The genome sequence of *Rickettsia* prowazekii and the origin of mitochondria

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We describe here the complete genome sequence (1,111,523 base pairs) of the obligate intracellular parasite *Rickettsia prowazekii*, the causative agent of epidemic typhus. This genome contains 834 protein-coding genes. The functional profiles of these genes show similarities to those of mitochondrial genes: no genes required for anaerobic glycolysis are found in either *R. prowazekii* or mitochondrial genomes, but a complete set of genes encoding components of the tricarboxylic acid cycle and the respiratory-chain complex is found in *R. prowazekii*. In effect, ATP production in *Rickettsia* is the same as that in mitochondria. Many genes involved in the biosynthesis and regulation of biosynthesis of amino acids and nucleosides in free-living bacteria are absent from *R. prowazekii* and mitochondria. Such genes seem to have been replaced by homologues in the nuclear (host) genome. The *R. prowazekii* genome contains the highest proportion of non-coding DNA (24%) detected so far in a microbial genome. Such non-coding sequences may be degraded remnants of 'neutralized' genes that await elimination from the genome. Phylogenetic analyses indicate that *R. prowazekii* is more closely related to mitochondria than is any other microbe studied so far.

The *Rickettsia* are α -proteobacteria that multiply in eukaryotic cells only. R. prowazekii is the agent of epidemic, louse-borne typhus in humans. Three features of this endocellular parasite deserve our attention. First, R. prowazekii is estimated to have infected 20-30 million humans in the wake of the First World War and killed another few million following the Second World War (ref. 1). Because it is the descendent of free-living organisms²⁻⁴, its genome provides insight into adaptations to the obligate intracellular lifestyle, with probable practical value. Second, phylogenetic analyses based on sequences of ribosomal RNA and heat-shock proteins indicate that mitochondria may be derived from the α proteobacteria^{5,6}. Indeed, the closest extant relatives of the ancestor to mitochondria seem to be the Rickettsia7-10. That modern Rickettsia favour an intracellular lifestyle identifies these bacteria as the sort of organism that might have initiated the endosymbiotic scenario leading to modern mitochondria¹¹. Finally, the genome of R. prowazekii is a small one, containing only 1,111,523 base pairs (bp). Its phylogenetic placement and many other characteristics identify it as a descendant of bacteria with substantially larger genomes²⁻⁴. Thus *Rickettsia*, like mitochondria, are good examples of highly derived genomes, the products of several types of reductive evolution.

The genome sequence of *R. prowazekii* indicates that these three features may be related. For example, prokaryotic genomes evolving within a cell dominated by a much larger, eukaryote genome and constrained by bottle-necked population dynamics will tend to lose genetic information^{12,13}. Predictable sets of expendable genes will tend to disappear from the prokaryotic genome when they are made redundant by the activities of nuclear genes. Likewise, non-essential sequences and otherwise highly conserved gene clusters may be obliterated by deleterious mutations that are fixed in clonal parasite or organelle populations because they cannot be eliminated by selection. This process is ongoing in the *Rickettsia* genomes, as shown by the identification of sequences that have recently become pseudogenes. Also, a large fraction (~25%) of non-coding sequences in this genome may be gene remnants that have been

degraded by mutation and have not yet been removed from the genome. Finally, transfer of genes from a mitochondrial ancestor to the nucleus of the host would both reduce the mitochondrial genome size and stabilize the symbiotic relationship. Phylogenetic reconstructions that identify genes in the *Rickettsia* genome as sister clades to eukaryotic homologues found in the nucleus or the organelle support this interpretation. *Rickettsia* and mitochondria probably share an α -proteobacterial ancestor and a similar evolutionary history.

General features of the genome

The circular chromosome of R. prowazekii strain Madrid E has 1,111,523 bp and an average G+C content of 29.1% (Figs 1, 2). The genome contains 834 complete open reading frames with an average length of 1,005 bp. Protein-coding genes represent 75.4% of the genome and 0.6% of the genome encodes stable RNA. We have assigned biological roles to 62.7% of the identified genes and pseudogenes; 12.5% of the identified genes match hypothetical coding sequences of unknown function and the remaining 24.8% represent unusual genes with no similarities to genes in other organisms (Table 1). Multivariate statistical analysis has shown that there is no major variation in codon-usage patterns among genes that are expressed in different amounts, indicating that codon-usage patterns in R. prowazekii may be dominated mainly by mutational forces¹⁴. G+C-content values at the three codon positions average 40.4, 31.2 and 18.6%, and these values are similar at different positions in the genome. We classified the open reading frames with significant sequence-similarity scores to gene sequences in the public databases into functional categories (Table 1) that allow comparisons with the metabolic profiles of other bacterial genomes^{15–23}.

