate synthase component II (trpD)	42.5%
HP0663	chorismate synthase (aroC)	47.2%
HP1380	prephenate dehydrogenase (tyrA)	30.2%
HP0157	shikimic acid kinase I (aroK)	36.1%
HP1277	tryptophan synthase, alpha subunit (trpA)	46.5%
HP1278	tryptophan synthase, beta subunit (trpB)	66.1%
Aspartate ra HP0649	aspartate ammonia-lvase (aspA)	55.5%
HP1189	aspartate-semialdehyde dehydrogenase	
HP1220	(asd) aspartokinase (lvsC) 48.0%	45.7%
HP0106	cystathionine gamma-synthase (metB)	47.7%
HP0290	diaminopimelate decarboxylase	
HP0566	(dap decarboxylase) (lysA) diaminonimelate enimerase (danE)	42.7%
HP0510	dihydrodipicolinate reductase (dapl)	95.3%
HP1013	dihydrodipicolinate synthetase (dapA)	39.5%
HP1050	homoserine kinase (thrB)	27.7%
HP0672	solute-binding signature and mitochondrial	
HP0212	signature protein (aspB)	47.3%
TH OLIE	(dapE)	42.3%
HP0626	tetrahydrodipicolinate N-succinyltransferase	26.104
HP0098	threonine synthase (thrC)	32.9%
Glutamate fa	amily	
HP0380	glutamate dehydrogenase (gdhA)	59.0%
HP0512 HP1158	glutamine synthetase (glnA)	48.6% 28.0%
Pvruvate far	nilv	20.5 /0
HP0941	alanine racemase, biosynthetic (alr)	32.4%
HP1468	branched-chain-amino-acid	62 506
HP0330	ketol-acid reductoisomerase (ilvC)	48.1%
Serine famil	y	
HP0107	cysteine synthetase (cysK)	45.7%
HP0096	phosphoglycerate dehydrogenase (serA)	32.5%
HP0736	phosphoserine aminotransferase (serC)	30.7%
HP0652 HP1210	phosphoserine phosphatase (serB)	36.5%
HP0183	serine hydroxymethyltransferase (glyA)	54.0%
		~
AND CARRI	ERS	э,
General		
<i>General</i> HP0220	synthesis of [Fe-S] cluster (nifS)	48.0%
General HP0220 Biotin HP0598	synthesis of [Fe-S] cluster (nifS)	48.0%
General HP0220 Biotin HP0598 HP0976	synthesis of [Fe-S] cluster (nifS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa	48.0% 34.9% te
General HP0220 Biotin HP0598 HP0976	synthesis of [Fe-S] cluster (nifS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoa aminotransferase (bioA)	48.0% 34.9% te 49.2%
General HP0220 Biotin HP0598 HP0976 HP1140	synthesis of [Fe-S] cluster (nifS) 8-aminor-7-oxononanoate synthase (bioF) adenosylmethionine-8-aminor-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenzy A carboxvase synthetase (birA)	48.0% 34.9% te 49.2% yme 36.9%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenzy A carboxylase synthetase (birA) biotin sulfoxide reductase (bisC)	48.0% 34.9% te 49.2% /me 36.9% 42.7%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotion operon repressor/biotin acetyl ocenzy A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC)	48.0% 34.9% te 49.2% yme 36.9% 42.7% 32.1% 26.2%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP029	synthesis of [Fe-S] cluster (nifS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenzy A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin Synthesise (bioD)	48.0% 34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP1406 HP0029 Folic acid	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operona prepresor/biotin acetyl coency A carboxylase synthetase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin synthetase (bioD)	48.0% 34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP1029 Folic acid HP1036	synthesis of [Fe-S] cluster (nifS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operator repressor/biotin acetyl coenzy A carboxylase synthetase (bioA) biotin suffixet reductase (bioC) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin synthetase (bioD) 7, 8-dinydro-6-hydroxymethylpterin-	48.0% 34.9% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP029 Folic acid HP1036 HP0587	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (bioA) biotin synthetase (bioC) biotin synthetase (bioC) biotin synthetase (bioD) 7, 8-ditlydro-6-hydroxymethylpterin- pyrophosphokinase (foIK) aminodegwrchorismate (vase (babC)	48.0% a4.9% te 49.2% me 36.9% 42.7% 32.1% 36.2% 3
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029 Folic acid HP1036 HP1036	synthesis of [Fe-S] cluster (nifS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operin ergressor/biotin acetyl ocenzy A carboxylase synthetase (biA) biotin synthetase (biA) biotin synthetase (biOB) dethiobiotin synthetase (biOD) 7, 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (foIK) aminodeoxychorismate lyase (pabC) dihydropterae synthase (foIP)	48.0% 34.9% te 49.2% me 36.9% 32.1% 36.2% 36.2% 36.0% 34.6% 34.6% 34.5%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029 Folic acid HP1036 HP1036 HP1232 HP1545 HP7038	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenz A carboxylase synthetase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin synthetase (bioD) 7.8-dihydro-6-hydroxymethytperin- pyrophosphotase (foIR) aminodeoxychorismate lyase (pabC) dihydropterate synthase (foIP) folypodyutamate synthase (foIC)	48.0% 34.9% te 49.2% me 36.9% 32.1% 36.2% 36.0% 34.6% 32.4% 34.5% 32.4% 34.5% 35.2%
General HP0220 Biotin HP0598 HP0976 HP1140 HP0407 HP1254 HP1406 HP0029 Folic acid HP10587 HP1545 HP0587 HP1545 HP0587 HP1545	synthesis of [Fe-S] cluster (nifS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (bioA) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioB) aminodexyr/onsimate lyase (pabC) dihydropteroate synthase (foIC) GTP cyclohydrolase 1 (foIE) methylen-eterahydrofolate dehydrogenase	48.0% 48.0% te 49.2% yme 36.9% 42.7% 32.1% 36.2% 36.0% 34.6% 32.4% 32.4% 32.5% 50.9%
General HP0220 Biotin HP0598 HP0976 HP1400 HP1404 HP1404 HP1406 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0587 HP1545 HP0587 HP1545 HP0587	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioD) 7, 8-ditlydro-6-hydroxymethylpterin- pyrophosphokinase (foIC) alminodegwychorismate lyase (pabC) ditlydropteroate synthase (foIC) GP cyclohydrolase I (foIC) methylene-terlahydrofolate dehydrogenase (foID)	48.0% 34.9% te 49.2% me 36.9% 42.7% 36.2% 36.2% 36.2% 36.2% 36.2% 36.2% 36.2% 32.4% 32.4% 32.4% 32.4% 32.4% 50.9% 48.4%
General HP0220 Biotin HP0588 HP0976 HP140 HP1404 HP1404 HP1406 HP0299 Folic acid HP1036 HP0587 HP132 HP1545 HP0928 HP0577 HP0928	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin operon repressor/biotin acetyl coency A carboxylase synthetase (bicA) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7.8-dillydro-8-hydroxymethylpterin- pyrophosphotinase (bioB) aminodeoxychorismate lyase (pabC) dihydroptenate synthase (foIP) folyloolydlutamate synthase (foIP) foTP cyclohydrolase 1 (foIE) methylene-tetrahydrotolate dehydrogenase (foID) para-aminobenzoate synthetase (pabB)	48.0% 34.9% te 49.2% me 36.9% 32.1% 36.0% 34.6% 32.4% 34.5% 35.2% 50.9% 48.4% 35.1%
General HP0220 Biolin HP0586 HP0976 HP140 HP140 HP1254 HP1254 HP1029 Folic acid HP0029 Folic acid HP10587 HP1232 HP1545 HP0587 HP0283 Heog28 He00577 HP0293 Haem and J He0153	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl coenzy A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin synthetase (bioD) 7.8-ditydro-8-hydroxymethylpterin- pyrophosphokase (loiK) aminodeoxychorismate (lyase (pabC) dihydroptercate synthase (foIC) GTP cyclohydrolase 1 (IoIE) methylene-aterhydrolade dehydrogenase (foID) para-aminobenzoate synthetase (pabB) porphyrin delta-aminolevulinic acid dehydratase	48.0% 34.9% te 49.2% me 36.9% 32.1% 36.0% 32.4% 36.0% 34.6% 32.4% 35.2% 50.9% 48.4% 35.1%
General HP0220 Biotin HP0576 HP0976 HP140 HP140 HP144 HP146 HP124 HP124 HP124 HP124 HP124 HP1254 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0583 Haem and µ	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (lolC) aminodeoxychorismate lyase (pabC) dihydropteroate synthase (lolC) GTP cyclohydrolase I (lolE) methylene-tetrahydrofolate dehydrogenase (toID) para-aminoleenzoate synthetase (pabB) porphyrin delta-aminolevulinic acid dehydratase (hemB)	48.0% 34.9% te 49.2% yme 36.9% 32.1% 36.2% 36.2% 36.2% 36.2% 34.6% 32.4% 34.5% 35.2% 50.9% 48.4% 35.1%
General HP0220 Biotin HP0588 HP1140 HP0976 HP1140 HP1406 HP1406 HP1406 HP1406 HP1036 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP0587 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP1545 HP15555 HP1555 HP15555 HP1555 HP15555 HP15555 HP15555 HP15555 HP	synthesis of [Fe-S] cluster (nlfS) 8-emino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotion sperion repressor/biofin acetyl coency A carboxylase synthetase (biA) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (bioD) aminodeoxychorismate lyase (pabC) dihydropterate synthase (foIP) folylpolyglutamate synthase (foIP) folylpolyglutamate synthase (foIP) folylpolyglutamate synthase (foIP) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthetase (pabB) parophyrin delta-aminolevulinic acid dehydratase (hemB) ferrochelatase (hemH)	48.0% 34.9% te 49.2% 49.2% 36.9% 32.1% 36.2% 36.2% 36.0% 34.5% 52.2% 50.9% 48.4% 35.2% 50.9% 48.4% 35.1%
General HP0220 Biotin HP0376 HP0976 HP0976 HP0976 HP1400 HP1400 HP1406 HP1029 HP0587 HP1236 HP0587 HP1238 HP0577 HP0293 Haem and p HP01376 HP0376 HP0376	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin operon repressor/biotin acetyl coency A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethobiotin synthetase (bioD) 7.8-dihydro-8-hydroxymethylpterin- pyrophosphotinase (foIR) aminodeoxychorismate lyase (pabC) dihydorpterave synthase (foIP) folyipolylutamate synthase (foIP) folyipolylutamate synthase (foIP) methylene-tetrahydrofolate dehydrogenase (foID) parkaminobenzoate synthetase (pabB) porphyrin detta-aminolevulinic acid dehydratase (hemB) glutamate-1-semialdehyde 2,1-aminomutase (hemL)	48.0% 34.9% te 49.2% yme 36.9% 36.9% 32.7% 36.2% 36.2% 36.2% 36.2% 32.4% 32.4% 32.4% 35.2% 50.9% 48.4% 35.1% 50.5% 33.4% 50.5% 33.4%
General HP0220 Biotin HP0598 HP0976 HP0976 HP0976 HP1400 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0408 H	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (birA) biotin sulfvater eductase (bioC) biotin synthesis protein (bioC) biotin synthesis (bioD) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioC) dinydropteroate synthetase (bioC) GTP cyclohydrolase I (toIE) methylene-tetrahydrotolate dehydrogenase (toID) para-aminobenzoate synthetase (pabB) oorphyrin detta-aminolevulinic acid dehydratase (hemB) glutamyl-IRNA reductase (hemA) glutamyl-IRNA reductase (hemA)	48.0% 34.9% te 49.2% me 36.9% 32.1% 36.2% 36.0% 34.5% 32.4% 32.4% 32.4% 32.4% 32.4% 33.45% 35.2% 50.3% 50.5% 33.4% 50.5% 33.4%
General HP0220 Biotin HP0376 HP140 HP0407 HP140 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0407 HP1406 HP0407 HP040 HP0407 HP0407 HP0407 HP040 HP0407 HP040 HP0407 HP0407 HP040	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (folC) dihydropteroate synthase (folC) GTP cyclohydrolase I (folE) methylene-tetrahydrofolate dehydrogenase (folD) para-aminobenzoate synthetase (pabB) porphyrin delta-aminolevulinic acid dehydratase (hemB) ferrochelatase (hemH) glutamyl-1-Bemildehyde 2,1-aminomutase (hemL) glutamyl-1-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxydase (hemN)	48.0% 34.9% 49.2% /me 36.9% 36.9% 32.1% 36.2% 36.0% 32.4% 32.4% 35.2% 50.9% 50.5% 33.4% 50.5% 51.3% 51.3% 51.3% 51.3%
General HP0220 Biotin HP0376 HP0376 HP0407 HP1400 HP1400 HP1406 HP1026 HP0577 HP0237 HP0577 HP0237 HP0577 HP0237 HP0577 HP0236 HP0376 HP0376 HP0259 HP0259 HP0226	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7.8-dilydro-8-hydroxymethylpterin- pyrophosphotinase (bioE) aminodeoxychorismate lyase (pabC) dihydroptenate synthase (foIP) folyloolydutamate synthase (foIP) folyloolydutamate synthase (foIP) foIP ocylodydrolase 1 (foIE) methylene-tetrahydrofolate dehydrogenase (horB) ferrochelatase (hemH) glutamate-1-semialdehyde 2,1-aminomutase (hemL) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN)	48.0% 34.9% te 49.2% me 36.9% 42.7% 36.2% 36.0% 36.0% 34.6% 32.2% 34.5% 35.2% 50.9% 50.5% 33.4% 50.5% 33.4% 50.5% 32.7%
General HP0220 Biotin HP0538 HP0538 HP0538 HP0536 HP047 HP1426 HP0407 HP1426 HP0407 HP1426 HP0428 HP0428 HP0428 HP0428 HP0428 HP0429 HP0427 HP1426 HP0427 HP1426 HP0427 HP047 HP0427 HP047 HP	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotion sperior repressor/biotin acetyl coency A carboxylase synthetase (birA) biotin suffixetase (bioC) biotin synthesis protein (bioC) biotin synthesis (bioE) dethiobiotin synthetase (bioD) 7.8-dilydaro-8-hydroxymethylpterin- pyrophosphokinase (bioE) dinyladpetrate synthase (bioD) GTP cyclohydrolase I (biE) methylene-tetrahydrololate dehydrogenase (foID) para-aminolevulinic acid dehydratase (hemB) ferrochelatase (hemH) glutamate-1-semialdehyde 21-aminomutase (hemL) glutamyLRNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN)	48.0% 34.9% te 49.2% me 36.9% 42.7% 32.1% 36.2% 36.2% 36.2% 35.2% 50.9% 33.4% 35.2% 50.9% 35.1% 50.5% 33.4% 32.3% 51.3% 32.4% 50.5% 33.4% 35.1% 50.5% 33.4% 32.7%
General HP0220 Biotin HP0376 HP0376 HP0376 HP0407 HP1254 HP1400 HP1036 HP1036 HP1036 HP0587 HP1545 HP0587 HP1545 HP0587 HP0587 HP0587 HP0587 HP0586 HP0587 HP0586 HP0238 HP0376 HP0376 HP0329 HP0365 HP1226 HP0231	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin operon repressor/biotin acetyl ocenzy A carboxylase synthetase (birA) biotin sulfvalde reductase (bioC) biotin synthesis protein (bioC) biotin synthesis (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) aminodeoxychorismate lyase (pabC) dihydropteroate synthase (foIC) aminodeoxychorismate lyase (pabC) dihydropteroate synthase (foIC) GTP cyclohydrolase I (toIE) methylene-tetrahydrofolate dehydrogenase (toID) pare-aminotexulinic acid dehydratase (hemE) ferrochelatase (hemH) glutamyl-Fiseniadehyde 2,1-aminomutase (hemI) oxydase (hemN) oxydase (hemN) oxydase (hemN) portphobilinogen daaminase (hemC)) protoporphyrinogen diaminase (hemC)	48,0% 48,0% 48,9% 56,9% 36,9% 32,1% 32,1% 32,1% 36,2% 36,2% 50,9% 34,6% 52,2% 50,9% 51,3%51,3% 51,3%
General HP0220 Biotin HP0376 HP1140 HP0477 HP1264 HP1264 HP1264 HP1026 HP0029 F0/c acid HP1036 HP02837 HP0577 HP0283 HP0577 HP0283 HP0065 HP0237 HP0283 HP0285 HP0283 HP0285 HP1226	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthese (bioB) dethiobiotin synthese (bioD) 7, 8-ditlydro-6-hydroxymethylpterin- pyrophosphokinase (bioR) aminodeoxychorismate lyase (babC) ditlydropferabiotiase (bioB) aminodeoxychorismate lyase (babC) ditlydropferabiotiase (bioR) folyboplylutamate synthase (foIP) folyboplylutamate synthase (foIP) folyboplylutamate synthase (foIP) aminodeoxychorismate lyase (babB) para-aminobenzoate synthetase (babB) para-aminobenzoate synthetase (babB) parbyrin delta-aminolevulinic acid dehydratase (hemL) glutamyl-RNA reductase (hemA) oxygen-independent corpropriyrinogen III oxidase (hemN) prohobilinogen deaminase (hemC) protoporphyrinogen oddase (hemE)	48.0% 34.9% 49.2% 36.9% 36.9% 36.2% 36.0% 36.2% 36.2% 36.2% 36.2% 35.2% 50.9% 44.5% 35.1% 50.5% 33.4% 50.5% 33.4% 50.5% 33.9% 51.3% 52.3%
General HP0220 Biotin HP0376 HP0376 HP0376 HP0407 HP1420 HP1400 HP1406 HP1029 HP1036 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0293 HP0587 HP0293 HP0587 HP0293 HP00587 HP0293 HP00587 HP0293 HP00586 HP0293 HP00586 HP0296 HP0296 HP0296 HP0296 HP0297 HP0297 HP0297 HP0297 HP0297 HP0297 HP0298 HP0297 HP0298 HP0297 HP0297 HP0298 HP0297 HP0298 HP0297 HP0298 HP0297 HP0297 HP0298 HP0297 HP02	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7.8-dillydro-8-hydroxymethylpterin- pyrophosphotinase (foIC) aminodeoxychorismate lyase (pabC) aminodeoxychorismate lyase (pabC) ditydopterae synthase (foIC) GTP cyclohydrolase I (foIC) folyipolyluramate synthase (foIC) GTP cyclohydrolase I (foIC) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthetase (pabB) porphrin detta-aminolevulinic acid dehydratase (hemB) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) oxygen-independent coproporphyrinogen III oxidase (hemC) protoporphyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemC) proporphyrinogen deaminase (hemC) proporphyrinogen deaminase (hemD) are and ulbratopendent coproporphyrinogen III oxidase (hemD) and ulbratopendent coproporthyrinogen III oxidase (hemC) protoporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemC)	48.0% 48.0% 48.9% 49.2% 36.9% 36.9% 36.2% 36.0% 36.2% 36.2% 36.2% 50.9% 51.3%
General HP0220 Biotin HP0538 HP0538 HP0538 HP0536 HP047 HP1420 HP1420 HP1426 HP0229 HP1545 HP0228 HP0547 HP0223 HP0547 HP0223 HP0545 HP0236 HP0236 HP0236 HP0236 HP0236 HP0237 HP0238 HP0236 HP0237 HP0238 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0236 HP0237 HP0257 HP057 HP057 HP057 HP057 HP057 HP057 H	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotin spynthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7. 8-dihydro-8-hydroxymethytperin- pyrophosphokinase (bioE) diminodeoxychorismate lyase (pabC) diminodeoxychorismate lyase (pabC) diminodeoxychorismate (lose) GTP cyclohydrolase I (lotE) methylene-tetrahydrololate dehydrogenase (foID) para-aminobenzoate synthetase (babB) borphyrin detta-aminolevulinic acid dehydratase (hemB) glutamate-1-semialdehyde 21-aminomutase (hemL) glutamyLRNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) oxygen-independent coproporphyrinogen III oxidase (hemE) protoporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemE) uroporphyrinogen III coxythase (hemE) uroporphyrinogen III coxythase (hemE) uroporphyrinogen III coxythase (hemE)	48,0% 34,9% 42,2% 36,9% 36,2% 36,0% 34,6% 52,2% 50,5% 33,4% 50,5% 33,4% 50,5% 33,4% 50,5% 32,2% 50,5% 32,2% 50,5% 32,2% 50,5% 50
General HP0220 Biotin HP0376 HP0376 HP140 HP0407 HP1406 HP1254 HP1406 HP1036 HP0577 HP0232 HP1645 HP0577 HP0233 HP0655 HP0239 HP0665 HP1226 HP0376 HP0239 HP0665 HP1228 HP0376 HP0239 HP0665 HP1228 HP0376 HP0396 HP0396 HP0396 HP0396 HP0396 HP0397 HP0396 HP0396 HP0396 HP0397 HP0396 HP0396 HP0397 HP0396 HP0397 HP0396 HP0397 HP0396 HP0397 HP0396 HP0397 HP0397 HP0396 HP0397 HP0396 HP0397 HP	synthesis of [Fe-S] cluster (nlfS) 8-emino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoa aminutransterase (bioA) biotin synthesis protein acetyl coency A carboxylase synthetase (biCA) biotin synthesis protein (biCC) biotin synthesis protein (biCC) biotin synthesise (bioB) dethiotion synthetase (biCD) 7.8-dihydro-8-hydroxymethylpterin- pyrophosphotiase (bioB) aminodeoxychorismate lyase (baCC) GTP cyclohydrolase (16IP) (GTP cyclohydrolase (16IP) GTP cyclohydrolase (16IC) GTP cyclohydrolase (16IP) GTP cyclohydrolase (16IP) GTP cyclohydrolase (16IP) GTP cyclohydrolase (16IP) GTP cyclohydrolase (16IP) GTP cyclohydrolase (16IP) Gtylopolylutamate synthase (GAP) glutamate-1semialdehydro (21-aminomutase (hemB) oxygen-independent coproportyrinogen III oxydae-independent copropo	48,0% 48,0% 48,0% 68,9% 36,9% 32,1% 32,1% 32,1% 36,0% 36,2% 36,0% 36,2% 50,5% 50,5% 51,3% 52,3% 52,3% 51,3% 51,3% 52,3% 52,3% 51,3%51,3% 51,3%
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General HP0220 Biotin HP0598 HP0598 HP0598 HP0598 HP1400 HP0407 HP1254 HP1406 HP1030 HP1036 HP1036 HP0587 HP1545 HP0287 HP1545 HP0287 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0583 HP0638 HP0239 HP0638 HP0239 HP0239 HP0239 HP0239 HP0239 HP0239 HP0239 HP0239 HP0239 HP0240 Mchybdopte HP0229 HP0240 Mchybdopte HP0580	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransterase (bioA) biotin operon repressor/biotin acetyl coenzy A carboxylase synthetase (birA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioD) 7, 8-dihydro-6-hydroxymethylpterin- pyrophosphokinase (bioC) dinydropteroate synthase (bioC) GTP cyclohydrolase I (biC) GTP cyclohydrolase I (biC) GTP cyclohydrolase I (biC) gera-aminodevylnic acid dehydratase (biD) porphyrin detta-aminolevulinic acid dehydratase (hemB) glutamyt-RNA reductase (hemA) glutamyt-RNA reductase (hemA) oxidase (hemN) porphobilinogen deaminase (hemC) protoportyrinogen III coxyrthase (hemE) unoporthyrinogen III coxyrthesis	48,0% 48,0% 48,0% 56,9% 56,9% 56,2%56,2% 56,2% 56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2%56,2% 56,2% 56,2%56,2%
General HP0220 Biotin HP0376 HP0596 HP1140 HP0470 HP1264 HP1264 HP1264 HP1029 HP0029 HP0029 HP0029 HP0029 HP0029 HP00237 HP0238 HP00237 HP0027 HP00	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin spythesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthese (bioB) dethiobiotin synthese (bioD) 7, 8-ditlydro-8-hydroxymethylpterin- pyrophosphotiase (bioB) aminodeoxychorismate lyase (pabC) ditlydropterate synthase (foIC) 67P oyclohydrolase (16IE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthesta (foIC) graphyrin delta-aminolevulinic acid dehydratase (hemE) glutamitet-1-semialdehyde 2,1-aminomutase (hemB) glutamitet-semialdehyde 2,1-aminomutase (hemB) glutamitet-semialdehyde 2,1-aminomutase (hemD) glutamyl-RNA reductase (hemA) oxygen-independent coproportyrinogen III oxidase (hemN) oxygen-independent coproportyrinogen III oxidase (hemD) erand ubiguinone 4-hydroxybenzoate cataprenytransferase (bioA) geranytranstransferase (ispA) octappenytrinogen dearbiosynthesis protein A (moaA) proble law endowe biosynthesis protein A (moaA)	48.0% 48.0% 48.0% 58.9% 58.9% 58.2% 58.2% 58.2% 50.9% 44.5% 55.2% 50.9% 53.2% 50.9% 50.5% 53.2% 51.3% 52.3% 51.3% 52.3% 51.3% 53.3%
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General HP0220 Biotin HP0538 HP0538 HP0538 HP0538 HP0456 HP0220 HP1426 HP1426 HP1028 HP0537 HP1232 HP1545 HP0237 HP0238 HP0326 HP0239 HP036 HP0239 HP039 HP039 HP039 HP039 HP039 HP039 H	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoa aminotransferase (bioA) biotion sportnovik repressor/biotin acetyl coency A carboxylase synthetase (birA) biotin sufficient repressor/biotin acetyl coency A carboxylase synthetase (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesise (bioB) dethiobiotin synthetase (bioD) 7.8-dihydro-8-hydroxymethylpterin- pyrophosphokinase (bioC) dihydropterate synthase (bioC) dihydropterate synthase (bioC) GTP cyclohydrolase I (bioE) methylene-tetrahydrololate dehydrogenase (bioD) para-aminotenzoate synthetase (babB) oxphyrin detta-aminolevulinic acid dehydratase (hemB) glutamate-1-semialdehyde 21-aminomutase (hemC) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) oxygen-independent coproporphyrinogen III oxidase (hemE) protoporthyrinogen deaminase (hemC) protoporthyrinogen III cosynthase (hemE) uroporphyrinogen III cosynthase (hemE) uroporphyrinogen III cosynthase (hemE) in olybdenum cofactor biosynthesis protein A (moaA) molybdenum cofactor biosynthesis protein (mozA)	48,0% 48,0% 448,0% 58,9% 58,2% 58,2% 50,5% 5
General HP0220 Biotin HP0376 HP140 HP0470 HP1404 HP1426 HP1254 HP1036 HP1036 HP0039 HP00687 HP1232 HP1545 HP0577 HP0238 HP0577 HP0238 HP0376 H	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotion sportno repressor/biotin acetyl coency A carboxylase synthetase (biA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) adminotocoxychorismate (bioB) dethiobiotin synthetase (bioD) 7, 8-ditydro-8-hydroxymethylpterin- pyrophosphotiase (toIC) folylpolylutamate synthase (foIC) folylpolylutamate synthase (foIC) folylpolylutamate synthase (foIC) folylpolylutamate synthase (foIC) giutamyt-FiNA reductase (hereA) oxygen-independent coproportyrinogen III oxidase (hernN) giutamyt-FINA reductase (hereA) oxygen-independent coproportyrinogen III oxidase (hernN) prohobilinogen deaminase (hereC) protoportyrinogen deaminase (hereC) protoportyrin	48.0% 48.0% 48.0% 48.0% 48.0% 58.9% 48.2% 58.9% 58.2% 50.9% 43.4% 55.9% 43.4% 50.5% 51.3% 50.5% 51.3% 51.3% 51.3% 51.3% 51.3% 52.7% 42.4% 37.9% 42.4% 37.9% 42.4% 37.9% 42.3% 22.6% 53.9% 43.3% 24.6% 53.9% 45.7% 53.9% 54.5% 55.9%