Non-coding DNA. The coding content of previously sequenced bacterial genomes is, on average, 91%, ranging from 87% in *Haemophilus influenzae* to 94% in *Aquifex aeolicum*. In comparison, a large fraction of the *R. prowazekii* genome, 24%, represents non-coding DNA (Fig. 3). A small fraction of this corresponds to



Figure 1 Overall structure of the *R. prowazekii* genome. The putative origin of replication is at 0 kb. The outer scale indicates the coordinates (in base pairs). The positions of pseudogenes are highlighted with death's heads. The distribution of genes is shown on the first two rings within the scale. The location and direction of transcription of rRNA are shown by pink arrows and of tRNA genes by black arrows. The next circle in shows GC-skew values measured over all bases in the genome. Red and purple colours denote positive and negative signs, respec-

tively. The window size was 10,000 nucleotides and the step size was 1,000 nucleotides. The central circles shows GC-skew values calculated for third positions in the codon only. GC-skew values were calculated separately for genes located on the outer strand (green) and on the inner strand (blue). To allow easier visual inspection, the signs of the values calculated for genes located on the inner strand have been reversed.

pseudogenes (0.9% of the genome) and less than 0.2% of the genome is accounted for by non-coding repeats. The remaining 22.9% contains no open reading frames of significant length and it has the low G+C content (mean 23.7%) that is characteristic of spacer sequences in the *R. prowazekii* genome¹⁴. A region of 30 kilobases (kb) located at position 886–916 kb contains as much as 41.6% non-coding DNA and 11.5% pseudogenes. The non-coding DNA in this region has a small, but significantly higher, G+C content (mean 23.7%) that non-coding DNA in other areas of the genome (mean 23.7%) (P < 0.001), indicating that it may correspond to inactivated genes that are being degraded by mutation (Fig. 3).

Origin of replication. The origin of replication has not been experimentally identified in the *R. prowazekii* genome, but we identified *dnaA* at ~750 kb. However, the genes flanking the *dnaA* gene differ from the conserved motifs found in *Escherichia coli* and *Bacillus subtilis* (*rnpA-rpmH-dnaA-dnaN-recF-gyrB*). In *R. prowazekii*, the genes *rnpA* and *rpmH* are located in the vicinity of *dnaA*, but in the reverse orientation compared to the consensus motif, and *dnaN*, *recF* and *gyrB* are located elsewhere.

The origin and end replication in microbial genomes are often associated with transitions in GC skew (G - C/G + C) values²⁴. In *R. prowazekii* we observe transitions in the GC skew values at

around 0 and 500–600 kb (Fig. 1). There is a weak asymmetry in the distribution of genes in the two strands, such that the first half of the genome has a 1.6-fold higher gene density on one strand and the second half of the genome has a 1.6-fold higher gene density on the other strand. The shift in coding-strand bias correlates with the shift in GC-skew values. As most genes are transcribed in the direction of replication in microbial genomes, the origin of replication may correspond to the shift in GC-skew values at the position that we have chosen as the start point for numbering. Indeed, several short sequence stretches that are characteristic of *dnaA*-binding motifs are found in the intergenic region of genes *RP001* and *RP885* at 0 kb, supporting this interpretation.

Stable RNA sequences and repeat elements. We identified 33 genes encoding transfer RNA, corresponding to 32 different isoacceptor-tRNA species. There is a single copy of each of the rRNA genes, with *rrs* located more than 500 kb away from the *rrl–rrf* gene cluster

Figure 2 Linear map of the *R. prowazekii* chromosome. The position and **J** orientation of known genes are indicated by arrows. Coding regions are colour-coded according to their functional roles. The positions of tRNA genes are indicated (inverted triangle on stalk). For additional information, see http://evolution.bmc.uu.se/~siv/gnomics/Rickettsia.html.

(Fig. 1). Comparison of the sequences from ten different *Rickettsia* species indicates that the disruption of the rRNA gene operon preceded the divergence of the typhus group and spotted fever group *Rickettisia* (S.G.E.A. *et al.*, unpublished observations). In addition, the genome contains a short sequence with similarity to a 213-nucleotide RNA molecule in *Bradyrhizobium japonicum* that may regulate transcription²⁵.

There are unusually few repeat sequences in this genome. We identified four different types of repeat sequence: all of these are located in intergenic regions. There is a sequence of 80 bp that is repeated seven times downstream of rpmH and rnpA in the dnaA region. A repetitive sequence of 325 bp is found at two intergenic regions that are more than 80 kb apart, downstream of the genes ksgA and rnh, respectively. A 440-bp-long repetitive sequence has been identified at two intergenic sites, 140 kb apart; one of these sites is downstream of rrf and the others downstream of pdhA and

Table 1 Asterisks indicate putative pseudogenes. Abbreviations of species names are: Bacteria: Acinetobacter calcoaceticus (B-Aca), Actonobacillus actinomycetemcomitans (B-Aac), Acyrthosiphon condii (B-Aco), Agrobacterium tumefaciens (B-Atu), Alcaligenes eutrophus (B-Aeu), Anabena sp. PCC7120 (B-Asp), Anabena variabilis (B-Ava), Anacystis nidulans (B-Ani), Azorhizobium caulinodans (B-Aca), Azosprillium brasiliense (B-Abr), Azotobacter vinelandii (B-Avi), Bacillus caldotenax (B-Bca), Bacillus stereothermophilus (B-Bst), Bacillus subtilis (B-Bsu), Bartonella bacilliformis (B-Bba), Bartonella henselae (B-Bhe), Bordetella pertussis (B-Bpe), Borrelia burgdorferi (B-Bbu), Bradyrhizobium japonicum (B-Bja), Brucella abortus (B-Bab), Brucella ovis (B-Bov), Caulobacter crescentus (B-Ccr), Chlamydia trachomatis (B-Ctr), Chloroflexus aurantiacus (B-Cau), Chromatum viosum (B-Cvi), citrus-greening-disease-associated bacterium (B-Cgr), Clostridium acetobutylicum (B-Cac), Clostridium pasteurianum (B-Cpa), Clostridium thermosaccharolyticum (B-Cts), Coxiella burnetii (B-Cbu), Erwinia chrysanthemi (B-Ech), Escherichia coli (B-Eco), Haemophilus influenzae (B-Hin), Helicobacter pylori (B-Hpy), Klebsiella pneumoniae (B-Kpn), Legionella pneumophila (B-Lpn), Leucothrix mucor (B-Lmu), Liberobacter africanum (B-Laf), Methylobacterium extorquens (B-Mex), Micrococcus luteus (Mlu), Moraxella catarrhalis (Mca), Mycobacterium leprae (Mle), Mycobacterium smegmatis (B-Msm), Mycobacterium tuberculosis (B-Mtu), Mycoplasma capricolum (B-Mca), Mycoplasma genitalium (B-Mge), Mycoplasma pneumoniae (B-Mpn), Paracoccus denitrificans (B-Pde), Pasteurella haemolytica (B-Pha), Plectonema boryanum (B-Pbo), Proteus mirabilis (B-Pmi), Proteus vulgaris (BPvu), Pseudomonas aeruginosa (B-Pae), Pseudomonas fluorescens (B-Pfl), Pseudomonas putida (B-Ppu), Pseudomonas syringae (B-Psy), Rhizobium meliloti (B-Rme), Rhizobium sp. NGR234 (B-Rsp), Rhodobacter capsulatus (B-Rca), Rhodobacter sphaeroides (B-Rsp), Rhodobacter sulfidophilus (B-Rsu), Rhodopseudomonas blastica (B-Rbl), Rhodospirillum rubrum (B-Rru), Rickettsia japonicum (B-Rja), Rickettsia rickettsii (B-Rri), Rickettsia typhi (B-Rty), Salmonella typhi (B-Sti), Salmonella typhimurium (B-Sty), Shigella flexneri (B-Sfl), Sprioplasma citri (B-Sci), Staphylococcus aureus (B-Sau), Staphyloccus carnosus (B-Sca), Streptococcus pneumoniae (B-Spn), Streptomyces clavuligerus (B-Scl), Streptomyces coelicor (B-Sco), Synechocystis PCC 6803 (B-Syn), Thermus aquaticus (B-Taq), Thermus thermophilus (B-Tth), Thiobacillus cuprinus (B-Tcu), Treponema hyodysenteriae (B-Thy), Vibrio alginolytics (B-Val), Vibrio cholera (B-Vch), Vibrio parahaemolyticus (B-Vpa), Vibrio proteolyticus (B-Vpr), Wolbachia sp. (B-Wsp), Yersinia entercolitica (B-Yen), Zooglea ramigera (B-Zra), Zymomonas mobilis (B-Zmo). Archaea: Methanococcus jannaschii (A-Mja), Sulfulobus acidocaldarius (A-Sac). Eukaryotes: Apis mellifera (E-Ame), Arabidopsis thaliana (E-Ath), Atratylodes japonica (E-Aja), Bos taurus (E-Bta), Candida albicans (E-Cal), Caenorhabidits elegans (E-Cel), Dictylostelium discoideum (E-Ddi), Flaveria trinervia (E-Ftr), Giardia theta (E-Gth), Glycine max (E-Gma), Haematobia irritans (E-Hir), Homo sapiens (E-Hsa), Marchantia polymorpha (E-Mpa), Mus musculum (E-Mmu), Prototheca wickerhamii (E-Pwi), Petunia hybrida (E-Phy), Pisum sativum (E-Psa), Porphyra purpurea (E-Ppu), Odontella sinensis (E-Osi), Reclinomonas americana (E-Ram), Rattus novergicus (E-Rno), (E-Sce). Rhizopus oryzae (E-Ror), Saccharomyces cerevisiae Schizosaccharomyces pombe (E-Spo), Solanum tuberosum (E-Stu), Spinacia oleracea (E-Sol).