General HP0220 Biotin HP0376 HP0598 HP0598 HP0598 HP1400 HP1400 HP1400 HP1406 HP1026 HP0587 HP1226 HP0587 HP0587 HP0587 HP0587 HP0237 HP0587 HP0237 HP0376 HP0376 HP0376 HP0376 HP0376 HP0378 HP0378 HP0381 HP0381 HP0685 HP1226 HP0237 HP0685 HP0239 HP0288 HP0685 HP0298 HP0298 HP0788 HP0788 HP0788 HP0788 HP0789 HP0789 HP0789 HP0799 HP0799	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) aminodeoxychorismate (bioB) dethiobiotin synthetase (bioD) 7.8-dillydro-8-hydroxymethylpterin- pyrophospholarolase (bioB) aminodeoxychorismate lyase (pabC) dihydropterate synthase (foIP) folyloolydutamate synthase (foIP) folyloolydutamate synthase (foIP) folyloolydutamate synthase (foIP) aminodeoxychorismate (bioE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthetase (pabB) borphyrin ditaaminolevulinic acid dehydratase (hemB) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) oxygen-independent coproporphyrinogen III oxidase (hemN) avgen-independent coproporphyrinogen III oxidase (hemS) arophybrinogen dearnase (hemC) protporphyrinogen dearnase (hemC) protporhyrinogen dearnase (hemS) avgen/independent coproporphyrinogen III oxidase (hemA) avgen/independent coproporphyrinogen III oxidase (hemS) avgen/independent coproporphyrinogen III oxidase (hemS) avgen/inde	48.0% 48.0% 48.0% 56.9% 56.9% 56.2% 56.2% 56.2% 50.9% 50.9% 50.9% 50.5% 51.5% 51.5% 51.5% 51.5% 51.5% 51.5% 51.5% 51.5% 51.9% 51.5% 51.9%
General HP0220 Biotin HP0376 HP0376 HP0376 HP0376 HP0376 HP0376 HP0376 HP0376 HP0376 HP0376 HP0376 HP0377 HP0233 HP0376 HP0377 HP0376 H	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotion sportnovike repressor/biotin acetyl coency A carboxylase synthetase (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) adhiotion sufficience (bioC) A carboxylase (bioB) dethiobiotin synthetase (bioD) 7.8-dillydra-8-hydroxymethylpterin- pyrophosphotolase (lofC) aminodeoxychorismate lyase (pabC) dillydrapterate synthase (foIC) GTP cyclohydrolase (lofC) GTP cyclohydrolase (lofC) methylene-tetrahydrofolate dehydrogenase (horD) glutamyl-RNA reductase (hereA) glutamate-1-semialdehyde 21-aminomutase (hermL) glutamyl-RNA reductase (hereA) oxygen-independent coproportyrrinogen III oxidase (hermN) oxygen-independent coproportyrrinogen III oxidase (hermD) prothopingen deaminase (hereC) protoportyrinogen second (hereC) protoportyrinogen forect oxygen-independent octaprenyl-diphosphate synthase (spB) <i>in</i> molyddopterin biosynthesis protein (moeA) molyddopterin biosynthesis protein (moeA) molyddopterin biosynthesis protein (moeA) molyddopterin converting factor, subunit 1 (maAC)	48.0% 48.0% 48.0% 58.9% 58.9% 58.2% 50.9% 50.9% 50.9% 50.9% 50.9% 51.3%
General HP0220 Biotin HP0376 HP140 HP047 HP1406 HP1254 HP1254 HP0587 HP1254 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0587 HP0580 HP0587 HP0580 HP0589 HP0580 HP0589 HP0580 HP0	synthesis of [Fe-S] cluster (nlfS) 8-emino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoa aminutransterase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) aminodeoxychorismate (yase (babC) aminodeoxychorismate lyase (babC) aminodeoxychorismate lyase (babC) aminodeoxychorismate lyase (babC) aminodeoxychorismate lyase (babC) (bi)topylutamate synthase (folP) (bi)topylutamate synthase (folP) (bi)topylutamate synthase (folP) (aftP oxclohydrolase 1 (biC) para-aminobenzoate synthestae (babB) porphyrin delta-aminolevulinic acid dehydratase (hemE) ferrochelatase (hemH) gutamate-1-semialdehyde 2,1-aminomutase (hemE) protoporphyrinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen dearboxylase (hemE) uroporphyrinogen elli cosynthase (hemE) uroporphyrinogen elli cosynthase (hemE) inolybdenum cofactor biosynthesis protein (mo2) molybdopterin biosynthesis protein (moeA) molybdopterin biosynthesis protein (moeA) molybdopterin converting factor, subunit 1 (moaE) molybdopterin converting factor, subunit 2 (moaE)	48.0% 48.0% 48.0% 48.0% 56.9% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.3% 52.2% 56.3% 52.2% 56.3% 52.2% 56.3% 52.2% 52.2% 52.5%
General HP0220 Biotin HP0376 HP1140 HP0477 HP1264 HP1264 HP1264 HP1264 HP1029 HP0287 HP0287 HP1284 HP0577 HP0283 HP0577 HP0283 HP0577 HP0283 HP0575 HP0283 HP0283 HP0283 HP0283 HP0283 HP0283 HP0285 HP1226 HP0283 HP0285 HP1226 HP0283 HP0285 H	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminouransferase (bioA) biotion sportnovike reductase (bioC) biotion synthesis protein (bioC) biotion synthesis protein (bioC) biotion synthesis protein (bioC) biotion synthesis (bioB) dethiobiotin synthese (bioD) 7, 8-ditlydro-6-hydroxymethylpterin- pyrophospholase (bioE) aminodeoxychorismate lyase (pabC) ditlydropterate synthase (foIC) GTP cyclohydrolase (16IE) methylene-tetrahydrofolate dehydrogenase (foID) para-aminobenzoate synthesta (foIC) detha-aminobenzoate synthesta (foIC) glutamite I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) glutamite-I-semialdehyde 2,1-aminomutase (hemE) gorphyrinogen dearniase (hemE) uroporphyrinogen dearniase (hemE) uroporphyrinogen dearniase (hemE) uroporphyrinogen dearnaviase (hemE) uroporphyrinogen dearnavi	48.0% 44.9% 44.9% 56.9% 56.9% 56.2% 56.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.2% 55.3% 55.2% 55.3%55.3% 55.3%55.3% 55.3% 55.3% 55.3% 55.3% 55.3%55.3%
General HP0220 Biotin HP0376 HP0598 HP0598 HP0407 HP1284 HP1406 HP1029 HP1036 HP0029 Folic acid HP1036 HP0587 HP0293 HP0577 HP0293 HP0577 HP0293 HP0577 HP0293 HP0376 HP0376 HP0239 HP0376 HP0239 HP0376 HP0239 HP0240 HP0289 HP0788 HP0788 HP0789 HP0789 HP0789 HP0789 HP0789	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) adhiotion sufficience (bioC) dethiobiotin synthetase (bioD) 7.8-dillydro-8-hydroxymethylpterin- pyrophosphotiase (lofD) aminodeoxychorismate lyase (pabC) dithydorpterate synthase (folP) folyioplyluramate synthase (folP) folyioplyluramate synthase (folP) folyioplyluramate synthase (folP) methylene-tetrahydrofolate dehydrogenase (folD) apra-aminobenzoate synthetase (pabB) borphyrin detta-aminotevulinic acid dehydratase (hemB) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) oxygen-independent coproporphyrinogen III oxidase (hemN) oxygen-independent coproporphyrinogen III oxidase (hemN) porphobilinogen deaminase (hemC) protoporphyrinogen dearinase (hemC) protoporphyrinogen dearinase (hemC) protoporphyrinogen dearinase (hemC) protein A (moaA) molydoopterin biosynthesis protein (moeA) molydoopterin converting factor, subunit 1 (moaD) molydoopterin converting factor, subunit 2 (mobE) molydoopterin converting factor, subunit 2 (mobA)	48.0% 48.0% 48.0% 48.0% 58.9% 58.2% 58.2% 58.2% 58.2% 50.9% 51.3%
General HP0220 Biotin HP02598 HP0598 HP0598 HP0470 HP1440 HP1400 HP1426 HP1029 HP0587 HP1236 HP0587 HP1236 HP0587 HP0587 HP0293 HP0577 HP0293 HP0577 HP0293 HP0376 HP0293 HP0381 HP0381 HP0298 HP0575 HP0298 HP0758 HP0758 HP0798 HP0798 HP0798 HP0798 HP0798 HP0799 HP0801 HP0789 HP0289 HP0789 HP0789 HP0789 HP0389 HP0789 HP0789 HP0380 HP0789	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosylmethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis (bioB) dethiobiotin synthetase (bioD) 7.8-dihydro-6-hydroxymethytperin- pryrohosphotaes (bioK) aminodeoxychorismate lyase (pabC) dihydropteradydrolase 1 (biE) methyden-etrahydrolate dehydrogenase (holD) porphyrin detta-aminolevulinic acid dehydratase (hemB) ferrocheltase (hemH) glutamate-1-semialdehyde 2,1-aminomutase (hemL) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) woyden-independent coproporphyrinogen III oxidase (hemD) protoporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemC) molydotperin biosynthesis protein (moeB) molydotperin converting factor, subunit 2 (moaE) molydotperin biosynthesis protein (moeB) molydotperin biosynthesis pro	48,0% 48,0% 448,0% 442,0% 36,0% 36,0% 34,4% 52,2% 50,5% 36,0% 34,4% 50,5% 33,3% 50,5% 33,3% 50,5% 31,3% 32,2% 50,5% 31,3% 31,9% 31,1%
General HP0220 Biotin HP0376 HP140 HP0470 HP1404 HP1426 HP1254 HP1426 HP1029 HP1026 HP1029 HP1026 HP0029 HP1026 HP0237 HP0238 HP0376 HP	synthesis of [Fe-S] cluster (nlfS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminotransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) aminodexychorismate (yase (babC) aminodexychorismate lyase (babC) aminodexychorismate lyase (babC) aminodexychorismate lyase (babC) (bi/protyclase (lofE) aminodexychorismate synthase (foIC) (aff P oclohydrolase 1 (biE) methylene-tetrahydrofolate dehydrogenase (biD) para-aminobenzoate synthase (foIC) (aff P oclohydrolase 1 (biE) methylene-tetrahydrofolate dehydratase (hemB) glutamyt-FINA reductase (hemA) oxgen-independent coproportyrinogen III oxidase (hemN) guidamyt-FINA reductase (hemE) uroporthyrinogen deaminase (hemC) protoporthyrinogen deaminase (hemE) uroporthyrinogen deaminase (hemE) uroporthyrinogen deaminase (hemE) iuroporthyrinogen deaminase (hemB) erand biguinone 4-hydroxybenzoate octaprenyltransferase (bibA) geranyltranstransferase (spA) octaprenyl-diposphate synthesis protein (moaD) molybdopterin biosynthesis protein (mocA) molybdopterin biosynthesis protein (mocA) molybdopterin biosynthesis protein (mocA) molybdopterin converting factor, subunit 1 (maaD) molybdopterin converting factor, subunit 2 (moaE) molybdopterin	48.0% 48.0% 48.0% 48.0% 48.0% 58.9% 42.7% 52.1% 52.2% 50.9% 42.4% 55.2% 50.9% 42.4% 55.2% 50.9% 51.3% 52.7% 51.3% 52.7% 51.3% 52.7% 51.3% 52.7% 51.3% 52.7% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 52.9% 51.3% 51.3% 52.9% 51.3% 51.3% 52.9% 51.3%
General HP0220 Biotin HP02508 HP1140 HP0407 HP1256 HP1426 HP1426 HP1426 HP1026 HP0587 HP0237 HP0587 HP0587 HP0237 HP0237 HP0236 HP0237 HP0058 HP0237 HP0238 HP0058 HP0237 HP0238 HP0238 HP028 HP0237 HP028 HP028 HP028 HP029 H	synthesis of [Fe-S] cluster (nIIS) 8-amino-7-oxononanoate synthase (bioF) adenosymethionine-8-amino-7-oxononanoate aminouransferase (bioA) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) biotin synthesis protein (bioC) dethiobiotin synthese (bioB) dethiobiotin synthese (bioB) dethiobiotin synthese (bioD) 7.8-dihydro-8-hydroxymethylterin- pyrophospholarolase (bioE) aminodeoxychorismate lyase (babC) dihydropterate synthase (foIP) folyloplylutamate synthase (foIP) folyloplylutamate synthase (foIP) folyloplylutamate synthase (foIP) for ycolvdyrolase (I (biD) para-aminobenzoate synthetae (pabB) borphyrin ditamate-1-semialdenyde 2,1-aminomutase (hemB) glutamyl-RNA reductase (hemA) oxygen-independent coproporphyrinogen III oxidase (hemN) porpholinogen deaminase (hemC) protoporphyrinogen deaminase (hemC) protoporphyrinogen deaminase (hemC) protoporphyrinogen deaminase (hemC) protoporphyrinogen deaminase (hemD) e and ubiguinone 4-hydroxybenzoate otoproprytinase (pab) molybdopterin biosynthesis protein (moeA) molybdopterin biosynthesis protein (moeA) molybdopteri	48.0% 48.0% 48.0% 48.0% 56.9% 56.9% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.2% 56.3% 56.2% 56.3%56.3% 56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3% 56.3%56.3% 56.3%56.3% 56.3%56.3% 56.3% 56.3%56.3%56.3%

HP0841	pantothenate metabolism flavoprotein (dfp)	31.3%
<i>Pyridoxine</i> HP1583	pyridoxal phosphate biosynthetic protein	
HP1582	A (pdxA) pyridoxal phosphate biosynthetic protein J (pdxJ)	34.2% 42.6%
Riboflavin	CTD evelop dralace II (ripA)	47.00
HP0802 HP0804	GTP cyclohydrolase II (1DA) GTP cyclohydrolase II (3,4-dihydroxy-2-butar 4-phosphate synthase (ribA, ribB) riboflavia biosynthasis protein (ribG)	47.2% ione 44.0%
HP1087	riboflavin biosynthesis protein (ribO) (ribC)	28.9%
HP1574 HP0002	riboflavin synthase beta chain (ribE)	52.4%
Thioredoxir HP1118	n, glutaredoxin and glutathione gamma-glutamyltranspeptidase (ggt)	53.2%
HP1458 HP0824	thioredoxin thioredoxin (trxA)	38.3% 51.5%
HP1164 Thiamine	thioredoxin reductase (trxB)	28.5%
HP0814 HP0843	thiamin biosynthesis protein (thiF) thiamin phosphate pyrophosphorylase/	34.6%
HP0845	hyroxyethylthiazole kinase (thiB) thiamin phosphate pyrophosphorylase/	35.7%
HP0844	thiamine biosynthesis protein (thi)	41.0%
Pyridine nu HP0329	cleotides NH(3)-dependent NAD+ synthetase (nadE)	37.5%
HP1355	nicotinate-nucleotide pyrophosphorylase (nadC)	36.3%
HP1356	quinolinate synthetase A (nadA)	34.2%
CELL ENVE	LOPE Incorroteins and porins	
HP1450	60 kDa inner-membrane protein	40.0%
HP0180 HP0175	cell binding factor 2	28.0% 34.9%
HP0078 HP0567	Hypothetical protein	28.4% 26.4%
HP1456	membrane-associated lipoprotein (lpp20)	98.9%
HP1564 HP0009	outer membrane protein outer membrane protein (omp1)	39.9%
HP0324	outer membrane protein (omp10)	0.0%
HP0472 HP0477	outer membrane protein (omp11) outer membrane protein (omp12)	0.0%
HP0638 HP0671	outer membrane protein (omp13)	0.0%
HP0706	outer membrane protein (omp15)	33.5%
HP0722	outer membrane protein (omp16) outer membrane protein (omp17)	43.3% 43.3%
HP0796	outer membrane protein (omp18)	0.0%
HP0896 HP0025	outer membrane protein (omp19) outer membrane protein (omp2)	0.0%
HP0912	outer membrane protein (omp20)	0.0%
HP0923	outer membrane protein (omp21)	0.0%
HP1107 HP1113	outer membrane protein (omp23) outer membrane protein (omp24)	0.0% 36.0%
HP1156	outer membrane protein (omp25)	0.0%
HP1177	outer membrane protein (omp26)	37.0%
HP1243 HP1342	outer membrane protein (omp28) outer membrane protein (omp29)	0.0%
HP0079	outer membrane protein (omp3)	0.0%
HP 1395 HP 1469	outer membrane protein (omp30) outer membrane protein (omp31)	0.0%
HP1501 HP0127	outer membrane protein (omp32) outer membrane protein (omp4)	0.0%
HP0227	outer membrane protein (omp5)	36.8%
HP0229 HP0252	outer membrane protein (omp6) outer membrane protein (omp7)	38.4%
HP0254	outer membrane protein (omp8)	37.6%
HP0839	outer membrane protein P1 (ompP1)	23.3%
HP0955 HP0655	prolipoprotein diacylglyceryl transferase (lgt protective surface antigen D15)34.4% 27.5%
HP1571	rare lipoprotein A (rIpA)	37.6%
HP0922	toxin-like outer membrane protein	29.5%
HP0289 Murain and	toxin-like outer membrane protein	30.6%
HP0830	amidase	40.6%
HP0738 HP0549	D-alanine:D-alanine ligase A (ddlA) glutamate racemase (glr)	28.5% 36.6%
HP0772	N-acetylmuramoyl-L-alanine amidase (amiA	26.8%
HP0597 HP1565	penicillin-binding protein 1A (PBP-1A) penicillin-binding protein 2 (pbp2)	35.0%
HP1125	peptidoglycan associated lipoprotein precur (omp18)	'sor 42.6%
HP0493	phospho-N-acetylmuramoyl-pentapeptide- transferase (mraY)	45.2%
HP0743	rod shape-determining protein (mreB)	37.7%
HP1372	rod shape-determining protein (mrec)	33.6%
HP0645 HP1543	soluble lytic murein transglycosylase (slt) toxR-activated gene (tagE)	32.2% 37.2%
HP1544	toxR-activated gene (tagE)	31.2%
HF 1100	(murG)	28.2%
HP0740	(murF)	25.7%
HP1494 HP1418	UDP-MurNac-tripeptide synthetase (murE) UDP-N-acetylenolpyruvoylglucosamine	36.0%
HP0648	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	J∠.1%
HP0623	UDP-N-acetylmuramate-alanine ligase (murC)	37.3%
HP0494	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	31.1%
Surface pol HP0003	ysaccharides, lipopolysaccharides and antig 3-deoxy-d-manno-octulosonic acid 8-phospl synthetase (kdsA)	ens nate 53.4%
HP0957	3-deoxy-d-manno-octulosonic-acid transfera	Se 006
HP0858	ADP-heptose synthase (rfaE)	40.6%
HP0859	(rfaF) ADP-L-glycero-D-mannoheptose-6-epimeras	33.2% e 32.7%
	(1967)	04.170

HP0855	alginate O-acetylation protein (algl)	41.8%	
HP0326	CMP-N-acetylneuraminic acid synthetase	31.006	
HP0230	CTP:CMP-3-deoxy-D-manno-octulosonate-	31.370	
1104000	cytidylyl-transferase (kdsB)	36.2%	
HP1392 HP0379	fucosyltransferase	25.7%	
HP0651	fucosyltransferase	39.2%	
HP0044	GDP-D-mannose dehydratase (rfbD)	62.1%	
HP0867 HP0159	lipid A disaccharide synthetase (IpxB) lipopolysaccharide 12-ducosyltransferase	32.0%	
111 0100	(rfal)	28.9%	
HP0208	lipopolysaccharide 1,2-glucosyltransferase	00.70	
HP0805	(rta) lippoligosaccharide 5G8 epitope biosynthe	26.7% sis-	
	associated protein (lex2B)	36.9%	
HP0826	lipooligosaccharide 5G8 epitope biosynthe	sis-	
HP1416	lipopolysaccharide 1,2-glucosyltransferase	39.2%	
	(rfaJ)	29.2%	
HP0679	lipopolysaccharide biosynthesis protein (wbpB)	12 8%	
HP1475	lipopolysaccharide core biosynthesis prote	in	
1100000	(kdtB)	49.0%	
HP0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	31.7%	
HP0619	lipopolysacharide biosynthesis glycosyl	01.7 /0	
LIBULAS	transferase (lic2B)	37.2%	
HP1105 HP1578	LPS biosynthesis protein	28.7%	
HP1581	methicillin resistance protein (IIm)	29.2%	
HP0857	phosphoheptose isomerase (gmhA)	44.5%	
HF 1275	{Pseudomonas aeruginosa}	39.6%	
HP1429	polysialic acid capsule expression protein		
Црорес	(kpsF)	46.0%	
HP0366	protein C	35.3%	
HP0178	spore coat polysaccharide biosynthesis		
	protein E	36.2%	
HF0421	protein J (capJ)	29.0%	
HP0196	UDP-3-0-(3-hydroxymyristoyl) glucosamine		
1001050	N-acyltransferase (IpxD)	39.5%	
HP 1052	(envA)	44.6%	
HP1375	UDP-N-acetylglucosamine acyltransferase		
	(IpxA)	41.8%	
Surface s	flaA1 protein	60.2%	
HP0325	flagellar basal-body L-ring protein (flgH)	32.7%	
HP0351	flagellar basal-body M-ring protein (fliF)	34.4%	
HP0246 HP1557	flagellar basal-body P-ring protein (ligi)	37.9%	
HP1559	flagellar basal-body rod protein (flgB)	01.010	
LIDASSO	(proximal rod protein)	31.0%	
HP 1558	(proximal rod protein)	46.0%	
HP1092	flagellar basal-body rod protein (flgG)	35.5%	
HP1585	flagellar basal-body rod protein (flgG)	47.7%	
HP1041 HP1035	flagellar biosynthesis protein (IIIA)	35.5%	
HP0684	flagellar biosynthesis protein (fliP)	43.4%	
HP0770	flagellar biosynthetic protein (flhB)	38.7%	
HP1419	flagellar biosynthetic protein (fliQ)	52.3%	
HP0173	flagellar biosynthetic protein (fliR)	26.4%	
HP0353 HP1420	flagellar export protein (filH) flagellar export protein ATP synthese (fill)	29.1%	
HP0870	flagellar hook (figE)	98.9%	
HP0908	flagellar hook (flgE)	30.5%	
HF III9	(HAP1) (flaK)	27.6%	
HP0752	flagellar hook-associated protein 2 (fliD)	28.9%	
HP0815	flagellar motor rotation protein (motA)	32.9%	
HP0816	flagellar motor switch protein (fliG)	37.0%	
HP1031	flagellar motor switch protein (fliM)	34.4%	
HP0753 HP0327	flagellar protein (fliS) flagellar protein G (flaG)	32.3% 23.3%	
HP0797	flagellar sheath adhesin hpaA	98.5%	
HP0584	flagellar switch protein (fliN)	39.7%	
HP0601	flagellin A (flaA)	99.8%	
HP0295	flagellin B homologue (fla)	32.9%	
HP1575	flhB protein (flhB)	40.5%	
HP1030 HP0907	TILY protein (TILY) Hook assembly protein flagella (flgD)	29.3% 25.5%	
HP1274	paralysed flagella protein (pfIA)	23.9%	
HP0751	polar flagellin (flaG)	21.9%	
HP0410	putative neuraminyllactose-binding haemagglutinin homologue (hpaA)	24.2%	
HP1192	secreted protein involved in flagellar motilit	y72.5%	
LD1/62	and a second a second of the second	y96.2%	
HD0000	secreted protein involved in flagellar motili	V00 20L	
HP0232	secreted protein involved in flagellar motili secreted protein involved in flagellar motili	y99.2%	
HP0232 CELLULA	secreted protein involved in flagellar motilit secreted protein involved in flagellar motilit AR PROCESSES	ly99.2%	
CELLULA General	secreted protein involved in itageilar motili secreted protein involved in flagellar motili AR PROCESSES	ly99.2%	
CELLULA General HP0392	secreted protein involved in nagenar motili secreted protein involved in flagellar motilit RPROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV)	26.8%	
CELLULA General HP0019 HP0393 HP0616	secreted protein involved in flageliar motili secreted protein involved in flageliar motili R PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV)	26.8% 31.7% 27.9%	
CELLULA General HP0019 HP0393 HP0616 HP1067	secreted protein involved in liageilar motili secreted protein involved in flageilar motili RR PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV)	26.8% 31.7% 99.2%	
CELLULA General HP0019 HP0393 HP0616 HP1067 HP0517 HP1490	secreted protein involved in liagellar motili secreted protein involved in flagellar motili R PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (cheV) GTP-binding protein (era) haermolvein	26.8% 31.7% 99.2% 95.6% 39.2%	
HP 1402 HP 0232 CELLULA General HP 0019 HP 0393 HP 0616 HP 1067 HP 0517 HP 1490 HP 1086	secreted protein involved in tiageilar motili secreted protein involved in tiageilar motili AR PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) faTP-binding protein (era) haemolysin Haemolysin (th)	26.8% 31.7% 27.9% 99.2% 95.6% 39.2% 40.2%	
HP0232 CELLULA General HP0019 HP0393 HP0616 HP1067 HP1087 HP1490 HP1086 HP0599	secreted protein involved in lagellar motili secreted protein involved in flagellar motili RR PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (cheV) Haemolysin Haemolysin (ty) haemolysin secretion protein precursor	26.8% 31.7% 27.9% 99.2% 95.6% 39.2% 40.2%	
HP0232 CELLULA General HP0019 HP0393 HP0616 HP1067 HP1490 HP1086 HP0599 HP0392	secreted protein involved in lagellar motili secreted protein involved in lagellar motili RR PROCESSES chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) chemotaxis protein (cheV) GTP-binding protein (cheV) Haemolysin (tly) haemolysin (tly) haemolysin (tly) haemolysin (tly) haemolysin (tly)	y99.2% 26.8% 31.7% 27.9% 99.2% 99.2% 95.6% 39.2% 40.2% 45.4%	

	(1910)	+0.+ <i>i</i> 0
HP0392	histidine kinase (cheA)	41.4%
HP0099	methyl-accepting chemotaxis protein (tlpA)	32.8%
HP0103	methyl-accepting chemotaxis protein (tlpB)	30.7%
HP0082	methyl-accepting chemotaxis transducer	
	(tlpC)	28.2%
HP0391	purine-binding chemotaxis protein (cheW)	34.3%
Cell division		
HP0331	cell division inhibitor (minD)	50.2%
HP0749	cell division membrane protein (ftsX)	25.7%
HP0978	cell division protein (ftsA) protein	31.9%
HP0748	cell division protein (ftsE)	37.6%
HP0286	cell division protein (ftsH)	41.2%
HP1069	cell division protein (ftsH)	98.6%
HP1556	cell division protein (ftsl)	30.6%
HP1090	cell division protein (ftsK)	39.8%
HP1560	cell division protein (ftsW) Escherichia coli	32.7%
HP0763	cell division protein (ftsY)	46.6%

HP0332	cell division topological specificity factor	22.00
HP0979	(minE) cell divison protein (ftsZ)	43.3%
Cell killing	cell filamentation protein (fic)	63.2%
HP0887 Chaperones	vacuolating cytotoxin 94.7%	
HP0010 HP0109	chaperone and heat shock protein (groEL) chaperone and heat shock protein 70	99.6%
LID0210	(dnaK) chaperone and heat shock protein C62.5	63.4%
	(htpG)	46.5%
HP0011 HP1332	co-chaperone (groES) co-chaperone and heat-shock protein	99.2%
HP0110	(dna) co-chaperone and heat-shock protein	42.7%
HP1024	(grpE) co-chaperone-curved DNA-binding protein	33.0% A
Chromoson	(CbpA) ne-associated protein	37.7%
HP1138 Detoxificatio	plasmid replication-partition related protein	40.4%
HP1563	alkyl hydroperoxide reductase (tsaA)	98.5%
HP0267	chlorohydrolase	42.6%
HP0243	(bacterioferritin)	95.8%
HP0389 HP1452	superoxide dismutase (sodB) thiophene and furan oxidizer (tdhF)	98.6% 37.6%
Protein and HP0355	peptide secretion GTP-binding membrane protein (lepA)	57.3%
HP0074 HP0786	lipoprotein signal peptidase (IspA) preprotein translocase subunit (secA)	97.0% 54.0%
HP1300 HP1255	preprotein translocase subunit (secY) protein translocation protein low temperatu	41.2%
HP1550	(secG) protein-export membrane protein (secD)	30.6%
HP1549	protein-export membrane protein (secF)	35.1%
HP1152	signal recognition particle protein (ffh)	41.4%
Transforma	trigger factor (tig) tion	27.6%
HP0520 HP0530	cag pathogenicity island protein (cag1) cag pathogenicity island protein (cag10)	96.5% 98.4%
HP0531 HP0532	cag pathogenicity island protein (cag11) cag pathogenicity island protein (cag12)	97.2% 98.9%
HP0534 HP0535	cag pathogenicity island protein (cag13) cag pathogenicity island protein (cag14)	98.0% 97.6%