pdhB. Finally, two similar sequences of 730 bp are located immediately next to each other at 850 kb.

Paralogous families. We have identified 54 paralogous gene families comprising 147 gene products. Of these, 125 have an assigned function. Most paralogues encode proteins with transport functions, such as the ABC transporters, the proline/betaine transporters and the ATP/ADP transporters. Five paralogous genes located next to each other at 115 kb encode putative integral membrane proteins with unknown functions.

Biosynthetic pathways

A striking feature of the *R. prowazekii* genome is the small proportion of biosynthetic genes compared with free-living proteobacterial relatives (such as *Haemophilus influenzae*, *Helicobacter pylori* and *E. coli*)^{15,19,20}. This scarcity of biosynthetic functions is also seen in diverse endocellular and epicellular parasites^{16–18,23}. This scarcity of biosynthetic functions is also seen in diverse endocellular and epicellular parasites^{16–18,23}.

Amino-acid metabolism. As many as 43 and 69 genes required for amino-acid biosynthesis are found in *Helicobacter pylori* and *Haemophilus influenzae*, respectively. In contrast, *Mycoplasma genitalium* and *Borrelia burgdorferi* contain only *glyA*, which encodes serine hydroxymethyltransferase. This gene is also found in *R. prowazekii* (Table 1). Serine hydroxymethyltransferase catalyses the conversion of serine and tetrahydrofolate into glycine and methylenetetrahydrofolate, respectively. A role in tetrahydrofolate metabolism may account for the ubiquity of *glyA* in bacteria.

Seven genes normally associated with lysine biosynthesis (*lysC*, *asd*, *dapA*, *dapB*, *dapD*, *dapE* and *dapF*) are also present in *R*. *prowazekii*. The biosynthetic pathways leading to lysine, methionine and threonine share the first two of these (*lysC* and *asd*). However, none of the downstream genes for threonine biosynthesis are found in *R. prowazekii*. Likewise, the lysine pathway is incomplete, and *lysA*, which encodes the enzyme that converts meso-diaminopime-late to lysine, is missing. The likely role of the upstream genes of this pathway in *R. prowazekii* is the biosynthesis of diaminopimelate, an essential envelope component. We have therefore classified these genes as 'cell-envelope' genes (Table 1).

We have identified other genes that are superficially involved in the metabolism of amino acids, but which apparently function in deamination pathways that divert amino acids into the tricarboxylic acid (TCA) cycle. For example, there is *aatA*, encoding aspartate aminotransferase, which catalyses the degradation of aspartate to oxaloacetate and glutamate. *tdcB* encodes threonine deaminase, which converts threonine into α -ketobutyrate. Another gene (*ilvE*) encodes branched-chain-amino-acid aminotransferase, which converts leucine, isoleucine or valine into glutamate. *pccA* and *pccB* encode propionyl-CoA carboxylase, which converts propionyl-CoA, an intermediate in the breakdown of methionine, valine and isoleucine, into succinyl-CoA. The *pccA* and *pccB* gene products show greatest similarity to the eukaryotic proteins that are located in the mitochondrial matrix.

Nucleotide biosynthesis. No genes required for the *de novo* syntheses of nucleosides have been found in the *R. prowazekii* genome. However, four genes required for the conversion of nucleoside monophosphates into nucleoside diphosphates (*adk, gmk, cmk* and *pyrH*) are present. There are also two genes encoding ribonucleotide reductase, which converts ribonucleoside diphosphates into deoxyribonucleoside diphosphates. Nucleoside diphosphate kinase (encoded by *ndk*), which converts NDPs and dNDPs to NTPs and dNTPs, is also present in *R. prowazekii*. Finally, there is a complete set of genes for the conversion of dCTP and dUTP into TTP, including *thyA*, which codes for thymidylate synthase. Thus, the *R. prowazekii* genome encodes all of the enzymes required for the interconversion of nucleoside monophosphates into all of the other required nucleotides. The nucleoside monophosphates are probably imported from the eukaryotic host.

Energy metabolism

Early in its infectious cycle, *R. prowazekii* uses the ATP of the host with the help of membrane-bound ATP/ADP translocases. However, *R. prowazekii* is also capable of generating ATP, which may compensate for the gradual depletion of cytosolic ATP later in the infection. *R. prowazekii*'s repertoire of genes involved in ATP production and transport include determinants for the TCA cycle, the respiratory-chain complexes, the ATP-synthase complexes and the ATP/ADP translocases (Table 1). Genes to support anaerobic glycolysis are absent.

Pyruvate dehydrogenase. Pyruvate is imported into mitochondria directly from the cytoplasm and converted into acetyl-CoA by pyruvate dehydrogenase. The genes encoding three components (E1–E3) of the pyruvate dehydrogenase complex are found in *R. prowazekii*, indicating that it too uses cytosolic pyruvate. Pyruvate dehydrogenase (E1) consists of two subunits (α and β) in *R. prowazekii*, mitochondria and Gram-positive bacteria; the corresponding genes are clustered in the genome. In contrast, proteobacteria such as *E. coli, Haemophilus influenzae* and *Helicobacter pylori* have a single subunit for the E1 component and these have little similarity to the α and β subunits of the E1 component in *R. prowazekii* and mitochondria (data not shown).

Two paralagous genes code for the dihydrolipoamide dehydrogenase (E3) in R. prowazekii. One of these most resembles mitochondrial homologues, whereas the other is most similar to bacterial homologues (data not shown). The presence of several paralogous gene families for pyruvate dehydrogenases complicates attempts to reconstruct a genome phylogeny based on these genes. ATP production. Genes encoding all enzymes in the TCA cycle are found in R. prowazekii. Proton translocation is mediated by NADH dehydrogenase (complex I), cytochrome reductase (complex III) and cytochrome oxidase (complex IV). Several clusters of genes code for components of the NADH dehydrogenase complex. Seven of these genes (nuoJKLM and nuoGHO) are located near to each other, but the order of genes is inverted relative to the order of this cluster in E. coli. An additional set of five genes is grouped in the order nuoABCDE, but the single genes nuoF and nuoN are distant from both of these clusters. Several proteins in the cytochrome bc_1 reductase complex, such as ubiquinol-cytochrome c reductase

(encoded by *petA*), cytochrome b (encoded by *cytb*) and cytochrome c_1 (encoded by *fbhC*), are present, as are several subunits of the cytochrome oxidase complex.