HP0536	cag pathogenicity island protein (cag15)	96.4%
HP0538	cag pathogenicity island protein (cag10)	95.3%
HP0540	cag pathogenicity island protein (cag19)	99.5%
HP0521 HP0541	cag pathogenicity island protein (cag2) cag pathogenicity island protein (cag20)	97.8%
HP0542 HP0543	cag pathogenicity island protein (cag21) cag pathogenicity island protein (cag22)	97.9% 95.5%
HP0544 HP0545	cag pathogenicity island protein (cag23) cag pathogenicity island protein (cag24)	99.0% 98.5%
HP0546 HP0547	cag pathogenicity island protein (cag25) cag pathogenicity island protein (cag26)	95.7% 92.9%
HP0522	cag pathogenicity island protein (cag3)	98.1%
HP0523	cag pathogenicity Island protein (cag4)	95.7%
HP0523 HP0524 HP0526	cag pathogenicity Island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6)	95.7% 99.1% 97.5%
HP0523 HP0524 HP0526 HP0527 HP0528	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8)	95.7% 99.1% 97.5% 94.6% 99.0%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence linoprotein (cag9)	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag9) competence licoprotein (comJ) competence licoprotein (comJ) competence licoprotein (cag4)	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP1006 HP1421 HP0222	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence licoprotein (comL) competence licoprotein (comL) completence licoprotein (caG) conjugative transfer regulon protein (trb8) Mu processing chini A (ter0).	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7%
HP0523 HP0524 HP0526 HP0527 HP0528 HP0529 HP1378 HP1361 HP106 HP1421 HP0333 HP0042	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag9) competence lipoprotein (comL) competence lipoprotein (comL) conjugat transfer protein (traG) conjugative transfer regulon protein (trbB) DNA processing chain A (dprA) trol protein	95.7% 99.1% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4%
HP0523 HP0524 HP0526 HP0527 HP0529 HP0529 HP1361 HP1361 HP1361 HP1421 HP0333 HP0424 HP0525 HP0441 HP0527	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) campetence licoprotein (comL) competence licoprotein (comL) completence licoprotein (cag1) conjugative transfer regulon protein (trb8) DNA processing chain A (dprA) trb1 protein virB11 homologue	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.5%
HP0523 HP0524 HP0526 HP0527 HP0528 HP1378 HP1361 HP1006 HP1421 HP00333 HP0042 HP0525 HP0425 HP0459	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence locus E (comE3) completence locus E (comE3) conjugative transfer regulon protein (tbB) DNA processing chain A (dprA) trbl protein virB11 homologue VirB4 homologue (virB4) virB4 homologue (virB4)	95,7% 99,1% 97,5% 97,5% 99,0% 98,9% 25,5% 26,7% 22,5% 30,7% 32,9% 31,4% 100,0% 23,5% 25,2% 25,2% 25,2%
HP0523 HP0524 HP0526 HP0527 HP0529 HP0529 HP1378 HP1361 HP1006 HP1421 HP00525 HP0042 HP0525 HP0042 HP0042 HP00459 CENTRAL II	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence locus E (comE3) competence locus E (comE3) conjugative transfer regulan protein (trbB) DNA processing chain A (dprA) trbI protein virB1 homologue virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4)	95,7% 99,1% 91,5% 94,6% 94,6% 99,0% 25,5% 26,7% 27,3% 27,3% 27,3% 30,7% 32,9% 31,4% 100,0% 23,5% 25,2% 25,3%
HP0523 HP0526 HP0527 HP0527 HP0528 HP0529 HP1378 HP0628 HP1378 HP0378 HP0378 HP0378 HP0323 HP0042 HP0525 CENTRAL II <i>General</i> HP1014	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completine tocus E (comE3) conjugati transfer grouton protein (trbB) DNA processing chain A (dprA) trib protein virB4 homologue (virB4) virB4 homologue (virB4)	95.7% 99.1% 99.1% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.2% 25.3%
HPU623 HP0524 HP0526 HP0527 HP0528 HP0528 HP0528 HP0528 HP0528 HP1528 HP1371 HP1026 HP1421 HP0032 HP0042 HP0047 HP041 HP0041 HP1014 HP1014 HP1014 HP1004	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completing clocus E (comE3) conjugati transfer grouton protein (trbB) DNA processing chain A (dprA) trbl protein virB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase	95.7% 99.1% 99.1% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 23.5% 25.2% 25.2% 25.2% 25.3% 33.2% 33.2%
HPU624 HP0524 HP0527 HP0527 HP0528 HP0528 HP0528 HP0528 HP0528 HP0528 HP0528 HP1378 HP1028 HP1024 HP0022 HP0025 HP00459 HP0459 CENTRAL II General HP1014 HP0049 HP0049 HP0049	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein VirB4 homologue (virB4) virB4 homologue (virB4) virB4 homologue (virB4) VITERMEDIARY METABOLISM 7chydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein	95.7% 99.1% 97.5% 94.6% 98.9% 25.5% 26.7% 22.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.3% 33.2% 33.2% 33.2%
HP0523 HP0524 HP0527 HP0527 HP0528 HP0529 HP0529 HP0529 HP0529 HP0529 HP0529 HP0529 HP0529 HP0331 HP0042 HP0333 HP0042 HP0459 CENTRAL II General HP0459 CENTRAL II General HP0459 HP0869 HP0900	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) comjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein VirB4 homologue (VirB4) virB4 homologue (VirB4) virB4 homologue (VirB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hynA)	95.7% 99.1% 97.5% 94.6% 98.9% 25.5% 25.5% 22.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.3% 25.3% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 41.4%
HP0523 HP0523 HP0527 HP0527 HP0528 HP0529 HP1327 HP0529 HP1381 HP1052 HP1381 HP1033 HP0045 HP0333 HP0042 HP0333 HP0045 HP0459 CENTRAL II General HP1014 HP1014 HP1014 HP1014 HP10459 HP0090 HP0990 HP0999	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (VirB4) virB4 homologue (VirB4) virB4 homologue (VirB4) VirB4 homologue (VirB4) VITERMEDIARY METABOLISM 7hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hypA)	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 26.7% 30.7% 32.9% 32.9% 32.9% 32.9% 25.3% 33.2% 33.2% 33.2% 33.2% 33.2%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP1378 HP10529 HP1378 HP10528 HP1381 HP1042 HP0525 HP0042 HP0525 HP0041 HP0459 CENTRAL II <i>General</i> HP0469 HP0869 HP0900 HP0899 HP0898	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trbl protein wirB4 homologue (wirB4) wirB4	95.7% 99.1% 97.5% 94.6% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 32.9% 22.5% 25.3% 30.7% 32.9% 25.2% 25.3% 33.2% 34.2% 33.2% 34.2%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP1378 HP10529 HP1378 HP10528 HP138 HP1042 HP0459 CENTRAL II General HP0459 HP0469 HP0089 HP0089 HP0898 HP0047	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (VirB4) virB4 homologue (VirB4) virB4 homologue (VirB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase (cdA) hydrogenase expression/formation protein (hypA) hydrogenase expression/formation protein (hypC) hydrogenase expression/formation protein (hypC)	95.7% 93.1% 97.5% 99.0% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 23.5% 25.2%25.2% 25.2%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP0528 HP0528 HP0528 HP0528 HP0528 HP0451 HP0454 HP0459 CENTRAL II General HP0459 HP0469 HP0360 HP0399 HP0898 HP0047 HP0197	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trbl protein wir84 homologue (wir84) wir84 homol	95.7% 99.1% 97.5% 99.0% 99.0% 98.9% 25.5% 26.7% 27.3% 30.7% 23.5% 23.2% 23.2% 25.2%25.2% 25.2%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0527 HP0528 HP1381 HP1052 HP1381 HP1042 HP0459 CENTRAL II HP0459 CENTRAL II General HP049 HP0490 HP0499 HP0899 HP0898 HP0047 HP0197 Amino suge HP1532	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) conjugati transfer regulon protein (trbB) DNA processing chain A (dprA) trb protein VirB4 homologue (VirB4) virB4 homologue (VirB4) virB4 homologue (VirB4) virB4 homologue (VirB4) VITERMEDIARY METABOLISM 7-a-hydroxysteroid dehydrogenase (hdhA) carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase carbonic anhydrase (cfA) hydrogenase expression/formation protein (hyp6) hydrogenase expression/formation protein (hyp6) glucosamine fructose-6-phosphate	96.7% 99.1% 97.5% 99.0% 99.0% 99.0% 26.5% 26.7% 22.3% 30.7% 32.9% 31.4% 100.0% 23.5% 25.3% 25.3% 37.0% 33.2% 37.0% 33.3% 28.1% 41.4% 38.5% 41.4% 38.5%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0527 HP0528 HP1381 HP1052 HP1381 HP1042 HP0459 CENTRAL II HP0459 CENTRAL II General HP0459 HP0899 HP0898 HP0047 HP0197 Amino suge HP1532 Phosphorus	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) comjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trbl protein VirB4 homologue (virB4) virB4 homolo	96.7% 991% 97.5% 98.0% 98.0% 25.5% 25.5% 25.3% 22.5% 22.5% 22.9% 23.3% 22.5% 22.5% 23.2% 22.5% 23.2% 23.2% 23.2% 23.2% 23.3% 23.2% 23.3% 23.2% 23.3% 23.2% 23.5% 23.2% 23.5% 23.2% 23.5% 2
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0527 HP0528 HP0528 HP0528 HP0528 HP0528 HP0528 HP0454 HP0454 HP0454 HP0454 HP0454 HP0454 HP0454 HP0454 HP0454 HP0454 HP0528 HP0047 HP0528 HP	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) completence lioporotein (com2) completence lioporotein (com2) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb1 protein wirB4 homologue (wirB4) wirB4 homolo	96.7% 9917% 97.5% 9917% 9917% 9917% 9920% 25.5% 25.5% 25.5% 25.2% 25.3% 25.2% 25.3% 33.3% 33.4% 100.0% 25.2% 25.3% 33.4% 33.2% 33.2% 34.2% 33.2% 34.2% 33.2% 34.2% 33.2% 34.2% 32.2%
HPU0523 HPD0524 HPD0527 HPD0527 HPD0528 HPD0527 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD052 H	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) comjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue (virB	96.7% 991% 97.5% 98.0% 98.0% 25.5% 83.9% 25.5% 25.3% 22.9% 25.3% 32.2% 25.3% 33.4% 100.0% 25.2% 25.3% 33.4% 100.0% 25.2% 25.3% 33.4% 33.2% 31.4% 33.2% 31.4% 33.2% 33.4% 33.2% 33.4% 33.2% 33.2% 33.2% 33.4% 33.5%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP1378 HP10529 HP1378 HP10529 HP1378 HP10529 HP1378 HP1378 HP1378 HP0459 HP0459 HP0459 HP0459 HP0459 HP0690	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) comjugate transfer regular protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologue (vir	96.7% 98.7% 97.5% 98.0% 98.0% 25.5% 25.5% 22.5% 22.5% 22.9% 22.5% 22.9% 22.5% 22.9% 23.2% 33.3%
HPU0523 HPD0524 HPD0527 HPD0527 HPD0528 HPD0527 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD0528 HPD041 HPD052 H	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologu	96.7% 991% 97.5% 98.0% 98.0% 25.5% 83.9% 25.5% 25.3% 25.3% 32.9% 32.2% 32.7% 22.5% 25.3% 33.4% 100.0% 25.2% 25.3% 33.4% 41.4% 33.2% 41.4% 33.2% 41.4% 33.5% 33.5% 33.5%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP1381 HP10529 HP1381 HP10529 HP1381 HP1032 HP0459 CENTRAL II HP0459 CENTRAL II General HP0459 HP0459 HP0898 HP0047 HP152 Phosphorus HP0520 HP0590 HP0690 HP	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein virB4 homologue (virB4) virB4 homologu	96.7% 991% 97.5% 98.0% 98.0% 25.5% 25.5% 25.3% 22.5% 22.3% 22.5% 22.9% 22.5% 22.9% 22.5% 22.9% 22.5% 22.9% 22.5% 33.3% 41.4% 38.5% 41.4% 38.5% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.3%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP1381 HP1052 HP1381 HP1052 HP1381 HP1045 HP0459 CENTRAL II HP0459 CENTRAL II General HP0459 HP0459 HP0689	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) DNA processing chain A (dprA) trbl protein wir84 homologue (wir84) wir84 homolo	96.7% 98.7% 97.5% 98.0% 98.0% 25.5% 98.0% 25.5% 72.3% 22.9% 25.3% 22.9% 25.3% 33.3% 33.2% 41.4% 33.2% 41.4% 38.5% 41.4% 38.5% 33.3% 41.4% 33.3%
HPU624 HP0524 HP0527 HP0527 HP0527 HP0528 HP0527 HP0528 HP1381 HP10529 HP1381 HP10529 HP1381 HP1042 HP0459 CENTRAL II General HP0459 HP0459 HP0630 HP0630 HP	cag pathogencity island protein (cag4) cag pathogencity island protein (cag5) cag pathogencity island protein (cag6) cag pathogencity island protein (cag7) cag pathogencity island protein (cag8) cag pathogencity island protein (cag8) cag pathogencity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) DNA processing chain A (dprA) trib protein virB4 homologue (virB4) virB4 homologue (vi	96.7% 98.7% 97.5% 98.0% 98.0% 25.5% 98.0% 25.5% 72.3% 22.9% 25.3% 32.9% 22.5% 22.9% 25.3% 33.3% 33.2% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 33.3% 45.6% 25.5% 97.1% 33.3%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0527 HP0528 HP1381 HP1052 HP1381 HP1052 HP1381 HP1045 HP0459 CENTRAL II General HP0459 HP0459 HP0639 HP06	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) virB4 homologue (virB4) virB4 homologu	96.7% 98.7% 97.5% 98.0% 98.0% 25.5% 98.0% 25.5% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 25.3% 26.3% 26.3% 26.3% 26.3% 26.5% 27.3% 26.5% 27.3% 27.5% 27.3% 27.5%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0527 HP0528 HP0529 HP1381 HP1052 HP1381 HP1006 HP1381 HP1042 HP0459 CENTRAL II General HP0459 HP0459 HP0689 HP06	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein wir84 homologue (wir84) wir84 homologue (wir84) wir85 homologue (wir86) homologue (wir84) wir85 homologue (wir86) homologue (wir86) homologu	96.7% 98.7% 97.5% 98.0% 98.0% 25.5% 98.0% 25.5% 72.3% 22.9% 25.3% 22.9% 25.3% 33.3% 33.2% 41.4% 33.2% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 33.3% 45.6% 25.5% 97.1% 44.5% 50.0% 25.5% 97.1% 44.5% 96.0% 96.5% 96.2% 96.2%
HPU0523 HPD0524 HPD0524 HPD0527 HPD0527 HPD0528 HPD0527 HPD0528 HPD0529 HP1381 HP1006 HP1381 HP1006 HP1381 HP1042 HP00526 HP0041 HP1014 HP1014 HP1018 HP0049 HP0049 HP0049 HP0049 HP0049 HP0049 HP0049 HP0049 HP0049 HP0049 HP0050	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) vir84 homologue (vir84) vir84 homologue (vir86) vir84 homologue (vir86) vir86 homologu	96.7% 98.7% 97.5% 98.0% 98.0% 25.5% 98.0% 25.5% 72.3% 22.8% 25.3% 32.2% 37.0% 33.3% 22.5% 22.5% 23.2% 25.3% 33.3% 28.1% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 33.3% 45.6% 26.5% 98.5% 100.0%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0527 HP0529 HP1381 HP1052 HP1381 HP1006 HP1381 HP10421 HP0459 CENTRAL II General HP0459 HP047 HP0197 HP0898 HP0047 HP0197 Amino suge HP0529 HP0898 HP0047 HP0197 Amino suge HP0529 HP0898 HP0047 HP0197 Amino suge HP0520 HP0898 HP0047 HP0520 HP0689	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb protein wirB4 homologue (wirB4) wirB4 homologu	96.7% 98.7% 97.5% 98.0% 92.5% 98.0% 22.5% 22.5% 22.3% 22.3% 22.3% 22.3% 22.5% 22.3% 22.3% 22.5% 22.3% 22.5% 33.3% 22.5% 33.3% 28.1% 33.2% 33.2% 33.2% 33.2% 33.2% 33.5% 33.3% 33.5% 33.5% 33.5% 33.3% 45.6% 25.5% 99.5% 100.0%
HPU623 HP0524 HP0524 HP0527 HP0527 HP0528 HP0529 HP1381 HP10529 HP1381 HP10529 HP1381 HP10421 HP0459 CENTRAL II HP0459 CENTRAL II HP0459 HP0451 HP0459 HP0459 HP0689 HP069	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com3) conjugati transfer eguton protein (trbB) DNA processing chain A (dprA) trb1 protein wir84 homologue (wir84) wir84 homologue (wir84)	96.7% 99.1% 97.5% 98.0% 98.0% 25.5% 98.0% 25.5% 22.5% 22.5% 22.5% 22.5% 22.5% 22.5% 22.5% 22.5% 22.5% 22.5% 22.5% 23.2% 25.3% 23.2% 25.3% 23.2% 25.3% 23.2% 25.3% 23.2% 25.5% 33.3% 45.6% 25.5% 33.3% 45.6% 25.5% 33.3%
HPU0523 HPD0524 HPD0526 HPD0527 HPD0527 HPD0528 HPD0527 HPD0528 HPD0529 HP1381 HP1006 HP1381 HP1006 HP1421 HP0333 HP00421 HP0459 CENTRAL II General HP0459 HP0047 HP0197 HP0050 HP0898 HP0047 HP152 HP0689 HP	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) vir84 homologue (vir84) vir84 homologue (vir84) vir85 homologue (vir86) vir85 homologue (vir86) vir88 homologue (vir86) vir88 homologue (vir86) vir88 homologue (vir86) vir88 homologue (vir86) vir88 homologue (vir86) vir86 homologu	96.7% 98.7% 97.5% 98.0% 92.5% 98.0% 22.5% 22.5% 22.5% 22.9% 25.3% 33.3% 32.2% 37.0% 33.2% 37.0% 33.2% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 38.5% 41.4% 39.7% 41.5%
HPU0523 HPO523 HPO526 HPO527 HPO528 HPO527 HPO528 HPO529 HP1381 HP1052 HPO529 HP1381 HP1062 HP0333 HP0421 HP0459 CENTRAL II General HP0459 HP0459 HP0459 HP0459 HP0459 HP0689 HP0	cag pathogenicity island protein (cag4) cag pathogenicity island protein (cag5) cag pathogenicity island protein (cag6) cag pathogenicity island protein (cag7) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) cag pathogenicity island protein (cag8) competence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) completence lioporotein (com2) vir84 homologue (vir84) vir84 homologue (vir84) vir85 homologue (vir86) vir85 homologue (vir86) vir86 homologu	96.7% 99.1% 97.5% 99.0% 99.0% 25.5% 99.0% 25.5% 93.0% 22.5% 22.5% 22.5% 22.9% 25.3% 33.3% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.2% 33.3% 41.4% 38.5% 33.3% 45.6% 25.5% 99.0% 33.3% 45.6% 25.5% 91.1% 33.3%

HP1270	subunit (NQO10)	-1.0%
1104074	subunit (NQO11) ((Paracoccus denitrificans)	42.6%
HP12/1	subunit (NQO12)	43.2%
HP1272	NADH-ubiquinone oxidoreductase, NQO13 subunit (NQO13)	40.2%
HP1273	NADH-ubiquinone oxidoreductase, NQO14 subunit (NQO14)	31.2%
HP1266	NADH-ubiquinone oxidoreductase, NQO3	31.6%
HP1263	NADH-ubiquinone oxidoreductase,	44.00
HP1262	NADH-ubiquinone oxidoreductase, NQO5	44.0%
HP1261	subunit (NQO5) NADH-ubiquinone oxidoreductase, NQO6	-1.0%
HP1260	subunit (NQO6) NADH-ubiquinone oxidoreductase, NQO7	62.2%
HP1267	subunit (NQO7)	40.7%
1101207	subunit (NQO8)	42.4%
HP1268	NADH-ubiquinone oxidoreductase, NQO9 subunit (NQO9)	41.2%
Amino acida HP1398	s and amines alanine dehydrogenase (ald)	39.6%
HP0294	aliphatic amidase (aimE)	75.4%
HP1238 HP1399	arginase (rocF)	31.8%
HP0943 HP0056	D-amino acid dehydrogenase (dadA) delta-1-pyrroline-5-carboxylate dehydrogena	26.2% se
HP0723	(Synechocystis sp.)	32.2%
HP0132	L-serine deaminase (sdaA)	45.8%
Anaerobic HP0666	anaerobic glycerol-3-phosphate dehydroger	nase,
HP0589	subunit C (glpC) ferredovin ovidoreductase, alpha subunit	27.2%
HP0590	ferredoxin oxidoreductase, apria subunit	43.2%
HP0591 HP0193	ferredoxin oxidoreductase, gamma subunit fumarate reductase, cytochrome b subunit	33.3%
HP0192	(frdC) fumarate reductase, flavoprotein subunit	58.8%
LIDOADA	(frdA)	69.4%
HP0191	(frdB)	70.8%
HP1110	pyruvate ferredoxin oxidoreductase, alpha subunit	41.0%
HP1111	pyruvate ferredoxin oxidoreductase, beta	13 7%
HP1109	pyruvate ferredoxin oxidoreductase, delta	17.00
HP1108	subunit pyruvate ferredoxin oxidoreductase, gamma	47.0% a
470	subunit	37.2%
HP0828	ATP synthase FO, subunit a (atpB)	37.7%
HP1136 HP1137	ATP synthase FO, subunit b (atpF) ATP synthase FO, subunit bÕ (atpFÕ)	28.3% 32.5%
HP1212	ATP synthase FO, subunit c (atpE)	41.2%
HP1132	ATP synthase F1, subunit alpha (atpA) ATP synthase F1, subunit beta (atpD)	85.6%
HP1135 HP1131	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit epsilon (atpC)	24.6% 32.7%
HP1135 HP1131 HP1133	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit epsilon (atpC) ATP synthase F1, subunit gamma (atpG)	24.6% 32.7% 37.8%
HP1135 HP1131 HP1133 Electron trai HP0146	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit epsilon (atpC) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q	24.6% 32.7% 37.8%
HP1135 HP1131 HP1133 Electron trai HP0146 HP0265	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gesilon (atpC) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cvtochrome c biogenesis protein (ccdA)	24.6% 32.7% 37.8% 44.2% 35.4%
HP1135 HP1131 HP1133 Electron trai HP0146 HP0265 HP0378 HP0147	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ccfs) categore aviance difference ubunit	24.6% 32.7% 37.8% 44.2% 35.4% 37.5%
HP1135 HP1131 HP1133 Electron trai HP0146 HP0265 HP0378 HP0147	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diffeme subunit, membrane-bound (fixP)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1135 HP1131 HP1133 <i>Electron trai</i> HP0146 HP0265 HP0378 HP0147 HP0144	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit option (atpC) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper binding subunit, membrane-bound (fixP)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% -
HP1135 HP1131 HP1133 <i>Electron trai</i> HP0146 HP0265 HP0378 HP0147 HP0144 HP0145	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, dileme subunit, membrane-bound (fixP) cytochrome c oxidase, heme b and copper binding subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9%
HP1135 HP1131 HP1133 <i>Electron trai</i> HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1461	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (coco) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c oxidase	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9% 43.9%
HP1135 HP1131 HP1133 <i>Electron trai</i> HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP1227 HP0277	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (vcf5) cytochrome c oxidase, ditmen subunit, membrane-bound (fixP) cytochrome c oxidase, ditmen subunit, membrane-bound (fixP) cytochrome codiase, neme b and copper binding subunit, membrane-bound (fixN) cytochrome c563 perxidase cytochrome c563 ferredoxin	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% - 43.9% 45.7% 48.5% 38.4% 52.5%
HP1135 HP1131 HP1133 <i>Electron tra</i> . HP0146 HP0265 HP0147 HP0144 HP0145 HP1461 HP145 HP1461 HP1227 HP0277 HP0588 HP1508	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, ditme subunit, membrane-bound (fixP) cytochrome c oxidase, dimeme subunit, membrane-bound (fixP) cytochrome coxidase, neme b and copper binding subunit, membrane-bound (fixN) cytochrome c551 peroxidase cytochrome c553 ferredoxin-like protein ferredoxin-like protein	24.6% 32.7% 37.8% 44.2% 35.4% 35.4% 37.5% 43.9% 43.9% 45.7% 48.5% 38.4% 52.5% 42.6% 29.4%
HP1135 HP1131 HP1133 Electron trai HP0146 HP0265 HP0147 HP0144 HP0144 HP0145 HP1461 HP1227 HP0277 HP0288 HP1461 HP1227 HP0277 HP0588 HP1161 HP1508	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) hsport (CccQ) cytochrome c biogenesis protein (ccdA) cytochrome c biogenesis protein (ycf5) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c553 ferredoxin-like protein ferredoxin-like protein flavadoxin (fitA) bhDPBH ftw.indexchutene.	24 6% 32.7% 37.8% 44.2% 35.4% 35.4% 37.5% 43.9% 43.9% 45.7% 43.9% 45.5% 52.5% 42.6% 52.5% 42.6% 42.6%
HP1135 HP1131 HP1133 Electron trai HP0146 HP0285 HP0147 HP0144 HP0145 HP1461 HP0277 HP0145 HP1461 HP0277 HP0588 HP1461 HP0277 HP0588 HP1161 HP0279 HP1161 HP0279 HP1161 HP0279 HP1161 HP0279 HP1161 HP0279 HP1161 HP0279 HP1161 HP0279 HP1177 HP0279 HP1177 HP0279 HP1177 HP0279 HP1177 HP0279 HP1177 HP0279 HP0177 HP	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport (bb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, dineme subunit, membrane-bound (fixP) cytochrome c oxidase, dineme subunit, membrane-bound (fixP) cytochrome c553 ferredoxin-like protein ferrodoxin-like protein	24.6% 32.7% 32.7% 35.4% 35.4% 35.4% 33.0% 43.9% 44.5% 33.0% 445.5% 33.4% 445.5% 33.4% 445.5% 33.4% 445.5% 44.5% 44.5% 44.5% 33.2%
HP1135 HP1131 HP1133 Electron trai HP0146 HP0285 HP0378 HP0147 HP0144 HP0145 HP1461 HP0277 HP0145 HP1461 HP0277 HP0588 HP1161 HP0587 HP1664 HP10642 HP0664 HP06634	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport (bb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, diheme subunit, membrane-bound (fixQ) cytochrome c oxidase, diheme subunit, membrane-bound (fixQ) cytochrome c553 ferredoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fidA) NAD(P)H-flavin oxidoreductase oyngen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, (tydD	24.6% 32.7% 32.7% 35.4% 35.4% 35.4% 33.0% 43.9% 44.5% 33.0% 445.5% 33.4% 445.5% 33.4% 445.5% 33.4% 45.5% 42.6% 33.4% 42.6% 42.6% 42.6% 42.6% 52.5% 42.6% 52.5% 42.6% 52.5% 42.5% 51.