The ATP-synthesizing complex is composed of the ATP synthase F_1 component (comprising five polypeptides, α , β , γ , ϵ and δ) and the F_0 component, a hydrophobic segment that spans the inner mitochondrial membrane. The genes encoding these components are normally clustered in one of the most highly conserved operon structures in microbial genomes. In *R. prowazekii*, however, the ATP-synthase genes encoding the α , β , γ , δ and ϵ subunits of the F_1 complex (*atpH*, *atpG*, *atpD* and *atpC*) are clustered in the common order, but *atpB*, *atpE* and *atpF*, encoding the A, B and C chains of the F_0 complex, are split from this cluster.

Replication, repair and recombination

R. prowazekii has a smaller set of genes involved in DNA replication than do free-living bacteria such as *E. coli*, *Haemophilus influenzae* and *Heliocobacter pyrlori*. Four genes have been identified that code for the core structure of DNA polymerase III, which includes the α (*dnaE*), ϵ (*dnaQ*), β (*dnaN*), γ and θ (*dnaX*) subunits. Extra subunits present in the *E. coli* DNA polymerase III are missing from *R. prowazekii*, as well as from *M. genitalium* and *B. burgdorferi*.

Genes encoding DNA-repair mechanisms are similar in the small genomes of the parasites *R. prowazekii*, *M. genitalium* and *B. burgdorferi*. Thus, genes involved in the repair of ultraviolet-induced DNA damage (*uvrABCD*) have been identified in all three genomes. In *R. prowazekii*, DNA-excision repair probably occurs by a pathway involving endonuclease III, poII and DNA ligase, as in *B. burgdorferi*.

The *R. prowazekii* genome has a limited capacity for mismatch repair. The DNA-mismatch-repair enzymes encoded by *mutL* and *mutS* are present, but *mutH* and *mutYare* not. There is a complete lack of *mut* genes in *M. genitalium*, but *mutL* and *mutHLY* have been identified in *B. burgdorferi* and *Chlamydia trachomatis*. The transcription-repair coupling factor (encoded by *mfD*) is found in *R. prowazekii*, *B. burgdorferi* and *C. trachomatis* but not in *M. genitalium*.

The *R. prowazekii* genome contains several genes involved in homologous recombination, such as *recA*, *recF*, *recJ*, *recN* and *recR*. A similar set of genes has been found in *A. aeolicus*²¹. The *rec* genes



Figure 3 G+C content in intergenic regions longer than 20 bp in the *R. prowazekii* genome. The empty circles correspond to spacer sequences located at 886 to

916kb, a region with an unusually large fraction of non-coding DNA and pseudogenes.

are scattered in the other small genomes of parasites. The *RecBCD* complex is missing in *R. prowazekii*, *M. genitalium* and *Helicobacter pylori* but it has been identified in *B. burgdorferi*.

Transcription and translation

R. prowazekii has three subunits (α , β and β') of the core RNA polymerase, as well as σ^{70} and one alternative σ factor, σ^{32} , which controls transcription of the genes encoding heat-shock proteins in *E. coli*. Genes involved in transcription elongation and termination, *nusA*, *nusB*, *nusG*, *greA* and *rho*, are also present. The gene encoding σ^{32} is absent in most other small genomes, such as those of *B. burgdorferi*, *Helicobacter pylori*, *M. genitalium* and *C. trachomatis*, although genes for heat-shock proteins are present.

An unusually large number of genes involved in RNA degradation are found in *R. prowazekii*. Of these, only four appear to be common to the bacterial genomes analysed so far (those encoding polyribonucleotide nucleotidyltransferase and ribonucleases HII, III and P). Four more ribonucleases (D, E, HI and PH) are present in *R. prowazekii*, but in none of the other small parasites.

Of the 33 identified tRNA genes, which code for 32 different tRNA isoacceptor species, two code for tRNA^{Phe}. There are two tRNA species for most of the amino acids that are encoded by fourcodon boxes; the exceptions are the four-codon boxes for proline and valine, for which we have identified only one isoacceptor-tRNA species, with U in the first anticodon position. *selC*, which codes for tRNA^{Sec}, and *selABD* are missing. *R. prowazekii* has a set of genes coding for tRNA modifications (*tgt, queA, trmD, truA, truB* and *miaA*) which resembles that of *Helicobacter pylori, C. trachomatis* and *B. burgdorferi; M. genitalium* has only *trmD* and *truA*.