HP1133 HP1131 HP1133 Electron tra. HP0146 HP0265 HP0378 HP0144 HP0144 HP14461 HP14461 HP1456 HP10588 HP15068 HP15068 HP15068 HP15068 HP15068 HP15068 HP1508	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport (cbb3-type cytochrome c oxidase subunit Q (ccoQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, dineme subunit, membrane-bound (fixP) cytochrome coxidase, dineme subunit, membrane-bound (fixP) cytochrome c oxidase, dineme subunit, membrane-bound (fixQ) cytochrome c553 ferredoxin-like protein ferrodoxin-like protein ferrodoxin	24.6% 37.6% 37.6% 44.2% 33.6%
HP1133 Electron tra, HP0146 HP0265 HP0378 HP0144 HP0144 HP01445 HP1445 HP1445 HP1445 HP14577 HP0277 HP0277 HP0277 HP0277 HP0534 HP16642 HP06534 HP06534 HP06532	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport chb3-type cytochrome c oxidase subunit Q (coco) cytochrome c biogenesis protein (cod) cytochrome c biogenesis protein (cod) cytochrome c oxidase, dineme subunit, membrane-bound fik/) cytochrome c oxidase, heme b and coppe binding subund fik/ cytochrome c 551 peroxidase cytochrome c551 peroxidase cytochrome c553 ferredoxin flexodoxin-like protein flexodoxin-like protein flexodoxin (IdA) valione-reactive Ni/Fe hydrogenase, cytoci b subunit (hydC) quinone-reactive Ni/Fe hydrogenase, cytoci subunit (hydC) flexoferose-reactive Ni/Fe hydrogenase, cytoci subunit (hydC) flexoferose-reactive Ni/Fe hydrogenase, large subunit (hydC) flex flexoferose-reactive flexoferose-reactive Ni/Fe hydrogenase, large subunit (hydC) flex flexoferose-reactive flexoferose-reactive Ni/Fe hydrogenase, large subunit (hydC) flex flexoferose-reactive flexoferose-reactive Ni/Fe hydrogenase, large	24 69% 37,8% 37,8% 44,2% 33,8% 33,5% 33,0%
HP1133 HP1133 Electron tra. HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP1447 HP0145 HP14277 HP0144 HP12277 HP0508 HP1162 HP10527 HP0633 HP0633 HP0631	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-tyne cytochrome c oxidase subunit Q (coco) cytochrome c biogenesis protein (ccd) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, menoheme subunit, membrane-bound (fixP) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c553 ferredoxin-like protein ferredoxin-like protein ferrodoxin-like protein ferrodoxin-like protein flavdcdoxin (fidA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, (pto guinone-reactive Ni/Fe hydrogenase, subunit (ydA) quinone-reactive Ni/Fe hydrogenase, large subunit (tydA)	24.6% 37.8% 37.8% 44.2% 35.4% 37.5% 43.9% 43.9% 43.5% 33.4% 43.5% 33.4% 43.5% 33.4% 43.5% 43.5% 445.5% 445.5% 445.6% 52.6% 42.6% 42.6% 42.6% 42.6% 42.6% 52.6% 42.6% 55.6% 66.5% 66.5%
HP1133 HP1133 Electron tra. HP0146 HP0285 HP0147 HP0378 HP0147 HP0378 HP0147 HP0374 HP0374 HP0374 HP0374 HP0374 HP0372 HP0583 HP0631 HP0631 HP0539	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) raport cbb3-type cytochrome c oxidase subunit Q (CocO) cytochrome c biogenesis protein (cocA) cytochrome c oxidase, dileme subunit, membrane-bound (fkP) cytochrome c oxidase, dileme subunit, membrane-bound (fkP) cytochrome c oxidase, dileme subunit, membrane-bound (fkN) cytochrome c553 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (ddA) NAD(P)H-flixt) roxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, farge subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subunit (VydA) ubiquinol cytochrome c oxidoreductases, cytochrome cbsubunit (NdC)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1133 HP1133 Electron tra. HP0146 HP0245 HP0378 HP0147 HP0144 HP0145 HP1461 HP1277 HP0588 HP1461 HP1277 HP0588 HP1618 HP1638 HP0633 HP0633 HP0633 HP0631 HP0538	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) raport cbb3-type cytochrome c oxidase subunit Q (coco) cytochrome c biogenesis protein (codA) cytochrome c oxidase, diteme subunit, membrane-bound (fkP) cytochrome c oxidase, diteme subunit, membrane-bound (fkP) cytochrome c553 for cotication codiase, diteme b and copper binding subunit, membrane-bound (fkN) cytochrome c553 for codiase, diteme b and copper binding subunit, membrane-bound (fkN) cytochrome c553 for codiase, monoheme subunit, membrane-bound (fkO) cytochrome c553 for codiase, monoheme subunit, Mathematication (fidA) NAD(P)H-fits) roxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, furgo subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (breh)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1133 HP1133 HP1133 HP0146 HP0146 HP0147 HP0147 HP0147 HP0144 HP0145 HP1461 HP1277 HP0588 HP1616 HP16277 HP0633 H	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, ditme subunit, membrane-bound (fixP) cytochrome c oxidase, ditme subunit, membrane-bound (fixP) cytochrome c563 for doxin-like protein forrdoxin-like protein forrdoxin-like protein forrdoxin-like protein forrdoxin-like protein forrdoxin-like protein forrdoxin-like protein forrdoxin (fidA) NAD(P)H-flwin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, large subunit (hydA) quinone-reactive Ni/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase,	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9% 43.9% 43.9% 45.7% 45.9% 38.4% 52.5% 45.7% 45.5% 52.5% 42.6% 22.4% 42.6% 52.6% 42.6% 52.6% 42.6% 52.6% 42.6% 52.6% 42.6% 52.6% 42.6% 53.8,4% 53.8,4% 53.8,4% 53.8,4% 45.9% 54.6
HP1133 HP1133 HP1133 HP0146 HP0146 HP0147 HP0147 HP0147 HP0147 HP0144 HP0145 HP1461 HP1277 HP0588 HP1461 HP1277 HP0588 HP1642 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0538 HP1539 HP1538 HP1540 Entmer-Doug	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, ditmen subunit, membrane-bound (fkP) cytochrome c oxidase, ditmen subunit, membrane-bound (fkP) cytochrome c oxidase, ditmen subunit, membrane-bound (fkN) cytochrome c563 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein flavdoxin (fldA) NAD(P)H-flavin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, large subunit (hydB) quinone-reactive Ni/Fe hydrogenase, small subunit (hydB) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, Rieske 2Fe-2S subunit (fbcF) <i>bard</i>	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9% 43.9% 45.7% 45.9% 45.7% 45.7% 52.5% 45.7% 52.5% 42.6% 45.7% 45.7% 45.7% 46.1% 32.7% 46.1% 33.3% 33.3% 33.3% 33.3%
HP1133 HP1133 HP1133 HP1133 HP0146 HP0265 HP0378 HP0147 HP0144 HP0144 HP0145 HP1461 HP1277 HP0588 HP1611 HP0277 HP0588 HP1613 HP0633 HP0633 HP0632 HP0631 HP1539 HP1538 HP1540 Enther-Douc HP1099	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, dimen subunit, membrane-bound (fkP) cytochrome c oxidase, dimen subunit, membrane-bound (fkP) cytochrome c oxidase, dimen subunit, membrane-bound (fkN) cytochrome c553 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (ftdA) NAD(P)H-flew in oxidoreductase quinone-reactive Ni/Fe hydrogenase, fyrd b subunit (hydA) ubiquinol cytochrome c oxidoreductase, quinone-reactive Ni/Fe hydrogenase, snall subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c553 ferredoxin (ftdA) NAD(P)H-flew Ni/Fe hydrogenase, snall subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c 5xidoreductase, cytochrome c 5xidoreductase, fieske 2Fe-2S subunit (fbcF) 5xrdf	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9% 43.9% 45.7% 43.9% 45.7% 52.5% 45.7% 33.4% 45.7% 52.5% 45.7% 51.4% 68.5% 68.5% 68.9% 33.2% 68.8% 33.2%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0265 HP0378 HP0147 HP0144 HP0145 HP1461 HP0277 HP0588 HP1611 HP0588 HP16053 HP0632 HP0631 HP0632 HP0631 HP1539 HP1538 HP1540 Entner-Douc HP109 HP1100	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CcoQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c553 ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (ftdA) NAD(P)H-flavin oxidoreductase oxgen-insensitive NAD(P)H nitroreductase quinone-reactive NI/Fe hydrogenase, large subunit (hydC) guinone-reactive NI/Fe hydrogenase, small subunit (hydC) ubiquinol cytochrome c oxidoreductase, cytochrome c52 subunit (hydC) guinone-reactive NI/Fe hydrogenase, small subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c 52 subunit (hydA) subunit (hydA)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.3% 45.7% 43.3% 45.7% 45.7% 45.7% 52.5% 45.7% 52.5% 42.6% 42.6% 42.6% 42.6% 42.6% 42.6% 42.6% 52.7% 54.7% 54.7% 54.7% 54.7% 53.3% 66.5% 67.5% 65.5%
HP1135 HP1137 HP1133 Electron tra HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP0147 HP0144 HP0145 HP1461 HP0145 HP1461 HP0254 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1508 HP1539 HP1540 Entner-Douch HP1538 HP1540 Entner-Douch HP1508 HP1508 HP1540 Entner-Douch HP1508 HP150	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit opsilon (atpC) ATP synthase F1, subunit opsilon (atpC) ATP synthase F1, subunit opsilon (atpC) apport chb3-type cytochrome c oxidase subunit Q (cocQ) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dineme subunit, membrane-bound fikP) cytochrome c oxidase, monoheme subunit, membrane-bound fikP) cytochrome c oxidase, monoheme subunit, membrane-bound fikP) cytochrome c oxidase cytochrome c553 ferredoxin ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin (IdA) ANAP(PI-Histin oxidereductase oxgen-insensitive NAD(P)H nitroreductase oxgen-insensitive NAD(P)H nitroreductase, cytochrome c subunit (PdC) quinone-reactive NI/Fe hydrogenase, cytoci subunit (hydC) quinone-reactive NI/Fe hydrogenase, cytoci subunit (hydC) quinone-reactive NI/Fe hydrogenase, cytoci subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (BcH) ubiquinol cytochrome c oxidoreductase, fease 22-e23 subunit (BcH)	24.6% 37.6% 37.6% 44.2% 37.6% 37.5% 33.0% 43.3% 43.3% 45.7% 33.3% 45.7% 33.4% 45.7% 33.4% 65.5% 68.5% 68.5% 68.5% 68.9% 33.3% 22.8% 33.2%
HP1135 HP1137 HP1133 Electron tra. HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP0147 HP0144 HP0145 HP1461 HP1461 HP16277 HP0583 HP0632 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP1539 HP1606 Entner-Douch HP109 Fermentation HP1000 Fermentation	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-tyne cytochrome c oxidase subunit Q (cboQ) cytochrome c biogenesis protein (ccd) cytochrome c oxidase, diheme subunit, membrane-bound (fixP) cytochrome c oxidase, memb and copper binding subunit, membrane-bound (fixN) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c oxidase, monoheme subunit, membrane-bound (fixO) cytochrome c553 ferredoxin-like protein ferredoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein flavodoxin (fidA) NAD(P)H-fixin oxidoreductase oxgen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase (nyD) quinone-reactive Ni/Fe hydrogenase, sensiti subunit (tydA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, ford 2-ketec3-deoxy-6-phosphogluconate aldolas (eda) (wiD)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 43.9% 44.5% 33.9% 445.5% 445.5% 445.5% 45.5% 45.5% 68.5% 68.9% 39.3% 68.5% 68.9% 39.2% 68.5% 60.3% 50.3% 50.7%
HP1135 HP1137 HP1133 Electron tra. HP0146 HP0276 HP0147 HP0144 HP0378 HP0147 HP0144 HP0378 HP0145 HP1461 HP1227 HP0648 HP1658 HP0653 HP0653 HP06532 HP0653 HP06532 HP06531 HP1538 HP1540 Entner-Douc HP1500 Entner-Douc HP1500 HP1	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (CocO) cytochrome c biogenesis protein (cocA) cytochrome c oxidase, diheme subunit, membrane-bound (fkP) cytochrome c oxidase, diheme subunit, membrane-bound (fkP) cytochrome c oxidase, montheme subunit, membrane-bound (fkN) cytochrome c oxidase, montheme subunit, membrane-bound (fkN) cytochrome c 553 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (fidA) NAD(P)H-fitty in oxidoreductase oxygen-insensitive NAD(P)H nitroreductase, quinone-reactive Ni/Fe hydrogenase, furgo subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subunit (tydC) quinone-reactive Ni/Fe hydrogenase, s	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1135 HP1137 HP1133 Electron tra. HP0146 HP0278 HP0147 HP0144 HP0378 HP0147 HP0144 HP0378 HP0147 HP0378 HP0147 HP0378 HP0378 HP0378 HP0378 HP0633 HP0633 HP0633 HP0633 HP0633 HP0631 HP0539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1540 Entner-Doug HP1539 HP1540 Entner-Doug HP1539 HP1540 Entner-Doug	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) raport cbb3-tyne cytochrome c oxidase subunit Q (CocO) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dileme subunit, membrane-bound (fkP) cytochrome c oxidase, fileme subunit, membrane-bound (fkP) cytochrome c oxidase, non-theme subunit, membrane-bound (fkN) cytochrome c553 ferredoxin ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subunit (tydC)	24.6% 32.7% 37.8% 44.2% 35.4% 33.5% 33.0% 43.9% 43.9% 43.9% 45.5% 33.4% 33.4% 34.5% 34.4% 52.5% 42.6% 22.4% 42.6% 42.6% 668.9% 689.9% 689.9% 690.9% 6
HP1135 HP1137 HP1133 Electron tra. HP0146 HP0146 HP0147 HP0147 HP0147 HP0147 HP0147 HP0144 HP0145 HP1461 HP1277 HP0588 HP1617 HP0631 HP0631 HP0633 HP0631 HP0631 HP0631 HP0631 HP0631 HP0538 HP1530 HP1530 HP1538 HP1540 Entner-Douc HP1007 HP1509 HP1508 HP1538 HP1540 Entner-Douc HP0691 HP1509 HP150	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) isport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkN) cytochrome c553 forredoxin ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin (fldA) NAD(P)H-flxin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase, quinone-reactive Ni/Fe hydrogenase, large subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subun	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0% 43.9% 43.9% 43.9% 43.9% 45.7% 52.5% 42.6% 33.4% 52.5% 42.6% 52.6% 42.6% 52.6% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 65.5% 65.5% 65.5%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0146 HP0147 HP0147 HP0147 HP0144 HP0145 HP1461 HP1277 HP0588 HP1617 HP0588 HP1608 HP1608 HP16083 HP0634 HP0634 H	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dilmen subunit, membrane-bound (fkP) cytochrome c oxidase, dilmen subunit, membrane-bound (fkP) cytochrome c563 for cytochrome c 563 for cytochrome c 563 for cytochrome c 563 for cytochrome c 563 for cytochrome c563 for cytochrome c cytochrome c cytochrome cytochrome c563 for cytochrome c cytochrome c cytochrome subunit (hydC) quinone-reactive Ni/Fe hydrogenase, large subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydC) dubiquinol cytochrome c oxidoreductase, cytochrome to subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome to subunit (fbcH) ubiquinol cytochrome c oxidoreductase, for cytochrome to cytochronate aldolas (cda) 6-phosphogluconate dehydratase n 3-oxoadipate coA-transferase subunit A (yyE) acatelik kinase (ackA) [Escherichia coli) phosphate accelytansferase (pta) phosphate accelytansferase (pta) phosphat	24.6% 32.7% 37.8% 33.2% 33.5% 33.5% 33.5% 33.9% 43.9% 45.7% 45.9% 45.7% 45.9% 52.5% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 68.5% 68.5% 68.9% 33.3% 28.8% 50.3% 50.7% 65.5%
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HP1135 HP1131 HP1133 Electron tra HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP0147 HP0147 HP0144 HP0145 HP1461 HP0284 HP1508 HP1	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit desilon (atpC) ATP synthase F1, subunit gamma (atpG) nsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (ccdA) cytochrome c oxidase, ditme subunit, membrane-bound (fixP) cytochrome c oxidase, ditme subunit, membrane-bound (fixP) cytochrome c oxidase, ditme subunit, membrane-bound (fixP) cytochrome c553 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (fidA) NAD(P)H-flwri oxidoreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase oxygen-insensitive NAD(P)H nitroreductase, cytochrome c coxidoreductase, cytochrome c coxidoreductase, cytochrome c coxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, cytochrome c subunit (fbcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (fbcH) duipanion-eractive Ni/Fe hydrogenase, large subunit (flyGB) 2-keto-3-dexy-6-phosphogluconate aldolas (eda) 6-phosphogluconate dehydratase <i>n</i> 3-coxadipate coA-transferase subunit A (xyID) 3-coxadipate coA-transferase subunit A (xyID) 3-coxadipate coA-transferase subunit B (xyE) phosphogluconate dehydratase <i>n</i> acetate kinase (ackA) [Escherichia coli) phosphate acety[transferase (pta) short-hain alcohol dehydrogenase phosphoenlopyruate synthase (ppsA) phosphoglycerate kinase	24 69% 327% 327% 337.8% 332.7% 333.0% 44.2% 33.0% 43.9% 45.7% 33.0% 45.7% 33.0% 45.7% 33.4% 45.7% 52.6% 52.6% 45.6% 68.5% 68.5% 68.9% 33.3% 28.8% 33.3% 28.8% 33.2% 65.5% 65.5% 65.5% 65.5% 65.5% 65.5% 65.2% 65.2% 65.5% 65.2% 65.2% 65.5% 65.2
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP0147 HP0144 HP0145 HP1227 HP0277 HP1268 HP12277 HP0583 HP0583 HP0583 HP0583 HP0631 HP0583 HP0631 HP0583 HP0583 HP0583 HP0583 HP0583 HP1540 Entner-Dout HP0590 HP1100 Fermentatio HP0590 HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 Gluconeoge HP0357 HP0	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport chb3-type cytochrome c oxidase subunit Q (cocol) cytochrome c biogenesis protein (cocf) cytochrome c oxidase, dineme subunit, membrane-bound (fixP) cytochrome c oxidase, neme b and copper binding subunit, membrane-bound (fixN) cytochrome c oxidase, nemo b and copper binding subunit, membrane-bound (fixN) cytochrome c oxidase, nemotheme subunit, membrane-bound (fixP) cytochrome c53 ferridoxin-like protein ferrodoxin-like sprotein subunit (tyQC) quinone-reactive Ni/Fe hydrogenase, cytoch subunit (tyQA) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c subunit (bcH) ubiquinol cytochrome c oxidoreductase, frasek 2F-2S subunit (bcH) socroalipate coA-transferase subunit A (yKD) acteate kinase (ackA) [Escherichia coli) phosphonenolpyruvate synthase (pas) phosphonenolpyruvate synthase (pas) phosphonenolpyruvate synthase (pas) phosphonenolpyruvate synthase (pas) enolase (eno)	24.6% 32.7% 37.8% 44.2% 43.9% 43.9% 43.9% 44.5% 33.9% 445.5% 445.5% 445.5% 445.5% 445.5% 445.5% 445.5% 445.5% 685.9% 685.9% 68.9% 39.3% 68.5% 665.5% 65.3% 65.5% 6
HP1135 HP1137 HP1133 Electron tra. HP0146 HP0265 HP0147 HP0144 HP0145 HP0147 HP0144 HP0145 HP0147 HP0144 HP0145 HP12277 HP0580 HP12277 HP0580 HP1621 HP0533 HP0631 HP0631 HP0631 HP0631 HP0631 HP1538 HP16062 HP0631 HP1538 HP16062 HP0631 HP1638 HP16094 HP1009 Fermentatio HP0690 HP1000 Fermentatio HP0690 HP1000 Fermentatio HP0395 Gluconeoge HP0385 Gluconeoge HP0385 HP0121 HP0395 Gluconeoge HP0385 HP0121 HP0378 HP037	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-tyne cytochrome c oxidase subunit Q (cboQ) cytochrome c biogenesis protein (ccd) cytochrome c oxidase, diheme subunit, membrane-bound (fixO) cytochrome c oxidase, mem b and copper binding subunit, membrane-bound (fixO) cytochrome c oxidase, neme b and copper binding subunit, membrane-bound (fixO) cytochrome c oxidase, neme b and copper binding subunit, membrane-bound (fixO) cytochrome c 553 ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein ferrodoxin-like protein guinone-reactive Ni/Fe hydrogenase (hyd) quinone-reactive Ni/Fe hydrogenase, cytoc b subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydC) quinone-reactive Ni/Fe hydrogenase, small subunit (hydC) acotate kinase (ackA) (Escherichia coii) phosphongluconate dehydratase nosis finctiose-16-bisphosphatase phosphonen/pirvuxte synthase (ppsA) phosphonen/pirvuxte synthase (ppsA) phosphonen/pirvuxte synthase (ppsA) phosphonen/pirvuxte synthase (ppsA) phosphonen/pirvuxte synthase (psA) fuccoice-bisphosphate adolase (tsr) fuccoice-bisphosphatese	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 43.9% 44.2% 43.9% 445.5% 445.5% 445.5% 45.7% 45.5% 38.4% 52.5% 52.5% 54.7% 54.7% 54.7% 56.5% 665.5% 665.5% 665.5% 673.2% 50.3% 50.3% 50.3% 50.7% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0% 52.4% 51.0%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP0147 HP0144 HP0277 HP0144 HP0277 HP0588 HP12277 HP0688 HP12277 HP0688 HP12277 HP0688 HP12277 HP0688 HP12277 HP0683 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0692 HP0095 HP0120 HP0095 HP0095 HP0036 HP0037 HP0036 HP0037 HP0036 HP0037 HP0036 HP0037 HP0036 HP0036 HP0037 HP0036 HP0037 HP0036 HP0037 HP0036 HP0037 HP0036 HP0036 HP0037 HP0036 HP00	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-tyne cytochrome c oxidase subunit Q (CocO) cytochrome c biogenesis protein (cocA) cytochrome c oxidase, diheme subunit, membrane-bound (fkP) cytochrome c oxidase, diheme subunit, membrane-bound (fkP) cytochrome c oxidase, diheme subunit, membrane-bound (fkN) cytochrome c 553 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (fidA) NAD(P)H-fitti) oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinone-reactive Ni/Fe hydrogenase, (ptO quinone-reactive Ni/Fe hydrogenase, seruit subunit (tydC) quinone-reactive Ni/Fe hydrogenase, seruit subunit (hydC) quinone-reactive Ni/Fe hydrogenase, seruit subunit (hydC) acotate coA-transferase subunit A (yiD) acotate kinase (ackA) [Escherichia coil) phosphotransace/Iase (pta) phosphotenolpyruvate synthase (psA) phosphoplycerate kinase enolase (eno) fructose-bisphosphate aldolase (tsr) glucose-epitaesphate isomerase (pgi)	24.6% 32.7% 37.8% 44.2% 35.4% 37.5% 33.0%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0275 HP0147 HP0144 HP0378 HP0147 HP0144 HP0378 HP0147 HP0378 HP0144 HP0277 HP0583 HP1461 HP1277 HP0583 HP1461 HP0631 HP0631 HP0633 HP0631 HP0631 HP0631 HP0631 HP0631 HP0539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1539 HP1540 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0357 HP0164 HP0363 HP0164 HP0357 HP0164 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0137 HP0154 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0136 HP0137 HP0136 HP0137 HP0146 HP0137 HP0146 HP0137 HP0146 HP0137 HP0146 HP037 HP0146 HP037 HP0146 HP037 HP0146 HP037 HP0146 HP037 HP0147 HP037 HP	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit gamma (atpG) raport cbb3-tyne cytochrome c oxidase subunit Q (CocO) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dileme subunit, membrane-bound (fkP) cytochrome c oxidase, fileme subunit, membrane-bound (fkP) cytochrome c oxidase, fileme subunit, membrane-bound (fkN) cytochrome c 553 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin-like protein ferredoxin (fdA) NAD(P)H-flixin oxidoreductase oxygen-insensitive NAD(P)H nitroreductase aquinone-reactive Ni/Fe hydrogenase, furge subunit (tydC) quinone-reactive Ni/Fe hydrogenase, small subunit (tydC) acteate kinase (ackA) (Escherichia coli) phospholgenone soliticate - 6.45isphosphatase phosphoransacetylase (pla) phospholgivcarte kinase enolase (eno) fructose-bisphosphate isomerase (pg)) glucose-6.phosphate isomerase (pg) glucose-6.phosphate	24.6% 32.7% 37.8% 44.2% 35.4% 33.5% 33.0%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0146 HP0147 HP0147 HP0144 HP0145 HP1461 HP1277 HP0548 HP1461 HP1277 HP05680 HP1605 HP1605 HP1605 HP0631 HP0633 HP0632 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0631 HP0632 HP0631 HP0632 HP0631 HP0632 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0631 HP0632 HP0631 HP0632 HP0631 HP0631 HP0632 HP0631 HP0632 HP0631 HP0632 HP0631 HP0631 HP0632 HP0631 HP0631 HP0632 HP0631 H	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit opsilon (atpC) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (Coco) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome co didase, dimene subunit, membrane-bound (fkP) cytochrome c553 for cytochrome cytochrome cytochrome cytochrome c553 for cytochrome	24.6% 32.7% 37.8% 44.2% 35.4% 33.5% 33.0% 43.3% 43.9% 43.9% 45.7% 33.4% 52.5% 52.5% 42.6% 52.5% 42.6% 52.6% 42.6% 52.6% 42.6% 51.4% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 65.5% 65.5% 73.2% 65.5% 73.5% 73.2% 65.5% 73.5% 74.5% 75.5%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0146 HP0147 HP0147 HP0147 HP0147 HP0147 HP0147 HP0144 HP0277 HP0588 HP1277 HP0588 HP1631 HP0631 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0634 HP0035 HP0154 HP0035 HP	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit denial (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (codA) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c563 for cytochrome c 563 for cytochrome c563 for cytochrome c synthese cytochrome b subunit (hcH) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c57 subunit (htpC) gotochrome c57 for cytochrome c coxidoreductase, cytochrome c1 subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (bcH) ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit (htpC) gotochrome c0, ficher cytochrome c subunit (htpC) gotochrome c1 subunit (btC) phosphogluconate dehydrogenase fnutose-bisphosphatase phosphoglycerate kinase enolase (col) phosphoglycerate kinase enolase (col) phosphoglycerate kinase enolase (col) phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglycerate kinase enolase (clk) glucose-c-phosphatase phosphoglyc	24.6% 32.7% 37.8% 44.2% 33.7% 33.7% 44.2% 43.9% 45.7% 45.9% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 68.5% 63.3% 65.5%
HP1135 HP1131 HP1133 Electron tra. HP0146 HP0146 HP0147 HP0147 HP0147 HP0144 HP0145 HP1461 HP1277 HP0588 HP1617 HP0583 HP0631 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0633 HP0634 HP0634 HP0639 HP0150 HP0150 HP0150 HP0150 HP0150 HP0151 HP0154 HP0251 HP0154 HP0154 HP0154 HP0154 HP0154 HP0154 HP0155 HP0154 HP0155 HP	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit denia (atpH) ATP synthase F1, subunit gamma (atpG) rsport ctb3-type cytochrome c oxidase subunit Q (CocQ) (CocQ) cytochrome c biogenesis protein (cdA) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c563 ferredoxin ferredoxin-like protein ferredoxin-like protein ferodoxin-like protein- ferodoxin-like protein- ferodoxin-like protein- ferodoxin-like protein- ferodoxin-like protein- ferodoxin-like protein- fizus-to-to-me c oxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, ficet 2F-2S subunit (fbcF) dordf 2-keto-3-dexy-6-phosphogluconate aldolase (eda) 6-phosphogluconate dehydratase n 3-oxoadipate co-A-transferase subunit A (yXD) 3-oxoadipate co-A-transferase subunit B (yKE) glucose-16-bisphosphatase phosphoglycerate kinase enolase (eno) phosphoglycerate kinase enolase (gk) glucose-6-phosphate aldolase (tsr) glucokinase (gk) glucose-6-phosphate isomerase (gpi) glyceraidehyde3-phosphate dehydrogenase (gap) phosphoglycerate mutase (pgm) triosephosphosphate isomerase (tpi) sphate pathway	24.6% 32.7% 37.8% 44.2% 33.7% 33.0% 44.2% 43.9% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 46.5% 53.3%
HP1135 HP1131 HP1133 Electron tra HP0146 HP0285 HP0147 HP0147 HP0144 HP0145 HP0147 HP0147 HP0144 HP0145 HP1461 HP0277 HP0277 HP0277 HP0277 HP0277 HP0277 HP02633 HP1608 HP1508 HP	ATP synthase F1, subunit delta (atpH) ATP synthase F1, subunit denia (atpH) ATP synthase F1, subunit gamma (atpG) rsport cbb3-type cytochrome c oxidase subunit Q (CocQ) cytochrome c biogenesis protein (vcf5) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c oxidase, dimene subunit, membrane-bound (fkP) cytochrome c Soldase, dimene subunit, membrane-bound (fkN) cytochrome c563 ferredoxin ferredoxin-like protein ferredoxin-like protein ferredoxin (ftA) NAD(P)H-flwinv oxidoreductase oxygen-insensitive NAD(P)H nitroreductase quinon-reactive Ni/Fe hydrogenase, large subunit (hydA) ubiquinol cytochrome c oxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, cytochrome c oxidoreductase, fieske 2Fe-2S subunit (fbcH) ubiquinol cytochrome c oxidoreductase, fieske 2Fe-2S subunit (fbcH) acoadipate coA-transferase subunit A (vxjD) 3-oxoadipate coA-transferase subunit A (vxjD) 3-oxoadipate coA-transferase subunit A (vxjD) 3-oxoadipate coA-transferase subunit A (vxjD) 3-oxoadipate coA-transferase (pa) short-hain alcohol dehydrogenase (pas) phosphoglycerate kinase enolase (eno) fructose-bisphosphate aldolase (tsr) glucokinase (gk) glucose-biphosphate dehydrogenase (pap) phosphoglycerate mutase (pgm) triosephosphate isomerase (pgi) glucose-biphosphate 1-dehydrogenase (pa) phosphoglycerate mutase (pgm) triosephosphate isomerase (pgi) glucose-biphosphate 3-pinemase (pgi)	24.6% 32.7% 37.8% 32.7% 33.2% 33.2% 44.2% 45.7% 43.9% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 45.7% 68.5% 68.5% 65.5%

UD1101	(devB)	29.2%
	(g6pD)	36.7%
HP1495 HP1088	transaldolase (tal) transketolase A (tktA)	33.5% 46.7%
HP0354 Sugare	transketolase B (tktB)	39.7%
HP0574	galactosidase acetyltransferase (lacA)	41.0%
TCA cycle	UDP-glucose 4-epimerase	43.1%
HP0779 HP0026	aconitase B (acnB) citrate synthase (gltA)	64.0% 47.8%
HP1325	fumarase (fumC)	63.7%
HP0509 HP0027	isocitrate dehydrogenase (icd)	98.0% 70.7%
FATTY ACIE	AND PHOSPHOLIPID METABOLISM	
General HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein)	
HP1348	dehydratase (fabZ) 1-acyl-dlycerol-3-phosphate acyltransferase	47.4%
LIDOSCI	(plsC) (Escherichia coli)	32.0%
	(fabG)	45.7%
HP0690	acetyl coenzyme A acetyltransferase (thiolase) (fadA)	52.0%
HP0950	acetyl-CoA carboxylase beta subunit (accD)	49.4%
HP1045 HP0557	acetyl-CoA synthetase (acoE)	52.3% 50.3%
HP0559	acyl carrier protein (acpP)	55.3%
HP0962 HP0558	beta ketoacyl-acyl carrier protein synthase	56.3%
HP0202	(fabF) beta-ketoacyl-acyl carrier protein synthase	50.0% III
LID0271	(fabH)	44.4%
HP0370	biotin carboxylase (accC)	52.1%
HP0871 HP0215	CDP-diglyceride hydrolase (cdh) CDP-diglyceride synthetase (cdsA)	73.9% 42.4%
HP0416	cyclopropane fatty acid synthase (cfa)	39.7%
HP0700 HP0195	diacylglycerol kinase (dgkA) enovl-(acyl-carrier-protein) reductase (NADE	45.8% -1)
1100004	(fabl)	45.8%
HP0201	(plsX)	37.8%
HP0808 HP0090	Holo-acp synthase (acpS) malonyl coenzyme A-acyl carrier protein	29.1%
LID1016	transacylase (fabD)	35.4%
	(pgsA)	35.4%
HP1357	phosphatidylserine decarboxylase proenzyr (psd)	ne 33.2%
HP1071 HP0499	phosphatidylserine synthase (pssA) phospholipase A1 precursor	99.6%
	(DR-phospholipase A)	33.8%
PURINES, P	YRIMIDINES, NUCLEOSIDES AND NUCLEC	TIDES
General HP0757	beta-alanine synthetase homologue	40.0%
2Õ-Deoxyrik	oonucleotide metabolism	
HP0372	deoxycytidine triphosphate deaminase (dcd)	28.2%
HP0865	deoxyuridine 50-triphosphate nucleotidohyda (dut)	rolase 41.4%
HP0364	ribonucleoside diphosphate reductase, beta	30.0%
HP0680	ribonucleoside-diphosphate reductase 1 alp	ob.010 oha
HP0825	thioredoxin reductase (trxB)	45.9%
Purine ribor	nucleotide biosynthesis	44 00%
HP0618	adenylate kinase (adk)	33.3%
HP1112 HP0255	adenylosuccinate lyase (purB)	49.5%
HP1434	formyltetrahydrofolate hydrolase (purU)	49.1%
HP1218	(purD)	31.8%
HP0854 HP0409	GMP reductase (guaC) GMP synthase (guaA)	31.8% 56.1%
HP0829	inosine-50-monophosphate dehydrogenase	58 5%
HP0198	nucleoside diphosphate kinase (ndk)	67.7%
HP0742	(prsA)	56.5%
HP1530	purine nucleoside phosphorylase (punB)	20.7%
HP1084	aspartate transcarbamoylase (pyrB)	38.7%
11-0918	hydrolysing) (pyrAb)	48.6%
HP1237 HP0349	carbamoyl-phosphate synthetase (pyrAa) CTP synthetase (pyrG)	39.7% 50.7%
HP0266	dihydroorotase (pyrC)	-1.0%
HP0581 HP1011	dihydroorotase (pyrC) dihydroorotate dehydrogenase (pyrD)	31.5% 41.5%
HP1257	orotate phosphoribosyltransferase (pyrE)	35.5%
HP0005 HP1474	thymidylate kinase (tmk))39.0% 33.9%
HP0777	uridine 50-monophosphate (UMP) kinase (pyrH)	50.4%
Salvage of I	nucleosides and nucleotides Ø30ovclic-nucleotide 20-phosphodiesterase	
1100570	(cpdB)	31.8%
HP1179	phosphopentomutase (deoB)	55.9%
HP1178 HP0735	purine-nucleoside phosphorylase (deoD) xanthine guanine phosphoribosyl transferas	55.5% se
Sugar-nucle	(gpt) eotide biosynthesis and conversions	27.1%
HP0043	mannose-6-phosphate isomerase (pmi) or	12 8%
HP0045	nodulation protein (noIK)	44.3%
HP0646 HP0683	UDP-glucose pyrophosphorylase (galU) UDP-N-acetylglucosamine pyrophosphoryla	65.6% Se
	(gImU)	40.0%
REGULATO	RY FUNCTIONS	
HP1032	alternative transcription initiation factor, sign	na-F
HP1168	(fliA) carbon starvation protein (cstA)	34.6% 59.8%
HP1442	carbon storage regulator (csrA)	43.3%
HP0278	guanosine pentaphosphate phosphohydrola	ଧୟ:୫୩୦ ase
HP0400	(gppA) penicillin tolerance protein (IvtB)	26.4% 30.6%

HP0775	penta-phosphate guanosine-30-pyrophospho)- 06 70
HP0224	nydrolase (spol) peptide methionine sulphoxide reductase	30.7%
III OLL I	(msrA)	66.8%
HP1025 HP1572	putative heat shock protein (hspR)	46.2%
HP0703	response regulator	44.2%
HP1021	response regulator	28.7%
HP1365	response regulator	32.4%
HP0166	response regulator (ompR)	51.0%
HP0714 HP0088	RNA polymerase sigma-54 factor (rpoN) RNA polymerase sigma-70 factor (rpoD)	43.5%
HP0792	sigma-54 interacting protein	97.7%
HP0164 HP1364	signal-transducing protein, histidine kinase signal-transducing protein, histidine kinase	27.1%
HP0244	signal-transducing protein, histidine kinase	
HP0048	(atoS) transcriptional regulator (bypE)	30.0%
HP1287	transcriptional regulator (tenA)	34.7%
HP0727	transcriptional regulator, putative	33.3%
REPLICATIO	N .	
Degradation	of DNA	07.00
HP0275 HP0259	AIP-dependent nuclease (addB) exonuclease VII. large subunit (xseA)	27.2% 37.6%
DNA replica	ation, restriction, modification, recombination	and repair
HP0142	A/G-specific adenine glycosylase (mutY)	38.2%
HP0050	(donA)	37.4%
HP0910	adenine specific DNA methyltransferase	0.0 4.01
HP1352	(HINDIIM) adenine specific DNA methyltransferase	33.4%
	(HINFIM)	62.5%
HP0263	adenine specific DNA methyltransferase (hoaim)	33.006
HP0481	adenine specific DNA methyltransferase	00.070
LD0260	(MFOKI)	29.3%
111 0200	(mod)	33.9%
HP0593	adenine specific DNA methyltransferase	20 50/-
HP1522	adenine specific DNA methyltransferase	30.0%
1100.170	(mod)	42.2%
HP0478	adenine specific DNA methyltransferase (VSPIM)	421%
HP0054	adenine/cytosine DNA methyltransferase	32.1%
HP0790 HP1529	anti-codon nuclease masking agent (prrB) chromosomal replication initiator protein	42.9%
111 1020	(dnaA)	34.9%
HP1121	cytosine specific DNA methyltransferase	27.00/
HP0051	cytosine specific DNA methyltransferase	37.0%
	(DDEM)	39.0%
HP0483	(HPHIMC)	38.7%
HP0701	DNA gyrase, sub A (gyrA)	97.4%
HP0501	DNA gyrase, sub B (gyrB)	46.0%
HP0548	DNA helicase, putative	38.8%
HP0615	DNA ligase (lig)	40.1%
HP1470	DNA mismatch repair protein (ividits) DNA polymerase I (polA)	40.0%
HP1460	DNA polymerase III alpha-subunit (dnaE)	42.0%
HP0500 HP1231	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit	26.0%
HP0500 HP1231	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit (hoIB)	26.0% 48.6%
HP0500 HP1231 HP1387 HP0717	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit (hoIB) DNA polymerase III epsilon subunit (dnaQ) DNA polymerase III gamma and tau subuni	26.0% 48.6% 35.1%
HP0500 HP1231 HP1387 HP0717	DNA polymerase III beta-subunit (dnaN) DNA polymerase III delta prime subunit (hoIB) DNA polymerase III epsilon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX)	26.0% 48.6% 35.1% its 39.0%
HP0500 HP1231 HP1387 HP0717 HP0012 HP1523	DNA polymerase III beta-subunit (dnaN) DNA polymerase III detta prime subunit (hoIB) DNA polymerase III desilon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA primase (dnaG)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7%
HP0500 HP1231 HP1387 HP0717 HP0012 HP1523 HP1393	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III epsilon subunit (dnaQ) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA recombinase (recG) DNA repair protein (recR)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3%
HP0500 HP1231 HP0717 HP0012 HP1523 HP1393 HP0116 HP0140	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III epsilon subunit (dnaO) DNA polymerase III gamma and tau subun (dnaX) DNA promase (dnaG) DNA recombinase (recG) DNA repair protein (recN) DNA repoisomerase I (topA)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3% 45.1%
HP0500 HP1231 HP1387 HP0717 HP012 HP1523 HP1523 HP0116 HP0400 HP0602	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA proymerase (dnaG) DNA recombinase (recG) DNA repair protein (recN) DNA topoisomerase I (topA) DNA topoisomerase II endonuclease III	26.0% 48.6% 35.1% ts 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6%
HP0500 HP1231 HP1387 HP0717 HP012 HP1523 HP1393 HP0116 HP0440 HP0602 HP0585	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA recombinase (recG) DNA recombinase (recG) DNA repair protein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) endonuclease III endonuclease III endonuclease III endonuclease III (th)	26.0% 48.6% 35.1% ts 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 40.1% 52.4%
HP0500 HP1231 HP1387 HP0717 HP012 HP1523 HP1523 HP016 HP016 HP0400 HP0602 HP0585 HP0705 HP1114	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA repoirmerase (ingA) DNA repoirmerase (ingA) DNA topoisomerase (itopA) endonuclease III (nth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 40.1% 53.4%
HP0500 HP1231 HP1387 HP0717 HP012 HP1523 HP1523 HP016 HP016 HP0400 HP0602 HP0585 HP0114 HP0705 HP1114 HP0821	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA repair protein (recG) DNA repair protein (recR) DNA topoisomerase I (topA) endonuclease III (topA) excinuclease III (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit C (uvrC)	26.0% 48.6% 35.1% ts 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 36.6% 40.1% 53.4% 53.4% 53.1% 31.5%
HP0500 HP1331 HP1387 HP0717 HP0717 HP1523 HP012 HP1523 HP0116 HP0440 HP0585 HP0705 HP0705 HP0705 HP0114 HP1114 HP0821 HP0213	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase (dnaG) DNA recombinase (rec0) DNA topoisomerase I (topA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) endonuclease III endonuclease III endonuclease III (mth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrB) excinuclease ABC subunit A (uvrB) excinuclease ABC subunit A (uvrB) excinuclease ABC subunit A (uvrB) excinuclease (lexA) duccse inhibited division orotein (didA)	26.0% 48.6% 35.1% 18 39.0% 36.6% 32.7% 28.3% 45.1% 36.6% 31.7% 36.6% 45.1% 53.4% 53.1% 53.1% 53.1% 53.9%
HP0500 HP1231 HP1337 HP0717 HP0717 HP1523 HP016 HP1523 HP016 HP0640 HP0685 HP0705 HP0705 HP0705 HP0705 HP1114 HP1526 HP0703	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA recombinase (recG) DNA repair protein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) endonuclease III endonuclease III endonuclease III endonuclease III excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease inhibited division protein (gidA) glucose-inhibited division protein (gidA)	26.0% 48.6% 35.1% 18 39.0% 36.6% 32.7% 36.6% 45.1% 31.7% 53.4% 53.4% 31.5% 53.3% 31.5% 53.3% 48.5% 32.9%
HP0500 HP1231 HP1387 HP0717 HP0717 HP0717 HP1623 HP1383 HP0116 HP0440 HP0440 HP0440 HP04602 HP0705 HP1114 HP0585 HP0705 HP114528 HP0705 HP1063	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA promisase (fraG) DNA repositionase (recO) DNA repositionase (recO) DNA topoisomerase I (topA) DNA topoisomerase I (topA) endonuclease III (nth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrC) glucose-inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase	26.0% 48.6% 35.1% 18 39.0% 36.6% 32.7% 32.7% 32.7% 31.7% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.3% 40.1% 53.9% 48.5% 32.9% 33.0%
HP0500 HP1231 HP1387 HP0717 HP0012 HP1523 HP1393 HP0116 HP0440 HP0705 HP1114 HP0821 HP0705 HP1114 HP0821 HP1526 HP0213 HP1563 HP1659	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA repoiser (dnaG) DNA repoiser (dnaG) DNA repoiser (dnaC) DNA topoisererase I (topA) endonuclease III (dnA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrC) exodeoxyribouclease (lexA) glucose-inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA)	26.0% 48.6% 35.1% 33.0% 36.6% 45.1% 28.3% 45.1% 31.7% 36.6% 40.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.2.9% 53.1% 53.2.9% 53.2.9% 53.2.9% 53.2.9% 53.2.9% 53.5%
HP0500 HP1231 HP1387 HP0717 HP0717 HP0717 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III genrina and tau subun (dnaX) DNA polymerase III genrina and tau subun (dnaX) DNA polymerase II (gnaM) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA)	26.0% 48.6% 35.1% 35.0% 36.6% 28.3% 45.1% 36.6% 45.1% 53.4% 53.1% 53.4% 53.4% 53.4% 53.1% 53.1% 53.9% 48.5% 32.9% 33.0% 33.0% 33.0%
HP0500 HP1231 HP1231 HP0717 HP0012 HP1523 HP0116 HP0440 HP0685 HP0705 HP1114 HP0585 HP0705 HP1526 HP0705 HP0583 HP0683 HP06877 HP06975	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase II (opA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyriboruclease (texA) glucose inhibited division protein (gidB) helicase heliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction enddeoxyribonuclease (ruvC) integrase/recombinase (xerC)	26.0% 48.6% 35.1% 18 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 53.6% 40.1% 53.4% 53.4% 53.4% 53.9% 32.9% 32.9% 32.9% 32.9% 33.0% 54.6% 34.7% 31.0% 33.0% 34.6% 34.7% 31.0% 31.0% 33.0% 34.6% 34.7% 31.0% 31.0% 33.0% 34.6% 34.0% 33.0% 33.0% 33.0% 34.6% 33.0%
HP0500 HP1231 HP1231 HP0717 HP0717 HP1623 HP0716 HP0440 HP0682 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0675 HP0875 HP0875	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA propismerase II (gnA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease III (th) excinuclease ABC subunit A (uvrC) excinuclease III (th) excinuclease III	26.0% 48.6% 35.1% 18 33.0% 36.6% 32.7% 32.3% 45.1% 31.7% 36.6% 40.1% 53.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 44.5% 32.9% 32.