In R. prowazekii, 21 genes encode 18 of the 20 aminoacyl-tRNA synthetases normally required for protein synthesis. There are two genes (gltX) encoding glutamyl-tRNA synthetase. As seen in several bacterial genomes²⁵, the gene coding for glutaminyl-tRNA synthetase, glnS, is missing. Three genes encoding subunits of the glutamyl-tRNA amidotransferase are present, indicating that a glutamyl-tRNA charged with glutamic acid may be transamidated to generate Gln-tRNA. The gene coding for asparaginyl-tRNA synthetase, asnS, is also missing from the R. prowazekii genome as well as from Helicobacter pylori, C. trachomatis and A. aeolicus²⁶. A transamidation process to form Asn-tRNA^{Asn} from Asp-tRNA^{Asn} has been proposed for the archaeon Haloferax volcanii²⁷ and this reaction may also occur in R. prowazekii. The valyl-tRNA synthetase is 38.3% identical to its homologue in Methanococcus jannaschii, but only 27.6% identical to its most similar homologue in bacteria, which is found in Bacillus stearothermophilus, possibly indicating a horizontal transfer event. The lysyl-tRNA synthetase (encoded by lysS) in R. prowazekii is a class I enzyme with no resemblance to the conventional class II lysyl-tRNA synthetases. Class I type of lysyltRNA synthetases have been observed previously in only B. burgdorferi, Pyrococcus woesii, Methanococcus jannaschii and a few other methanogens²⁶.

Regulatory systems

As in other genomes of small parasites, *R. prowazekii* has a reduced set of regulatory genes. There are a few members of two-component regulatory systems, such as the proteins encoded by *barA*, *envZ*, *ntrY*, *ntrX*, *ompR* and *phoR*. *spoT*, which is involved in the stringent response, has been identified in B. burgdorferi, Helicobacter pylori and M. genitalium. Only remnants of genes coding for aminoterminal fragments of proteins similar to those encoded by *spoT* and *relA* are identifiable in *R. prowazekii*. No fragments of *spoT* encoding the carboxy-terminal segments of the protein have been identified in the genome.

Cell division and protein secretion

Proteins involved in detoxification, such as superoxide dismutase, and those involved in thiophen and furan oxidation are present in *R*.

prowazekii. Two genes encoding haemolysins have also been identified, and an *R. typhi* homologue of *tlyC* exhibits haemolytic activities when expressed in *E. coli* (S. Radulovic, J. M. Troyer, B. Noden, S.G.E.A. and A. Azad, unpublished observations).

The data indicate that the basic mechanisms of cell division and secretion in *R. prowazekii* are similar to those in free-living proteobacteria. There is a common set of bacterial chaperones (encoded by *dnaK*, *dnaJ*, *hslU*, *hslV*, *groEL*, *groES* and *htpG*) and genes involved in the *secA*-dependent secretory system (*secABDEFGY*, *ffH* and *ftsY*). *R. prowazekii* has a significantly larger set of genes involved in peptide secretion than does *M. genitalium*.

Membrane-protein analysis

Many studies of *R. prowazekii* have focused on outer-surface membrane proteins because of their potential importance in bacterial detection and vaccination. The superficial lipopolysaccharide (LPS) molecule is important in the pathogenesis of *R. prowazekii*. LPS consists of a polysaccharide that is covalently linked to lipid A, the biosynthesis of which is catalysed by products of *lpxABCD*, all of which are present in the *R. prowazekii* genome. These genes are clustered in *E. coli*, but *lpxA* and *lpxD* are separate from *lpxB* and *lpxC* in *R. prowazekii*. Three genes involved in the biosynthesis of the 3-deoxy-D-manno-octulosonic acid (KDO) residues reside in the *R. prowazekii* genome (*kdsA*, *kdsB* and *kdtA*). Only one gene (*rfaJ*) with a putative function in outer-core biosynthesis has been identified.