HP0500 HP1387 HP0717 HP0717 HP0717 HP1523 HP1523 HP0160 HP0585 HP0705 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA primase (dnaG) DNA repositionase (recG) DNA repositionase (recG) DNA repositionase (recO) DNA topolisomerase I (topA) DNA topolisomerase I (topA) endonuclease III (nb) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease (hexA) glucose-inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction DNA helicase (ruvB)	26.0% 48.8% 35.1% 18 39.0% 36.8% 32.7% 28.3% 45.1% 31.7% 53.4%53.4% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4% 53.4%53.5% 53.4%53.5% 53.4% 53.4%53.5% 53.5%53.5% 53.5%53.5% 53.5%53.5% 53.5%53.5% 53.
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1383 HP1383 HP0383 HP0385 HP0385 HP0385 HP0383 HP06877 HP0675 HP0675 HP0675 HP0675 HP0675	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit G (uvrC) excideoxyribonuclease (texA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidA) Holliday junction DNA heicase (truA) Holliday junction endodeoxyribonuclease (turC) integrase/recombinase (xerC) membrane bound endonuclease (truC) membrane bound endonuclease (truC) membrane bound endonuclease (truC)	26.0% 48.6% 48.6% 35.1% 15 39.0% 36.6% 32.7% 32.3% 45.1% 31.7% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 32.9% 32.9% 33.0% 54.6% 34.7% 31.8% 54.6% 34.7% 31.8% 54.6% 54.6% 54.7% 54.6% 54.6% 54.7% 54.8\% 54.8\% 54.8\% 54.8\% 54.8\% 54.8\% 54.
HP0500 HP1387 HP7387 HP0717 HP0012 HP1523 HP1333 HP1052 HP0385 HP00585 HP00585 HP0053 HP0053 HP0057 HP0057 HP0057 HP0057 HP0057 HP0057 HP0057 HP0057 HP0057	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (texA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) methyrates-(texA) ANA helicase (rucA) primosomal protein replication factor (priA) recombinase (recA)	26.0% 48.6% 48.6% 53.0% 36.6% 32.7% 328.3% 45.1% 31.7% 53.4% 53.4% 53.4% 53.4% 53.4% 53.3.0% 54.5% 32.2% 33.0% 54.6% 34.7% 31.8% 34.7% 31.8% 41.0% 36.3%
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0555 HP0116 HP0400 HP0555 HP0705 HP0705 HP0523 HP1653 HP1059 HP0675 HP0975 HP0775 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA proprimase (fraG) DNA reportinase (recG) DNA reportinase (recG) DNA reportinase (recO) DNA topoisomerase I (ropA) DNA topoisomerase I (ropA) DNA topoisomerase I (ropA) DNA topoisomerase I (ropA) DNA topoisomerase I (ropA) excinuclease III (nth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) glucose inhibited division protein (gidB) helicase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction DNA helicase (ruvB) Holiday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNARprotein-cysteline methyltransferse (rdA) primosomal protein replication factor (priA) recombinasi policetrandef DNA descrite hol holiand DNA repair protein (recR) primosomal protein replication factor (priA) recombinasi policetrandef DNA descrite transferse (recA)	26.0% 48.6% 48.6% 35.1% its 39.0% 36.6% 32.7% 46.1% 31.7% 36.6% 40.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 54.6% 31.7% 33.0% 33.0% 33.0% 33.0% 33.7% 33.1%% 54.6%
HP0500 HP1387 HP0717 HP0717 HP0717 HP0717 HP0717 HP1523 HP1393 HP016 HP040 HP0685 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077 HP075 HP077 HP075 HP077 HP075 HP077 HP075 HP077	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrB) excinuclease ABC subunit A (uvrB) excinuclease ABC subunit A (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction endodeoxyribonuclease (ruvC) membrane bound endonuclease (ruc) methylate-DNARporetin-cysteine methylitransferase (dat1) primosomal protein replication factor (priA) recombinase (recA)	26.0% 48.6% 48.6% 53.0% 53.0% 53.0% 53.9% 53.7% 53.9% 53.7% 53.4% 53.4% 53.4% 53.4% 53.9% 53.9% 53.9% 54.6%
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1383 HP1533 HP0385 HP0385 HP0385 HP0385 HP0383 HP06877 HP0675 HP0323 HP0675 HP0323 HP0675 HP0323 HP0675 HP0323 HP0675 HP0323 HP0675 HP0323 HP0675 HP0325 HP0337 HP0337 HP0337 HP0357 HP0337 HP0357 H	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III genrine subunit (dnaX) DNA polymerase III genrine and tau subun (dnaX) DNA polymerase III genrine and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truC) methylater-DNARportein-cysteine methylatersa (terA) recombinase (terA) recombinate (terA)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 28.3% 45.1% 31.7% 53.4% 53.1% 53.4% 53.1% 53.4% 53.4% 53.1% 53.4% 32.9% 32.9% 32.9% 32.9% 32.9% 34.7% 31.9% 53.6% 36.3% 53.6% 30.0% 54.6% 31.9% 53.6% 31.9% 53.6% 36.3% 53.1% 53.1% 54.5% 53.1% 54.5% 55
HP0500 HP1387 HP7387 HP0717 HP0012 HP1523 HP1523 HP1533 HP0525 HP0025 HP00585 HP00585 HP0053 HP0053 HP0053 HP0053 HP0057	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase II (opA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidA) Holliday junction DNA helicase (ruvA) Holliday junction endodeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) methyritaed-DNANprotein-cysteine methyritansferse (dat1) primosomal protein replication factor (priA) recombinational DNA repair protein (recR) rep helicase, single-stranded DNA-depende ATPase (rep) restriction modification system S subunit ribonuclease H (mNA)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 45.1% 31.7% 53.6% 45.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.4% 53.4% 53.1% 53.4% 53.30% 54.6% 34.7% 54.6% 34.7% 54.5% 31.1% 54.5% 31.1% 55.5% 31.1% 55.5% 33.3% 33.94% 33.94% 33.94% 58.4%
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0555 HP0116 HP0440 HP0675 HP0705 HP0705 HP0705 HP0705 HP0675 HP0675 HP0675 HP0955 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0676 HP0387 HP0387 HP0676 HP0387 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA proprimase (fraG) DNA reporimase (recO) DNA reporimerase I (topA) DNA topoisomerase I (topA) excinuclease III (mth) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrC) excinuclease ABC subunit A (uvrC) excinuclease ABC subunit A (uvrC) excinuclease ABC subunit A (uvrC) excinuclease ABC subunit A (uvrC) excideoxyritouclease (inxA) glucose-inhibited division protein (gdB) helicase (truC) Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvA) Holliday junction ENA helicase (ruvB) Holliday junction endodeoxyritonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) primosomal protein replication factor (priA) recombinasi DNA repair protein (recR) rep helicase (recA) resombinational DNA repair protein (recR) replicative DNA helicase (dnaB) restriction modification system S subunit ribonuclease HII (rmhA) ribonuclease HII (rmhA)	26.0% 48.6% 48.6% 53.0% 53.0% 53.0% 53.0% 53.7% 28.3% 46.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.5% 54.6% 54.6% 54.6% 54.6% 54.6% 54.6% 54.6% 55.5% 54.6% 55.5%
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP1523 HP0586 HP0705 HP0676 HP0705 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase III gemma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit G (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (rucA) methytate-DNARportein-cysteine methytitransferase (dat1) primosomal protein replication factor (priA) recombinase (recA) replicative DNA helicase (dnaB) replicative DNA helicase (dnaB)	26.0% 48.6% 48.6% 53.0% 53.0% 53.0% 53.9% 53.4% 53.4% 53.4% 53.4% 53.4% 53.9% 54.6\% 54.6\%
HP05201 HP1387 HP0717 HP0717 HP0717 HP0717 HP0717 HP0715 HP1523 HP1333 HP0715 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077 HP0675 HP0775 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidA) Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nuvA) Holliday junction endodeoxyribonuclease (tuvC) integrase/recombinase (xerC) integrase/recombinase (xerC) membrane bound endonuclease (nuc) methylate-DNANportein-cysteine methylate-DNANportein-cysteine Mathylate-DNANportein-cysteine ferp helicase (fepA) resonibinational DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mNA) ribonuclease H (mNA) single-strandeDNA-binding protein (sb) single-strandeDNA-binding protein (sb) single-strandeDNA-binding protein (sb)	26.0% 48.6% 53.1% 18 39.0% 36.6% 32.7% 28.3% 46.1% 31.7% 36.6% 40.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.9% 40.9% 53.4% 53.1% 53.9% 40.9% 53.1% 53.9% 40.9% 53.1% 53.9% 54.6% 54.6% 54.6% 53.1% 53.3% 54.6% 53.1% 53.3% 53.2% 55.3% 55.4% 53.3% 53.
HP0500 HP1387 HP7387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0525 HP0025 HP0025 HP00585 HP0052 HP00585 HP0052 HP00585 HP0052 HP0052 HP0057 HP0057 HP0057 HP00575 H	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase II (opA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyriboruclease (tevA) glucose inhibited division protein (gidB) glucase (max) Holiday (unction DNA helicase (ruvA) Holiday (unction DNA helicase (ruvA) Holiday (unction enddeoxyribonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNARprotein-cysteine methyltransferse (dat1) primosomal protein replication factor (priA) recombinational DNA repair protein (recR) rep helicase, (indB) restriction modification system S subunit ribonuclease HII (mhB) single-stranded-DNA-specific exonuclease (rec) site-specific recombinase	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 45.1% 31.7% 53.6% 45.1% 31.7% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.6% 27.8% 30.0% 54.6% 34.7% 54.6% 54.6% 54.6% 54.6% 54.6% 55% 11.0% 56.5% 11.0% 56.5% 11.0% 56.5% 11.0% 56.5% 11.0% 56.4% 33.8% 33.9,4% 33.3% 56.4% 33.6% 21.3% 56.4% 33.6% 35.5% 33.0% 33.0% 33.0% 33.6% 35.5% 33.0%33.0% 33.0%33.0% 33.0% 33.0% 33.0% 33.0% 33.0%33.0% 33.0% 33.0% 33.0%33
HP0500 HP1387 HP0717 HP0717 HP0717 HP0717 HP0717 HP0718 HP1523 HP1523 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077 HP0	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA proprimase (fraG) DNA repair protein (reCN) DNA repoisomerase I (topA) DNA topoisomerase I (topA) excinuclease III (nth) excinuclease ABC subunit A (uvrA) excinuclease (III (th) excinuclease (III (th) excinuclease (III (th) excinuclease (III (dnA) glucose inhibited division protein (gdB) heliCase (III (th) (th) A helicase (ruvA) Hoiliday junction DNA helicase (ruvA) Hoiliday junction ENA helicase (ruvA) Hoiliday junction endodexynthonuclease (ruvC) primosomal protein replication factor (prIA) recombinase (recA) resombinational DNA repair protein (recR) rep helicase (dnaB) restriction modification system S subunit ribonuclease HI (mhB) single-stranded DNA-specific exonuclease (recJ) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme S protein (recS) yipe I restriction enzyme S protein (rcF)	26.0% 48.6% 48.6% 53.0% 53.0% 53.0% 53.0% 53.9% 53.7% 45.1% 53.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 54.6% 55.1%
HP05201 HP1337 HP0717 HP0012 HP1337 HP0717 HP0012 HP1523 HP1333 HP1333 HP0625 HP016 HP0705 HP0705 HP0705 HP0705 HP0705 HP0877 HP0675 HP0877 HP0675 HP0877 HP0675 HP0987 HP0675 HP09911 HP1323 HP1053 HP09911 HP1322 HP09661 HP0387 HP0951 HP0951 HP0961 HP0387 HP0953 HP0961 HP0387 HP0953 HP0953 HP0954 HP0954 HP0954 HP0954 HP0954 HP0954 HP0954 HP0954 HP0954 HP0954 HP0955 HP0055	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (holB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) excideoxyribonuclease (texA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) heiliday junction DNA helicase (truA) Holliday junction DNA helicase (truA) Holliday junction DNA helicase (truA) Holliday junction DNA helicase (truC) membrane bound endonuclease (truC) methytate-DNANprotein-cysteine methytitransferase (dat1) primosomal protein replication factor (priA) recombinase (treCA) repolitave DNA helicase (dnaB) restriction modification system S subunit ribonuclease H (mNA) single-stranded DNA-specific exonuclease (recJ) single-stranded-DNA-specific exonuclease (rec) piel restriction express Protein (freiGN) piel restriction express Protein (freiGN) p	26.0% 48.6% 48.6% 53.1% 15 39.0% 36.6% 32.7% 28.3% 45.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.9% 40.1% 53.3% 32.9% 33.0% 54.6% 34.7% 31.5% 58.9% 34.7% 31.5% 58.9% 33.6% 32.9% 33.8% 32.8% 33.8% 33.8% 32.8% 33.8% 32.8%
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HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1533 HP0555 HP0114 HP0675 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0675 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA proprimase (fraG) DNA repair protein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit C (uvrC) excideoxy/thoruclease (iexA) glucose-inhibited division protein (gdB) heliCase Holiday junction DNA helicase (ruvA) Holiday junction DNA helicase (ruvB) Holiday junction ENA helicase (ruvB) Holiday junction endodeoxy/honuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (casE) primosomal protein replication factor (prIA) recombinasio (teA) primosomal protein replication factor (prIA) recombinase (recA) resombinational DNA repair protein (recR) rep helicase, (dnaB) restriction modification system S subunit ribonuclease HI (mhB) indonuclease HI (mhC) integrase/recombinase transcription-repair coupling factor (trCF) type I restriction enzyme K protein (hsdM) type I restriction enzyme K protein (hsdM)	26.0% 48.6% 48.6% 53.0% 53.0% 53.0% 53.0% 53.7% 46.1% 53.1% 53.1% 53.1% 53.1% 53.4% 53.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.5% 54.6% 54.6% 53.3% 53.8%
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HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP1523 HP0525 HP0025 HP0025 HP00585 HP0055 HP0053 HP0052 HP0053 HP0057 H	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase II (opA) DNA topoisomerase I (topA) DNA topoisomerase I (topA) exclauclease ABC subunit A (uvrA) exclauclease ABC subunit B (uvrB) exclauclease ABC subunit B (uvrB) exclauclease ABC subunit B (uvrB) exclauclease ABC subunit G (uvrC) exodedow/tibonuclease (tevA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) heliciase Holiday junction DNA helicase (ruvA) Holiday junction endodeoxynibonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNANprotein-cysteine methylitas-bingde-tonArepair protein (recR) rep helicase, (indA) prosomal protein replication factor (priA) recombinational DNA repair protein (recR) rep helicase (HnNA) ribonuclease H (mNA) ribonuclease H (mNB) single-stranded-DNA-specific exonuclease (rec) site-specific recombinase transcription-reopiar coupling factor (trCF) type I restriction enzyme R protein (hsdR) type I restriction enzyme R protein (hsdR)	26.0% 48.6% 35.1% its 39.0% 36.6% 32.7% 45.1% 31.7% 36.6% 31.7% 31.7% 36.6% 31.7% 31.9% 31.9% 32.9% 442.9% 33.0% 53.4% 33.0% 54.6% 33.0% 54.6% 33.1% 33.6% 33.7% 33.4% 33.6% 37.7% 55.4% 37.7% 55.4% 55.5% 55.5% 55.5% 55.5% 55.5% 55.5% 55.5% 55.5% 55.5% 55.5% 55.
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP15333 HP1523 HP0555 HP0715 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA proprime (dnaS) DNA recombinase (recC) DNA repair protein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) excinuclease ABC subunit G (uvrC) excideday/thoruclease (revA) glucose inhibited division protein (gdB) helicase (nuvC) Holliday junction DNA helicase (ruvA) Holliday junction DNA helicase (ruvB) Holliday junction endodecxynchonuclease (ruvC) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylitate-DNANprotein-cysteine methylitrabiferses (dat1) primosomal protein replication factor (prA) recombinase (recA) resombinational DNA-repair protein (recR) rep helicase, (dnaB) restriction modification system S subunit ribonuclease HI (mhB) single-stranded-DNA-specific exonuclease (rec) ype I restriction enzyme K protein (hsdM) ype I restriction enzyme M protein (hsdM)	26.0% 48.6% 48.6% 53.0% 53.0% 53.0% 53.0% 53.7% 45.1% 53.1% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 53.4% 54.6% 54.6% 54.6% 54.6% 54.6% 54.6% 54.6% 54.6% 55.3% 51.5% 54.6% 55.3% 51.5% 54.6% 55.3% 55.3% 50.7% 55.3%
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP15333 HP06585 HP0016 HP0114 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP0705 HP077 HP0675 H	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase (II gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (II (uvrC) exodeoxyribonuclease (II (uvrC) integrase/recombinase (recr) Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nucA) methytate-DNARQprotein-cysteine methytitransferase (dat1) primosomal portein (replication factor (priA) recombinase (recA) recombinase (recA) recombinase (recA) reportein replication factor (priA) recombinase (H (nnHB) single-stranded-DNA-specific exonuclease (rec) site-specific recombinase (rec) site-specific recombinase (rec) methytate-DNA-specific exonuclease (rec) site-specific recombinase (rec) replicative DNA helicase (naB) restriction morgyme B protein (redS) ype I restriction enzyme B protein (risdR) ype	26.0% 48.6% 53.1% 18 39.0% 36.6% 32.7% 45.1% 31.7% 53.4% 53.9% 32.9% 32.9% 32.9% 31.7% 53.9% 32.5% 53.5% 53.5% 53.7% 53.
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1533 HP1523 HP0585 HP0385 HP0625 HP0585 HP0635 HP0635 HP0635 HP0635 HP0637 HP	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase (dnaG) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidA) glucose-inhibited division protein (gidA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction A repair protein (terCi) integrase/recombinase (xerC) integrase/recombinase (xerC) integrase/recombinase (terA) recombinase (terA) recombinase (terA) recombinase (terA) recombinase (terA) resolution and DNA-terpair protein (terCi) rep helicase (thMB) single-strand-DNA-specific exonuclease (rec) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme K protein (hsdK) type II restriction enzyme K protein (hsdK)	26.0% 48.6% 48.6% 53.1% its 39.0% 36.6% 32.7% 45.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.9% 40.1% 53.9% 40.9% 53.4% 53.9% 32.9% 33.6% 33.0% 54.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.7% 53.7% 53.4% 53.3% 53.7% 53.4% 53.3% 53.7% 53.4% 53.3% 53.7% 53.4% 53.3% 53.7% 53.4% 53.3% 53.7% 53.7% 53.4% 53.7% 53
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0525 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP0555 HP05555 HP05555 HP05555 HP05555 HP05555 HP05555 HP055555 HP055555 HP05555555 HP05555555555	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase (dnaG) DNA recombinase (recG) DNA repair protein (recN) DNA topoisomerase I (topA) DNA topoisomerase I (topA) exclauclease ABC subunit B (uvrB) exclauclease ABC subunit B (uvrB) exclauclease ABC subunit B (uvrB) exclauclease ABC subunit G (uvrC) exodedow/tibonuclease (truA) glucose inhibited division protein (gidA) glucose-inhibited division protein (gidB) helidiasy junction DNA helicase (ruA) Holiday junction ENA helicase (ruA) Holiday junction endodeoxy/tibonuclease (ruxC) integrase/recombinase (xerC) integrase/recombinase (xerC) methylated-DNANprotein-cysteine methylitabited DNA helicase (nuC) methylated-DNANprotein-cysteine methylitabited DNA helicase (nuC) methylated-DNANprotein-cysteine methylitabited DNA helicase (nuC) methylated-DNANprotein-cysteine methylitabited DNA-binding protein (recR) rep helicase, ingle-stranded DNA-depende ATPase (rep) single-stranded-DNA-specific exonuclease (rec) siste-specific recombinase transcription-reayme K protein (hsdK) ype I restriction enzyme K protein (hsdK) ype II restriction enzyme K p	26.0% 48.6% 48.6% 53.1% 10 30.0% 36.6% 32.7% 45.1% 33.0% 53.1% 53.1% 53.1% 53.4% 53.1% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.3% 53.0% 54.6% 33.0% 55.3% 11% 56.5% 11 33.8% 53.4% 53.3% 53.4% 53.3% 53.4% 55.3% 55
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0555 HP0114 HP0602 HP0705 HP075	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noiB) DNA polymerase III germe subunit (dnaX) DNA polymerase III germe and tau subun (dnaX) DNA polymerase (II germe and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase I (topA) ducase inhibited division protein (gidA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase Holliday junction DNA helicase (ruvA) Holliday junction enyme K protein (recR) recombinational DNA repair protein (recR) recombinational DNA repair protein (recR) repleicase, single-stranded DNA-depende ATPase (rec) replicase H (mhA) ribonuclease H (mhA) ribon	26.0% 48.6% 48.6% 48.6% 48.6% 48.6% 53.0% 53.0% 53.9% 53.9% 53.7% 53.9% 53.4% 53.9% 53.4% 53.9% 54.6% 31.5% 54.9% 33.0% 54.6% 34.7% 33.8% 39.0% 55.3% 51.3% 53.8% 33.6% 32.8% 33.6% 33.6% 33.6% 33.6% 33.6% 33.7% 55.3% 50.7% 55.3%
HP05201 HP1337 HP1377 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0585 HP0685 HP075	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase III gamma and tau subun (dnaX) DNA polymerase (II gamma and tau subun (dnaX) DNA topoisomerase I (topA) DNA topoisomerase ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (IeVA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) heilicase Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nuvA) Holliday junction DNA helicase (nucA) membrane bound endonuclease (nuc) methytate-DNANQprotein-cysteine methytitransferase (dat1) primosomal protein (replication factor (priA) recombinase (recA) recombinase (recA) reportine estimated DNA-specific exonuclease H (mA) reportine estimated DNA-specific exonuclease (rec) single-stranded-DNA-specific exonuclease (rec) single-stranded-DNA-specific exonuclease (rec) single-stranded-DNA-specific exonuclease (rec) ype I restriction enzyme K protein (redK) ype I restriction enzyme K protein (risdK) ype II restrictio	26.0% 48.6% 48.6% 53.1% 15 39.0% 36.6% 32.7% 28.3% 46.1% 31.7% 56.6% 40.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.1% 53.4% 53.1% 53.1% 54.6% 53.1% 54.9% 55.9% 55.9% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 57.0% 56.9% 57.0% 57.
HP0500 HP1387 HP1387 HP0717 HP0012 HP1523 HP1523 HP1523 HP1523 HP0555 HP0555 HP0035 HP0555 HP0033 HP0675 HP0033 HP0677 HP0575 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP0033 HP06775 HP00345 HP00357 HP00575 HP00357 HP00575 HP00357 HP005757	DNA polymerase III beta-subunit (dnaN) DNA polymerase III deta prime subunit (noIB) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase III gemma and tau subun (dnaX) DNA polymerase (dnaG) DNA topoisomerase I (topA) DNA topoisomerase I (topA) excinuclease ABC subunit A (uvrA) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit B (uvrB) excinuclease ABC subunit G (uvrC) exodeoxyribonuclease (tevA) glucose inhibited division protein (gidA) glucose inhibited division protein (gidB) helicase Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truA) Holiday junction DNA helicase (truC) methylated-DNA/Byrotein-cysteine methylated-DNA/Byrotein-cysteine methylated-DNA/Byrotein-cysteine methylated-DNA/Byrotein-cysteine methylated-DNA-binding protein (tecR) rep helicase (teA) recombinase (teA) resombination a DNA-helicase (funB) heliotay et al. (http: binde-Structure) methylated-DNA-specific exonuclease (teC) site-specific recombinase transcription-repair coupling factor (trcF) type I restriction enzyme K protein (teAS) type II restriction enzyme K protein (teAS) ty	26.0% 48.6% 48.6% 53.1% 53.0% 53.0% 53.90% 53.90% 53.9% 53.9% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 53.4% 53.1% 58.9% 40.1% 58.9% 40.1% 58.9% 40.1% 58.9% 40.0% 58.9% 31.6% 58.9% 31.6% 58.9% 33.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.6% 33.7% 59.3% 50.7% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 57.0% 56.3% 50.7% 57.0% 56.3% 50.7% 57.0% 56.3% 50.7% 57.0% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 56.3% 50.7% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.0% 57.3% 57.7% 57.3

HP1471	type IIS restriction enzyme R protein	
HP1366	(BCGIB) type IIS restriction enzyme R protein	28.2%
HP1208	(MBOIIR) ulcer associated adenine specific DNA	37.1%
HP1209	methyltransferase ulcer-associated gene restriction endonucle	93.4% ase
HP1347	(iceA)	95.5%
		10.170
Degradation	of RNA	
HP1213	polynucleotide phosphorylase (pnp) DNA-dependent RNA polymerase	38.9%
HP1293	DNA-directed RNA polymerase, alpha subu (rpoA)	nit 35.3%
HP1198	DNA-directed RNA polymerase, beta subun (rpoB)	it 47.8%
Transcriptio	n factors	50.00
HP0866 HP1514	transcription elongation factor GreA (greA) transcription termination factor NusA	50.3%
HP0001	(nusA) transcription termination factor NusB (nusB)	39.1% 30.2%
HP1203	transcription termination factor NusG (nusG)	41.0%
HP0550	transcription termination factor Rho (rho)	56.6%
RNA proces HP0640	sing poly(A) polymerase (papS)	374%
HP0662	ribonuclease III (rnc)	37.3%
TRANSLATI	N	
<i>General</i> HP0944	translation initiation inhibitor, putative	45.6%
Aminoacyl t HP1241	RNA synthetases alanyl-tRNA synthetase (alaS)	44.9%
HP0319	arginyl-tRNA synthetase (argS)	35.8%
HP0886	cysteinyl-tRNA synthetase (cysS)	97.3%
HP0476 HP0643	glutamyl-tRNA synthetase (gltX) glutamyl-tRNA synthetase (gltX)	43.1% 39.8%
HP0960	glycyl-tRNA synthetase, alpha subunit (glyQ)	60.1%
HP0972 HP1190	glycyl-tRNA synthetase, beta subunit (glyS) histidyl-tRNA synthetase (hisS)	33.6% 32.4%
HP1422 HP1547	isoleucyl-tRNA synthetase (ileS) leucyl-tBNA synthetase (leuS)	49.7% 45.9%
HP0182 HP0417	lysyl-tRNA synthetase (lysS) methionyl-tRNA synthetase (metS)	58.6% 42.4%
HP0403	phenylalanyl-tRNA synthetase, alpha subuni	10 706
HP0402	phenylalanyl-tRNA synthetase, beta subunit	40.7%
HP0238	prolyl-tRNA synthetase (proS)	30.0%
HP1480 HP0123	seryI-tRNA synthetase (serS) threonyI-tRNA synthetase (thrS)	48.3% 42.1%
HP1253 HP0774	tryptophanyl-tRNA synthetase (trpS) tyrosyl-tRNA synthetase (tyrS)	52.6% 54.7%
HP1153 Degradation	valyI-tRNA synthetase (valS)	43.7%
HP0570	aminopeptidase a/i (pepA)	38.5%
HP0794	ATP-dependent clp protease (cipA) ATP-dependent clp protease proteolytic	40.3%
HP1379	ATP-dependent protease (lon)	43.9%
HP0223 HP1374	ATP-dependent protease (sms) ATP-dependent protease ATPase subunit	41.0%
HP0264	(CIPX) ATP-dependent protease binding subunit	56.3%
HP0169	(clpB) collagenase (prtC)	97.7% 40.1%
HP0516 HP0515	heat-shock protein (hsIU) ORF1 heat-shock protein (hsIV)	98.4% 57.1%
HP0470 HP0657	oligoendopeptidase F (pepF) processing protease (ymxG)	97.9% 24.2%
HP1485 HP1350	proline dipeptidase (pepQ) protease	35.2% 40.6%
HP1012 HP1435	protease (pqqE) protease IV (PspA)	29.6% 41.7%
HP0404	protein kinase C inhibitor (SP:P16436)	40.2%
HP1584	sialoglycoprotease (gcp)	35.7%
Nucleoprote	ins	30.270
HP0835 Protein mod	histone-like DNA-binding protein HU (hup)	44.6%
HP0363	L-isoaspartyl-protein carboxyl methyltransfer (pcm)	ase 43.0%
HP1299	methionine amino peptidase (map)	43.0%
LID1122	cyclosporin-type rotamase (ppi)	58.1%
1100700	rotamase (slyD)	40.4%
Ribosomal p	proteins: synthesis and modification	41.0%
HP1201 HP1200	ribosomal protein L1 (rpl1) ribosomal protein L10 (rpl10)	52.0% 30.4%
HP1202 HP1068	ribosomal protein L11 (rpl11)	63.8%
HP0084	(prmA) ribosomal protein L 13 (rol13)	38.4%
HP1309	ribosomal protein L16 (rp114)	65.9%
HP1312	ribosomal protein L16 (rp116)	62.4%
HP1292 HP1303	ribosomal protein L17 (rp117) ribosomal protein L18 (rp118)	48.3%
HP1147 HP1316	ribosomal protein L19 (rpl19) ribosomal protein L2 (rpl2)	50.9% 58.9%
HP0126 HP0296	ribosomal protein L20 (rpl20) ribosomal protein L21 (rpl21)	54.8% 46.1%
HP1314 HP1317	ribosomal protein L22 (rpl22) ribosomal protein L23 (rpl23)	44.9% 31.7%
HP1308 HP0297	ribosomal protein L24 (rpl24) ribosomal protein L27 (rpl27)	52.2% 64.7%
HP0491 HP1311	ribosomal protein L28 (rpL28) ribosomal protein L29 (rpl 29)	41.7% 45.6%
	(puto)	41.8%
HP1319 HP0551	ribosomal protein L3 (rpl3) ribosomal protein L31 (rpl31)	49.3%
HP1319 HP0551 HP0200	ribosomal protein L3 (rpl3) ribosomal protein L31 (rpl31) ribosomal protein L32 (rpl32)	49.3%
HP1319 HP0551 HP0200 HP1204 HP1447	ribosomal protein L3 (rpl3) ribosomal protein L31 (rpl31) ribosomal protein L32 (rpl32) ribosomal protein L33 (rpl33) ribosomal protein L34 (rpl34)	49.3% 41.7% 55.1% 70.5%
HP1319 HP0551 HP0200 HP1204 HP1447 HP0125 HP1297	ribosomal protein L3 (rpl3) ribosomal protein L31 (rpl3) ribosomal protein L32 (rpl32) ribosomal protein L33 (rpl33) ribosomal protein L34 (rpl34) ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36)	49.3% 41.7% 55.1% 70.5% 50.8% 81.6%
HP1319 HP0551 HP0200 HP1204 HP1447 HP0125 HP1297 HP1318 HP1307	ribosomal protein L3 (rpl3) ribosomal protein L31 (rpl31) ribosomal protein L32 (rpl32) ribosomal protein L33 (rpl33) ribosomal protein L34 (rpl34) ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribosomal protein L4 (rpl4) ribosomal protein L5 (rpl5)	49.3% 41.7% 55.1% 70.5% 50.8% 81.6% 40.6% 53.1%
HP1319 HP0551 HP0200 HP1204 HP1204 HP125 HP1297 HP1318 HP1307 HP1304 HP1304 HP1199	ribosomal protein L3 (rpl3) ribosomal protein L31 (rpl31) ribosomal protein L32 (rpl32) ribosomal protein L33 (rpl33) ribosomal protein L34 (rpl34) ribosomal protein L35 (rpl35) ribosomal protein L36 (rpl36) ribosomal protein L51 (rpl5) ribosomal protein L5 (rpl5) ribosomal protein L71/12 (rpl71/12)	49.3% 41.7% 55.1% 70.5% 50.8% 81.6% 40.6% 53.1% 44.4% 65.0%

HP0399	ribosomal protein S1 (rps1)	30.5%
HP1320 HP1295	ribosomal protein S10 (rps10) ribosomal protein S11 (rps11)	58.2% 56.2%
HP 1197	ribosomal protein S12 (rps12)	79.0%
HP1296	ribosomal protein S13 (rps13)	55.8%
HP 1040	ribosomal protein S15 (rps15)	57.8%
HP 1151	ribosomal protein S16 (rpS16)	46.8%
HP1244	ribosomal protein S17 (rps17)	55.2%
HP1315	ribosomal protein S19 (rps19)	61.1%
HP 1554	ribosomal protein S20 (rps20)	49.6%
HP0562	ribosomal protein S21 (rps21)	42.4%
HP 1313	ribosomal protein S4 (rps4)	51.2%
HP1302	ribosomal protein S5 (rps5)	65.5%
HP1246 HP1196	ribosomal protein S6 (rps6) ribosomal protein S7 (rps7)	32.1%
HP 1305	ribosomal protein S8 (rps8)	45.0%
HP0083 HP1047	ribosomal protein S9 (rps9) ribosome-binding factor A (rbfA)	26.3%
RNA modifi	cation	
HP1141	methionyl-tRNA formyltransferase (fmt)	37.5%
HP0361	pseudouridylate synthase I (hisT)	32.2%
HP1448	ribonuclease P, protein component (rnpA)	29.3%
HF 1002	ribosyltransferase-isomerase (queA)	39.3%
HP1513	selenocystein synthase (selA)	36.2%
HP 1148 HP 1415	tRNA (guanine-NT)-meinyitransierase (trmb)	39.1%
100001	transferase (miaA)	30.7%
HPU281 Translation	tRINA-guanine transglycosylase (tgt)	45.6%
HP0247	ATP-dependent RNA helicase, DEAD-box	
ID CONTRACTOR	family (deaD)	37.7%
HP0077 HP0171	peptide chain release factor RE-1 (prtA) peptide chain release factor RE-2 (prfB)	52.6% 49.6%
HP 1256	ribosome releasing factor (frr)	43.7%
HP1195 HP0177	translation elongation factor EF-G (TUSA) translation elongation factor EF-P (efp)	67.5% 45.1%
HP1555	translation elongation factor EF-Ts (tsf)	43.1%
HP1205 HP1208	translation elongation factor EF-Tu (tufB)	89.5%
HP1048	translation initiation factor IF-2 (infB)	45.4%
HP0124	translation initiation factor IF-3 (infC)	43.4%
FRANSPOR	AND BINDING PROTEINS	
General		
HP0179	ABC transporter, ATP-binding protein	66.7% 311%
HP0715	ABC transporter, ATP-binding protein	52.3%
HP1576	ABC transporter, ATP-binding protein (abc)	48.2%
71-1400	(HI1087)	37.8%
HP1220	ABC transporter, ATP-binding protein (yhcG)	31.5%
HP1577	ABC transporter, permease protein (yaeE)	43.1%
HP0607	acriflavine resistance protein (acrB)	29.7%
HP1432 HP1427	histidine and glutamine-rich protein histidine-rich, metal binding polypeptide	50.0%
	(hpn)	100.0%
HP1206 HP1082	multidrug-resistance protein (netA) multidrug-resistance protein (msbA)	26.2%
HP0600	multidrug-resistance protein (spaB)	29.7%
HP1181	multidrug-efflux transporter	29.1%
HP0498	sodium- and chloride-dependent trans-	01.770
-IP0214	porter sodium-dependent transporter (huNaDC-1)	30.8%
Amino acida	peptides and amines	55.5 /6
HP0940	amino acid ABC transporter, periplasmic	4.50
-IP0939	binding protein (yckK) amino acid ABC transporter, permease	41.5%
	protein (yckJ)	46.9%
HP1017	amino acid permease (rocE)	41.7%
HP0301	dipeptide ABC transporter, ATP-binding	44.070
COCO CL	protein (dppD) dipontido APC transportor ATP hinding	59.5%
11 0002	protein (dppF)	54.8%
HP0298	dipeptide ABC transporter, periplasmic	30.8%
HP0299	dipeptide ABC transporter, permease	00.070
100000	protein (dppB)	49.3%
11 0300	(dppC)	52.5%
HP 1506	glutamate permease (gltS)	56.9%
7F 11/1	protein (glnQ)	51.9%
HP 1172	glutamine ABC transporter, periplasmic	22.20
HP 1169	glutamine-binding protein (ginH) alutamine ABC transporter, permease	32.2%
10 11 20	protein (glnP)	27.6%
HP1170	giutamine ABC transporter, permease prote (glnP)	in 30.9%
HP0250	oligopeptide ABC transporter, ATP-binding	
HP 1252	protein (oppD) oligopentide ABC transporter, periplasmic	39.1%
II ILOL	oligopeptide-binding protein (oppA)	28.7%
HP1251	oligopeptide ABC transporter, permease	50.6%
HP0251	oligopeptide ABC transporter,	00.070
	permease protein (oppC)	31.4%
HP0818	osmoprotection protein (proWX)	30.4%
HP0055	proline permease (putP)	51.4% 20.1%
HP0133	serine transporter (sdaC)	44.6%
Anions		
HP0475	motypdenum ABC transporter, ATP-binding protein (modD)	38.4%
HP0473	molybdenum ABC transporter, periplasmic	
-IP0474	molybdate-binding protein (modA)	95.9%
04/4	protein (modB)	28.7%
HP0313	nitrite extrusion protein (narK)	23.6%
arbohvdrei	es, organic alcohols and acids	J-1.070
HP0143	2-oxoglutarate/malate translocator (SODIT1)	37.0%
HP1091 HP0724	aipna-ketoglutarate permease (kgtP) anaerobic C4-dicarboxylate transport	45.5%
	protein (dcuA)	53.8%
HP 1174	giucose/galactose transporter (gluP)	53.6% 55.5%
HP0140	L-lactate permease (IctP)	58.7%

Cations HP0791	cadmium-transporting ATPase, P-type	
HP0969	(cadA) cation efflux system protein (czcA)	97.5% 37.3%
HP1328	cation efflux system protein (czcA)	28.9%
HP1329 HP1503	cation eniux system protein (czcA) cation-transporting ATPase, P-type (copA)	30.3%
HP1073 HP1072	copper ion binding protein (copP) copper-transporting ATPase, P-type (copA)	92.4% 93.9%
HP0471	glutathione-regulated potassium-efflux syste	em
HP0687	iron(II) transport protein (feoB)	33.6%
HP1561	binding protein (ceuE)	27.5%
HP1562	iron(III) ABC transporter, periplasmic iron- binding protein (ceuE)	28.2%
HP0888	iron(III) dicitrate ABC transporter, ATP-bindir protein (fecE)	ng 34.4%
HP0889	iron(III) dicitrate ABC transporter, permease	04.470
HP0686	protein (TecD) iron(III) dicitrate transport protein (fecA)	38.3% 29.7%
HP0807 HP1400	iron(III) dicitrate transport protein (fecA) iron(III) dicitrate transport protein (fecA)	28.5% 26.3%
HP1344	magnesium and cobalt transport protein	26.204
HP1183	NA+/H+ antiporter (napA)	26.6%
HP1552 HP1077	Na+/H+ antiporter (nhaA) nickel transport protein (nixA)	49.2% 98.7%
HP0490	putative potassium channel protein, putative	25.7%
Nucleoside	s, purines and pyrimidines	
HP1290	nicotinamide mononucleotide transporter (pnuC)	28.0%
HP1180	pyrimidine nucleoside transport protein (nupC)	32.9%
Other		
HP0876	(frpB)	27.6%
HP0915	iron-regulated outer membrane protein (froB)	28.1%
HP0916	iron-regulated outer membrane protein (froB)	28 804
HP1129	biopolymer transport protein (exbD)	29.7%
HP1130 HP1339	biopolymer transport protein (exbB) biopolymer transport protein (exbB)	33.5% 46.8%
HP1340	biopolymer transport protein (exbD)	35.8%
HP1446	biopolymer transport protein (exbb)	36.2%
HP1512	(frpB)	26.6%
HP0653 HP1341	nonheme iron-containing ferritin (pfr) siderophore-mediated iron transport protein	99.4%
	(tonB)	37.2%
OTHER CA	TEGORIES	
General HP0924	4-oxalocrotonate tautomerase (dmpl)	37.7%
HP1034	ATP-binding protein (ylxH)	36.3%
HP1139	SpoOJ regulator (soj)	47.4%
HP0827 Adaptation	ss-DNA binding protein 12RNP2 precursor	46.8%
HP1496	general stress protein (ctc)	26.5%
HP1483	gerC2 protein (gerC2)	33.3%
HP0927	heat shock protein (htpX)	32.8%
HP0927 HP0280 HP1228	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA)	32.8% 27.2% 38.2%
HP0927 HP0280 HP1228 HP0970	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-cobalt-cadmium resistance protein (pccP)	32.8% 27.2% 38.2%
HP0927 HP0280 HP1228 HP0970 HP1444	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB)	32.8% 27.2% 38.2% 21.1% 42.1%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD)	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (lnvA) nickel-cobelt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (lnvA) nickel-coblet-admium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein (muh)	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 <i>Colicin-rela</i>	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-cobelt-admium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ted functions	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 <i>Colicin-rela</i> HP1126 HP0128	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-coblet-admium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/ellurit resistance cluster	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 <i>Colicin-rela</i> HP1126 HP128	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mvIN protein (mvIN) ted functions colicin tolerance-like protein (toIB) phage/colicin-fleurite resistance cluster terY protein	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 28.9% 36.0% 33.5% 25.7% 25.6%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 <i>Colicin-rela</i> HP126 HP126 HP0428 <i>Drug and a</i> HP1431	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mvIN protein (mvIN) ted functions colicin tolerange-like protein (toIB) phage/colicin/felurite resistance cluster terY protein naiog sensitivity 158 (rNN (adenosine-N6,N6-)dimethyl-	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6%
HP0927 HP0280 HP1228 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0855 <i>Colicin-rela</i> HP1126 HP1248 HP0428 <i>Drug and a</i> HP1431 HP0606	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-cobalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mvIN protein (mvIN) ted functions colicin tolerange-like protein (toIB) phage/colicin/tellurite resistance cluster terY protein nalog sensitivity 156 rtNA (dancosine-N6,N6-)dimethyl- transferase (ksgA) membrane lusion protein (mtrC)	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 35.5% 24.2%
HP0827 HP0280 HP1228 HP0970 HP1444 HP09970 HP0967 HP0967 HP0967 HP1248 HP1248 HP1248 HP1248 Drug and a HP1431 HP0606 HP0630 HP1478	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-coblet.cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mvIN protein (mvIN) ted functions colicin tolerange-like protein (toIB) phage/colicin/tellurite resistance cluster terY protein nalog sensitivity 156; rtNA (adenosine-N6,N6;-dimethyl- transferase (ksgA) membrane fusion protein (mtrC) modulator of drug advivity (mda66) phendarovite, add Mearboydase	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.6% 25.6% 24.2% 62.3% 39.7%
HP0827 HP0280 HP1228 HP0970 HP1444 HP09970 HP0315 HP0967 HP1248 HP1248 HP1248 Drug and a HP1431 HP0428 Drug and a HP0428 HP0428 HP0430 HP0440 HP0430	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-obalt-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mvIN protein (mvIN) ted functions collicin tolerance-like protein (toIB) phage/collicin/télluufte resistance cluster teY' protein nalog sensitivity 158; rtNA (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacrylic acid desarboxylase tetracycline resistance protein tetA(P),	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 24.2% 62.3% 39.7%
HP0827 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 <i>Collicin-rela</i> HP1426 HP1428 Drug and a HP1431 HP1431 Transposol	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-cobelt-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (surE) virulence associated protein (surE) virulence associated protein (surE) virulence factor mvIN protein (mvIN) ted functions collicin tolerance-like protein (toIB) phage/collicin/tellurite resistance cluster ten' protein nalog sensitivity 165 rRNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative <i>r-telated</i> functions	32.8% 27.2% 38.2% 42.1% 42.1% 70.2% 28.9% 36.0% 33.5% 25.6% 25.6% 35.6% 24.2% 62.3% 39.7%
HP0827 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0885 <i>Collicin-rela</i> HP1426 HP1428 HP0428 <i>Drug and a</i> HP1431 HP1431 Transpose0 HP1476 HP1476	heat shock protein (hpX) heat shock protein B (ibpB) invasion protein B (ibpB) invasion protein (invA) nickel-cobelt-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein C (vapD) virulence associated protein D (vapD) virulence associated protein (mvIN) ted functions colicin tolerance-like protein (mvIN) ted functions colicin tolerance-like protein (mvID) majog sensitivity 165 (rINA) (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mtC) modulator of drug activity (mda68) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative -related functions IS200 insertion sequence from SARA17 IS200 insertion sequence from SARA17	32.8% 27.2% 38.2% 21.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7% 25.6% 25.6% 35.5% 62.3% 39.7% 27.0% 33.3%
HP0027 HP0280 HP1228 HP0970 HP1248 HP0970 HP1444 HP0315 HP0315 HP0325 Colicin-rela HP1128 HP1248 Drug and a HP1431 HP0626 HP1431 HP0626 HP1476 HP1080 HP1476 HP0180 HP01476 HP0180 HP01476 HP0180 HP01476 HP0180 HP01476 HP0180 HP	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (lnvA) nickel-coblet-cadmium resistance protein (nccB) small protein (smpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (surE) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein malog aesitivity 165 (rINA) (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative netated functions 18200 insertion sequence from SARA17 18200 insertion sequence from SARA17 18200 insertion sequence from SARA17	32.8% 27.2% 38.2% 21.1% 42.1% 37.7% 28.9% 36.0% 33.5% 25.7% 25.6% 35.5% 24.2% 39.7% 27.0% 23.9% 27.0%
HP0827 HP0280 HP1228 HP0970 HP1444 HP0930 HP1444 HP0315 HP0970 HP1248 HP0885 <i>Colicin-rela</i> HP128 HP1431 HP0282 <i>Drug and a</i> HP1431 HP0680 HP1476 HP165 <i>Transposor</i> HP1085 HP0141 HP0988 HP0998 HP0998 HP0998	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein C (supD) virulence associated protein C (supD) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellurtle resistance cluster ten' protein meliog aensitvity 16\$ rRNA (adenosine-N6,N6)-dimethyl- transferase (ksqA) membrane fusion protein (mtC) modulator of drug activity (mda6) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative r-related functions 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15205 transposase (tnpA)	32.8% 272% 38.2% 211% 42,1% 42,1% 42,1% 37.7% 28.9% 36.0% 33.5% 25.7% 25.7% 25.6% 35.5% 35.5% 24.2% 62.3% 24.2% 24.2% 23.9% 33.9% 33.9% 97.2%
HP0827 HP0280 HP1228 HP0970 HP1444 HP0930 HP0315 HP0967 HP1248 HP0315 Colicin-rela HP128 HP128 HP128 HP128 HP128 HP128 HP1431 HP0280 HP1431 HP0630 HP1476 HP1165 Transposol HP0414 HP1088 HP099	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (linvA) nickel-coblet-admium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellurite resistance cluster teY protein malorg aesivity 185 rfNA (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mtC) modulator of drug activity (mda66) phenylacrylic adid decarboxylase tetracycline resistance protein sequence from SARA17 IS200 insertion sequence from SARA17	32.8% 272% 38.2% 211% 42.1% 37.7% 70.2% 28.9% 36.0% 33.5% 25.7% 25.5% 62.3% 33.9% 27.0% 27.0% 33.9% 33.9% 27.0% 27.0%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0970 HP1444 HP0935 HP0967 HP1434 HP10967 HP1435 HP1431 HP0626 HP1431 HP1435 HP1086 HP0428 HP1098 HP0988 HP0998 HP10985 HP10975 HP1	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein B (lbpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin-fellurite resistance cluster terY protein malorg sensitivity 16S rRNA (adenosine-N6,N6-)-dimethyl- transfarse (ksgA) 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 15205 transposase (tnpA) 15805 transposase (tnpA) 15805 transposase (tnpA) 15805 transposase (tnpA)	32.8% 272% 38.2% 211% 42.1% 37.7% 70.2% 28.9% 33.5% 25.5% 25.5% 24.2% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 27.0%27.0% 27
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0967 HP1444 HP0967 HP1288 Colicin-rela HP0428 Drug and a HP1431 HP0428 HP0428 HP0428 HP0428 HP0428 HP0428 HP1455 HP044 HP1455 HP0437 HP0989 HP0987	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (livA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/ellurite resistance cluster terY protein malog sensitivity transferase (ksgA) membrane tusion protein (mtC) 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 15205 transposase (tnpA) 15805 transposase (tnpB)	32.8% 272% 32.2% 21.1% 42.1% 7.7% 7.2% 28.9% 36.0% 25.5% 25.5% 25.5% 25.5% 25.5% 22.5% 22.2% 33.9% 37.2% 33.9% 37.2% 33.9% 37.2% 33.9% 33.9% 37.2% 33.9% 33.9%
HP0927 HP0280 HP1228 HP0970 HP1444 HP0930 HP0976 HP1248 HP0967 HP1248 HP0967 HP1248 Drug and a HP1431 HP1431 HP1436 HP1436 HP1436 HP1436 HP1436 HP1436 HP1437 HP0988 HP0988 HP0988 HP0988 HP1036 HP1036 HP1036 HP1036 HP1037 HP0988 HP0997 HP1034 HP1034 HP1034	heat shock protein (htpX) heat shock protein B (lbpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein homolog (vacB) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellurite resistance cluster teY' protein malog sensitivity 155 (rtNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane tusion protein (mtrC) modulator of drug activity (mda66) phenylacylic 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 15205 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpA) 15605 transposase (tnpB) 15605 transposase (tnpB) 15605 transposase (tnpB) 15605 transposase (tnpB) 15605 transposase (tnpB)	32.8% 272% 38.2% 21.1% 42.1% 7.7% 70.2% 28.9% 33.5% 25.7% 25.5% 25.5% 25.5% 25.5% 25.5% 25.5% 27.2% 27.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 97.2% 93.4% 93.4%
HP0327 HP0227 HP1228 HP0270 HP1444 HP0370 HP1444 HP0316 HP0316 HP0316 HP0328 HP0328 HP128 HP128 HP128 HP1431 HP0428 Transposol HP1476 HP0428 Transposol HP1476 HP0428 Transposol HP1476 HP0428 HP0437 HP0437 HP0438	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-cobelt-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (surE) virulence associated protein (surD) diversion (surD) editoriance-like protein (mvIN) ted functions colicin tolerance-like protein (tolB) phage/colicin/tellurite resistance cluster terY protein naiog sensitivity 165 rRNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative <i>r-leited functions</i> 15200 insertion sequence from SARA17 153605 transposase (mpA) 153605 transposase (mpB) 153605 transposase (mpB)	22.8% 272% 38.2% 211% 42.1% 28.9% 28.9% 28.9% 25.6% 25.6% 25.6% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 24.2% 24.3% 27.2%27.2% 27
HP0927 HP0280 HP1228 HP0270 HP1444 HP0930 HP1444 HP0930 HP1248 Colicin-rela HP128 Colicin-rela HP128 Drug and a HP1431 HP0285 Colicin-rela HP1431 HP0285 Transposol HP1476 HP0385 HP0473 HP0477 HP1096 HP1096 HP1097 HP1096 HP1096 HP1096 HP1097 HP1096 HP1097 HP1096 HP1097 HP1096 HP1097 HP1096 HP1097	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein C (vapD) virulence associated protein C (vapD) virulence associated protein C (vapD) et al. (vapD) virulence associated protein C (vapD) virulence associated protein (mvIN) ted functions colicin tolerance/like protein (mvIN) ted functions colicin tolerance/like protein (mvIC) maiog sensitivity 168 (rINA) (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mrIC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative <i>n-related functions</i> 15200 insertion sequence from SARA17 15806 transposase (mpA) 15806 transposase (mpA) 15806 transposase (mpA) 15806 transposase (mpA) 15806 transposase (mpB) 15806 tr	32.8% 272% 38.2% 211% 42.1% 28.9% 33.5% 25.6% 25.6% 33.5% 25.6% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.9% 33.4% 33.4% 33.4% 33.4%
HP0927 HP0280 HP1228 HP0270 HP0370 HP0370 HP0375 HP	heat shock protein (htpX) heat shock protein B (ibpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (mcB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein C (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) phage/colicin /tellunter resistance cluster terY protein malog aesitivity 165 (rNA) (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mrtC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-feated functions 15200 insertion sequence from SARA17 15200 insertion sequence fupA) 15605 transposase (InpA) 15605 transposase (InpA) 15605 transposase (InpA) 15605 transposase (InpB) 15605 trans	22.8% 272% 38.2% 211% 42.1% 37.7% 70.2% 28.9% 25.7% 25.6% 25.6% 25.6% 25.6% 25.6% 27.0%27.0% 27.0%27.0% 27.0% 27.0% 27.0% 27.0% 27.0%27.0% 27.0% 27.0% 27.0%27
HP0027 HP0280 HP1228 HP0270 HP0370 HP1444 HP0375 HP1444 HP0375 Colicin-rela HP1431 HP0285 Colicin-rela HP1431 HP0285 Colicin-rela HP1431 HP0285 Colicin-rela HP1431 HP0285 HP0473 HP0473 HP0670 HP1535 HP0078 HP0473 HP0078 HP0478 HP057 HP057 HP057 HP057 HP057 HP0778 HP057 HP0778 HP077	heat shock protein (hpX) heat shock protein B (hpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (surE) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (tolB) phage/colicin/faluntie resistance cluster terY protein nalog aesitivity 165 (rINA) (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mtC) putative hrafetad functions 15200 insertion sequence from SARA17 15200 inser	22,8% 272% 38,2% 211% 42,1% 37,7% 70,2% 28,9% 25,5% 25,5% 25,5% 25,5% 25,5% 25,5% 25,5% 25,5% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 27,2% 28,9% 27,2% 28,9% 27,2% 28,9% 27,2% 28,9% 27,2% 28,9% 27,2% 28,9% 27,2% 27,2% 28,9% 27,2% 28,9% 27,2% 28,9% 27,2% 28,9% 27,2% 27,2% 27,2% 28,9% 27,2%27,2% 27,2%27,2% 27,2% 27,2% 27,2%27,2% 27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2%27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2%27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2% 27,2%27,2% 27,2%27,2% 27,2% 27,2%27
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HP0927 HP0280 HP1228 HP0270 HP1444 HP0370 HP1444 HP0315 HP0375 HP1248 Drug and a HP1126 HP1248 Drug and a HP1431 HP0285 Colicin-rela HP1431 HP0285 Colicin-rela HP1431 HP0285 Transposol HP1431 HP0289 HP1035 HP0474 HP0389 HP1098 HP1097 HP1634 HP1038	heat shock protein (hpX) heat shock protein B (hpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein CompO (vacB) virulence factor mviN protein (mvIN) ted functions colicin telerancelike protein (toIB) phage/colicin fellunter resistance cluster ten' protein naiog sensitivity 168 (rINA) (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative <i>r-telated functions</i> 15200 insertion sequence from SARA17 15200 insertion sequence from SARA17 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpA) 15806 transposase (tnpB) 15806 transposase (tnb	32.3% 32.2% 38.2% 27.2% 38.2% 21.1% 21.1% 21.5% 28.9% 25.5% 25.5% 25.5% 25.5% 25.5% 24.2% 33.9% 27.2% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 27.2% 33.9% 33.9% 33.9% 33.9% 33.4% 33.4% 34.4%35.2%36.4% 36.4%36.4% 36.4%36.4% 36.4%36.4% 36.4%36.4%37.4% 37.4%37.4% 37.4%37.4% 37.4%37.4% 37.4% 37.4%37.4% 37.4%37.4% 37.4%37.4% 37.4% 37.4%37.4%37.4% 37.4%37.4%37.4% 37.4%
HP0927 HP0280 HP1228 HP0270 HP1444 HP0370 HP1444 HP0315 HP0376 HP1288 Colicin-rela HP1431 HP0285 Colicin-rela HP1288 Colicin-rela HP1431 HP0285 Colicin-rela HP1431 HP0285 Colicin-rela HP1431 HP0285 HP1431 HP0285 HP1431 HP0285 HP1431 HP0285 HP1437 HP0385 HP1437 HP0385 HP1437 HP0385 HP1437 HP0385 HP1437 HP0385 HP1437 HP0385 HP1437 HP0385 HP1437 HP0385 HP0387	heat shock protein (hpX) heat shock protein B (hpB) invasion protein (invA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein CompO (vacB) voluence associated protein (surE) virulence associated protein (surE) phage/colicin/tellunte resistance cluster phage/colicin/tellunte resistance cluster ten' protein nalog sensitivity 168 rfNA (adenosine-N6,N6-)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda66) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative <i>r-telated functions</i> 15200 insertion sequence from SARA17 15805 transposase (tnpA) 15805 transposase (tnpA) 15805 transposase (tnpA) 15805 transposase (tnpA) 15805 transposase (tnpA) 15805 transposase (tnpB) 15805 transp	32,3% 32,2% 38,2% 27,2% 38,2% 21,1% 21,1% 21,2% 37,7% 28,3% 21,2% 35,5% 24,2% 35,5% 24,2% 39,7% 27,2% 97,2%97,2% 97,2%97,2% 97,2% 97,2% 97,2% 97,2%97,2% 97,2% 97,2% 97,2%97,2%
HP0927 HP0280 HP1228 HP0270 HP0370 HP1444 HP03970 HP1444 HP03970 HP1288 HP0315 Colicin-rela HP1431 HP128 Drug and a HP1431 HP0285 Colicin-rela HP1431 HP0285 HP0370 HP1431 HP0380 HP1431 HP0380 HP0470 HP0381	heat shock protein (IntpX) heat shock protein B (IbpB) invasion protein (IntpA) notest cook protein (surA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (surE) virulence associated protein D (vapD) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (toIB) phage/colicin/fellurite resistance cluster terY protein nalog aesitivity 165 (rINA) (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda6) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-felated functions IS500 insertion sequence from SARA17 IS500 insertion s	22,3% 32,2% 38,2% 27,2% 38,2% 21,1% 21,1% 22,3% 37,7% 22,3% 33,5% 24,2% 33,5% 24,2% 33,3%34,3% 33,3% 33,3% 33,3%34,3% 33,3% 33,3%34,3% 33,3%34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 33,3%34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 34,3% 33,3%35,3% 34,3% 34,3% 34,3% 34,3% 33,3%35,3% 34,3% 34,3% 34,3%35,3% 34,3% 34,3% 34,3%35,3% 34,3% 34,3%35,3% 34,3% 34,3%35,3% 34,3% 34,3%35,3% 34,3%35,3% 34,3%35,3% 34,3% 34,3%35,3% 34,3%35,3% 34,3%35,3% 34,3%36,3% 34,3%36,3% 34,3%36,3% 36,3%37,3% 36,3%37,3% 37,3%37,3% 37,3%37,3% 37,3%37,3% 37,3%37,3% 37,3%37,3% 37,3%37,3% 37,3%37,3%
HP0927 HP0280 HP1228 HP0270 HP0270 HP0270 HP0270 HP0270 HP0270 HP0270 HP0270 HP0270 HP0270 HP1248 HP0270 HP1248 HP0270 HP1431 HP0270 HP	heat shock protein (IntpX) heat shock protein B (IbpB) invasion protein (IntpA) notest cook protein (surpB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence factor mviN protein (mviN) ted functions colicin tolerance-like protein (toIB) phage/colicin/fellurite resistance cluster terY protein nalog aesitivity 165 (rINA) (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mr(C) modulator of drug activity (mda6) phenylacrylic acid decarboxylase tetracycline resistance protein tetA(P), putative n-felated functions IS200 insention sequence from SARA17 IS200 insention sequenc	32.3% 32.2% 38.2% 27.2% 38.2% 21.1% 21.1% 22.9% 37.7% 22.9% 35.5% 24.2% 33.3% 32.5% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.3% 33.4% 33.4% 34.4%34.4% 34.4%34.4% 34.4% 34.4%34.4% 34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4% 34.4%34.4%34.4% 34.4%34.4%34.4% 34.4%
HP0827 HP0280 HP0280 HP0280 HP0370 HP0370 HP1444 HP0380 HP0370 HP1484 HP0385 Colicin-rela HP1484 HP0385 Colicin-rela HP1431 HP0428 Drug and a HP1431 HP0680 HP1431 HP0697 HP1431 HP0698 HP0498 HP0998 HP0431 HP0998 HP0379 HP0398 HP0438 HP0431 HP0379 HP0431 HP0321 HP0321 HP0322 HP1321 HP1321 HP1321 HP1321 HP1321 HP1321 HP1321 HP1321 HP1321 HP1321 <tr< td=""><td>heat shock protein (IntpX) heat shock protein B (IbpB) invasion protein (IntpA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (mvIN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellurite resistance cluster terY protein nalog aestivity 185, rRNA (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda6) phenylacrylic acid decarboxylase tetraxycline resistance protein tetA(P), putative hrelated functions 18200 insertion sequence from SARA17 18200 inser</td><td>32,3% 272% 38,2% 272% 38,2% 211% 211% 22,3% 23,5% 24,2% 24,2% 24,2% 33,5% 24,2% 24,2% 24,2% 39,7% 24,2% 24,2% 39,7% 27,0% 33,9%33,9% 33,9% 33,9% 33,9%34,9% 33,9% 33,9% 33,9%34,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9%33,9% 33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9%33,9% 33,9%34,9% 33,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9%34,9%34,9% 34,9%34,9%34,9% 34,9%34,9%34,9</td></tr<>	heat shock protein (IntpX) heat shock protein B (IbpB) invasion protein (IntpA) nickel-coblet-cadmium resistance protein (nccB) stationary-phase survival protein (surE) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein D (vapD) virulence associated protein (mvIN) ted functions colicin tolerance-like protein (tolB) phage/colicin/fellurite resistance cluster terY protein nalog aestivity 185, rRNA (adenosine-N6,N6)-dimethyl- transferase (ksgA) membrane fusion protein (mrC) modulator of drug activity (mda6) phenylacrylic acid decarboxylase tetraxycline resistance protein tetA(P), putative hrelated functions 18200 insertion sequence from SARA17 18200 inser	32,3% 272% 38,2% 272% 38,2% 211% 211% 22,3% 23,5% 24,2% 24,2% 24,2% 33,5% 24,2% 24,2% 24,2% 39,7% 24,2% 24,2% 39,7% 27,0% 33,9%33,9% 33,9% 33,9% 33,9%34,9% 33,9% 33,9% 33,9%34,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9% 33,9%33,9% 33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9% 33,9%33,9% 33,9%33,9% 33,9%34,9% 33,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9% 34,9%34,9%34,9%34,9% 34,9%34,9%34,9% 34,9%34,9%34,9

HP0258	concented	hypothetical	integral	membrane		Ц
111 0200	protein	пуровновови	integral	membrane	32.7%	Н
HP0284	conserved protein	hypothetical	integral	membrane	29.2%	H
HP0362	conserved	hypothetical	integral	membrane	00.0%	Н
HP0415	conserved	hypothetical	integral	membrane	28.8%	H
HP0467	protein	hypothetical	integral	membrane	44.4%	Н
	protein				100.0%	H
HP05/1	protein	nypotnetical	integral	membrane	29.5%	Н
HP0644	conserved	hypothetical	integral	membrane	20.206	Н
HP0677	conserved	hypothetical	integral	membrane	00.0 10	H
HP0693	protein conserved	hypothetical	integral	membrane	28.5%	H
100740	protein				46.7%	F
HP0/18	protein	nypotnetical	integral	membrane	33.5%	F
HP0737	conserved	hypothetical	integral	membrane	33 306	Н
HP0758	conserved	hypothetical	integral	membrane	00.070	Н
HP0759	protein conserved	hypothetical	integral	membrane	47.6%	H
100707	protein				31.1%	Н
HFU/6/	protein	пурошецса	integrai	membrane	25.2%	Н
HP0851	conserved protein	hypothetical	integral	membrane	373%	Н
HP0920	conserved	hypothetical	integral	membrane	00.001	H
HP0946	conserved	hypothetical	integral	membrane	36.3%	Н
HP0052	protein	hypothetical	integral	membrane	35.9%	Н
	protein			·	38.5%	Н
HP0983	protein	hypothetical	integral	membrane	32.8%	H
HP1044	conserved	hypothetical	integral	membrane	20.6%	H
HP1061	conserved	hypothetical	integral	membrane	30.0%	F
HP1080	protein	hypothetical	integral	membrane	35.0%	Н
	protein	in in it is in	····		44.0%	Ē
HP1162	protein	nypotnetical	integrai	membrane	27.6%	H
HP1175	conserved	hypothetical	integral	membrane	40.6%	Н
HP1184	conserved	hypothetical	integral	membrane	40.0%	Н
HP1185	protein conserved	hypothetical	integral	membrane	23.5%	Н
	protein				55.5%	H
HP1225	conserved protein	hypothetical	integral	membrane	31.6%	H
HP1234	conserved	hypothetical	integral	membrane	20.00%	Н
HP1235	conserved	hypothetical	integral	membrane	23.0%	Н
HP1330	protein conserved	hypothetical	integral	membrane	30.9%	F
	protein	hi na ada adia al			41.7%	Ì
HP1331	protein	nypotnetical	integral	membrane	33.6%	F
HP1343	conserved protein	hypothetical	integral	membrane	491%	H
HP1363	conserved	hypothetical	integral	membrane		Н
HP1407	conserved	hypothetical	integral	membrane	33.1%	H
UD1/66	protein	hypothotical	intogral	mombrano	22.4%	Н
	protein				30.9%	Н
HP1484	protein	nypotnetical	integral	membrane	41.2%	H
HP1486	conserved	hypothetical	integral	membrane	22.006	Н
HP1487	conserved	hypothetical	integral	membrane	23.070	Н
HP1509	protein conserved	hypothetical	integral	membrane	30.7%	H
1104540	protein	he an adda ad a al			34.3%	H
HP 1548	protein	nypotnetical	integrai	membrane	30.6%	F
HP0138	conserved	hypothetical	iron-sul	fur protein	41.2%	Н
HP0151	conserved	hypothetical	membra	ane protein	21.8%	ŀ
HP0575 HP1258	conserved	hypothetical	membra	ane protein Indrial	38.8%	υ
LID1402	protein 4	hypothotical	nifl Llike	protoin	23.2%	G
HP0032	conserved	hypothetical	protein	protein	37.0%	H
HP0035 HP0086	conserved	hypothetical	protein		34.1% 28.7%	Н
HP0094	conserved	hypothetical	protein		29.8%	Н
HP0100 HP0102	conserved	hypothetical	protein		29.3%	H
HP0105 HP0117	conserved	hypothetical hypothetical	protein		39.7% 34.2%	
HP0162	conserved	hypothetical	protein		36.7%	Н
HP0216 HP0233	conserved	hypothetical hypothetical	protein		33.9% 30.5%	Н
HP0248	conserved	hypothetical	protein		30.7%	Н
HP0274 HP0285	conserved	hypothetical	protein		30.8%	H
HP0309 HP0310	conserved	hypothetical hypothetical	protein		31.3% 33.7%	Н
HP0318	conserved	hypothetical	protein		47.2%	Н
HP0328 HP0334	conserved	hypothetical	protein		30.7%	H
HP0347	conserved	hypothetical	protein		31.8%	H
HP0374	conserved	hypothetical	protein		24.7%	Н
HP0388 HP0395	conserved	nypothetical hypothetical	protein protein		39.8% 39.9%	Н
HP0396	conserved	hypothetical	protein		33.7%	
HP0419	conserved	hypothetical	protein		43.0% 38.2%	
HP0465 HP0466	conserved	hypothetical	protein protein		95.5% 95.7%	
HP0468	conserved	hypothetical	protein		97.1%	
HP0469 HP0496	conserved conserved	nypothetical hypothetical	protein protein		95.1% 99.2%	
HP0507	conserved	hypothetical	protein		37.2% 95.3%	
HP0552	conserved	hypothetical	protein		37.8%	
HP0553 HP0639	conserved	hypothetical	protein protein		30.0% 41.0%	
HP0654	conserved	hypothetical	protein		32.0%	
HP0656 HP0707	conserved conserved	hypothetical	protein protein		30.0% 40.1%	
HP0709 HP0710	conserved	hypothetical	protein		49.6% 33.7%	
HP0716	conserved	hypothetical	protein		30.2%	

HP0734 HP0741	conserved hypoin	encar	UNUNCILL		/ . / . / M/
HP0741	conserved hypoth	etical	protein		31.0%
IDOTIC	conserved hypoth	etical	protein		30.2%
HPU/45	conserved hypoth	etical	protein		33.7%
HP0747	conserved hypoth	etical	protein		32.4%
HP0760	conserved hypoth	etical	protein		36.1%
HP0810	conserved hypoth	etical	protein		31.0%
HP0813	conserved hypoth	etical	protein		32.5%
HP0823	conserved hypoth	etical	protein		27.8%
HP0860	conserved hypoth	etical	protein		52.1%
HP0890	conserved hypoth	etical	protein		32.2%
HP0891	conserved hypoth	etical	protein		33.8%
HP0892	conserved hypoth	etical	protein		39.1%
HP0894	conserved hypoth	etical	protein		39.8%
HP0926	conserved hypoth	etical	protein		30.7%
HPU934	conserved hypoth	etical	protein		33.0%
HP0900	conserved hypoth	otical	protein		21106
UD0066	conserved hypoth	otical	protein		20.106
HP0900	conserved hypoth	otical	protein		29.1%
HP1020	conserved hypoth	etical	nrotein		31.5%
HP1037	conserved hypoth	etical	nrotein		95 996
HP1046	conserved hypoth	etical	protein		32.6%
HP1049	conserved hypoth	etical	protein		39.7%
HP 1066	conserved hypoth	etical	protein		41.3%
HP 1149	conserved hypoth	etical	protein		24.7%
HP 1160	conserved hypoth	etical	protein		34.7%
HP 1182	conserved hypoth	etical	protein		34.6%
HP1214	conserved hypoth	etical	protein		21.5%
HP1221	conserved hypoth	etical	protein		42.4%
HP1240	conserved hypoth	etical	protein		22.5%
HP1242	conserved hypoth	etical	protein		42.3%
HP1259	conserved hypoth	etical	protein		44.6%
HP1284	conserved hypoth	etical	protein		36.8%
HP1291	conserved hypoth	etical	protein		26.3%
HP1335	conserved hypoth	etical	protein		33.9%
HP1337	conserved hypoth	etical	protein		27.2%
HP 1338	conserved hypoth	etical	protein		30.2%
HP 1394	conserved hypoth	etical	protein		33.0%
HF 1401	conserved hypoth	stical	protein		21.0%
HP 1413	conserved hypoth	etical	protein		41.0%
HP 1414	conserved hypoth	etical	protein		27.4%
HF 1417 UD1/22	conserved hypoth	otioal	protein		40.206
HP1//26	conserved hypoth	otical	protein		40.3%
HP1428	conserved hypoth	etical	protein		37.8%
HP1443	conserved hypoth	etical	protein		37.9%
HP1449	conserved hypoth	etical	protein		39.0%
HP1453	conserved hypoth	etical	protein		26.8%
HP1459	conserved hypoth	etical	protein		30.1%
HP1504	conserved hypoth	etical	protein		23.9%
HP1510	conserved hypoth	etical	protein		30.6%
HP1533	conserved hypoth	etical	protein		25.4%
HP1570	conserved hypoth	etical	protein		40.5%
HP1573	conserved hypoth	etical	protein		42.2%
HP1587	conserved hypoth	etical	protein		39.0%
HP1588	conserved hypoth	etical	protein		32.0%
HP1589	conserved hypoth	etical	protein		35.1%
HP0713	conserved hypoth	etical	protein		
Baaaa	(plasmid pHPM180	J)			41.8%
HP0028	conserved hypoth	etical	secreted	protein	42.1%
HPUI39	conserved nypoth	etical	secreted	protein	37.1%
HP0160	conserved hypoth	etical	secreted	protein	30.0%
HP0190	conserved hypoth	otical	secreted	protein	24 206
HP0235	conserved hypoth	otical	secreted	protein	24.3%
	concerved hypoth	otical	encroted	protein	20.206
HP0257	concerved hypoth	etical	secreted	protein	36.4%
HP0257 HP0320		etical	secreted	protein	29.8%
HP0257 HP0320 HP0506	conserved hypoth	Subul	00010100	protein	20.070
HP0257 HP0320 HP0506 HP0518	conserved hypoth	etical	secreted	protoin	96 996
HP0257 HP0320 HP0506 HP0518 HP0785	conserved hypoth conserved hypoth conserved hypoth	etical	secreted		96.9% 26.6%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949	conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical	secreted secreted	protein	96.9% 26.6% 39.7%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical	secreted secreted secreted secreted	protein	96.9% 26.6% 39.7% 29.4%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical etical	secreted secreted secreted secreted secreted	protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980 HP1075	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted	protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980 HP1075 HP1098	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted secreted	protein protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9% 27.0%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980 HP1075 HP1098 HP1117	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted secreted secreted	protein protein protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9% 27.0% 32.3%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP1216	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted secreted secreted secreted secreted	protein protein protein protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9% 27.0% 32.3% 31.9%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980 HP1075 HP1098 HP1117 HP11216 HP1285	conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth conserved hypoth	etical etical etical etical etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted secreted secreted secreted secreted	protein protein protein protein protein protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0%
HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP1098 HP1075 HP1098 HP1175 HP1286 HP1286	conserved hypoth conserved hypoth	etical etical etical etical etical etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted secreted secreted secreted secreted secreted secreted	protein protein protein protein protein protein protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5%
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HP0257 HP0320 HP0506 HP0518 HP0785 HP0949 HP0977 HP0980 HP1075 HP1098 HP117 HP1216 HP1285 HP1286 HP1286 HP1464 HP1488	conserved hypoth conserved hypoth	etical etical etical etical etical etical etical etical etical etical etical etical etical	secreted secreted secreted secreted secreted secreted secreted secreted secreted secreted secreted secreted secreted	protein protein protein protein protein protein protein protein protein protein protein protein protein	96.9% 26.6% 39.7% 29.4% 57.4% 42.9% 27.0% 32.3% 31.9% 38.0% 37.5% 27.4% 29.8%
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