We have identified a set of genes involved in the biosynthesis of murein and diaminopimelate and a set involved in the biosynthesis of fatty acids. These includes: *fabD*, which is involved in the last step of the initiation phase of fatty-acid biosynthesis; four genes involved in the elongation cycle of fatty-acid biosynthesis (*fabFGHI*); and three genes involved in the first three steps of the synthesis of polar head groups (*cdsA*, *pssA* and *pgsA*). Finally, post-translational processing and addition of lipids to an N-terminal cysteine require the gene products prolipoprotein diacylglycerol transferase (*lgt*), prolipoprotein signal peptidase (*lspA*) and apolipoprotein:phosholipid *N*-acyl transferase (*lnt*). These are found in the genome with several genes involved in the degradation of fatty acids, such as *fadA* which encodes the 3-ketoacyl-CoA thiolase.

Virulence

The R. prowazekii genome contains several homologues of the VirB gene operon found in Agrobacterium tumefaciens. This gene family encodes proteins that direct the export of the T-DNA-protein complex across the bacterial envelope to the plant nuclei²⁸. R. prowazekii has two homologues of VirB4 and one homologue each of VirB8, VirB9, VirB10, VirB11 and VirD4. The latter five genes are clustered with the gene trbG, which is involved in conjugation in Agrobactrium tumefaciens. Homologues of the single-stranded DNA-binding proteins VirD2 and VirE2 are missing. In Agrobacterium tumefaciens, these proteins are bound to the transferred T-DNA, indicating different functions for the homologues of the VirB genes in R. prowazekii. Indeed, VirB proteins are homologous to components of the E. coli transport system for plasmids, as well as to components of the Pt1 transport machinery in Bordetella pertussis, which exports pertussis toxin²⁸. A set of genes coding for VirB4 and several other VirB proteins has been identified in the cag pathogenicity island of Helicobacter pylori. In this species, the VirB proteins facilitate export of a factor that induces interleukin-8 secretion in gastric epithelial cells²⁸. Thus, R. prowazekii may encode components of a transport system for both conjugal DNA transfer and protein export.

The virulence of *Staphylococcus aureus* has been correlated with the production of capsular polysaccharides in phagocytic assays and mouse lethality assays^{29,30}. A cluster of ten capsule genes (capA-M) is involved in capsule biosynthesis in *S. aureus* strain M³¹. We have identified three *R. prowazekii* genes with sequence similarities to *S. aureus cap* genes. Two of these (capD and capM) are separated by ten

genes, most of which are unknown genes or genes involved in the biosynthesis of LPS or techoic acid. Thus, *R. prowazekii* may produce components of a microcapsular layer that is involved in virulence.

Reductive evolution

Genome sequences of organisms enjoying an endosymbiotic lifestyle are at risk. The activities of homologous nuclear genes may render genes of the endosymbiont expendable and as a consequence they become vulnerable to obliteration by mutation. Good candidates for such purged genes in *Rickettsia* and mitochondria are genes required for amino-acid biosynthesis, nucleoside biosynthesis and anaerobic glycolyis. These and other genes would have been deleted when an ancestral genome first lived in a nucleated cell. Once genes essential to a free-living mode are lost, the endosymbiont becomes an obligate resident of its host.

Likewise, small, bottle-necked populations of bacteria infecting a eukaryotic cell will tend to accumulate deleterious mutations because selection cannot remove them from such clonal populations¹³. The accumulation of such harmful but non-lethal mutations is referred to as 'Muller's ratchet'³² or 'near-neutral evolution'^{33,34}. The consequence of accumulation of these mutations will be the inactivation and eventual deletion of non-essential genes.

The first mutation that inactivates an expendable gene is likely to initiate a sequence of events in which subsequent mutations freely transform it, by degrees, from a pseudogene, to unrecognizable sequence, to small fragments, to extinction. In this sequence, mutations are released from amino-acid-coding constraints. Thus nucleotide substitutions will reflect the mutation bias of the genome. This bias can be estimated roughly by frequencies of third-position bases in the codons. For R. prowazekii, the bias of the third-position bases is 18% G+C rather than the 29% G+C average for the genome. So, as sequences age in R. prowazekii, their composition should gradually approach the low G+C content of third codon positions. Nearly one-quarter of the R. prowazekii genome is composed of non-coding sequences, with a G+C content lower than that of coding sequences (25% G+C compared to 30%; P < 0.001). Thus, much of the non-coding sequence may be remnants of coding sequences that are in the process of being eliminated from the genome.

The gene encoding S-adenosylmethionine synthetase (*metK*), which catalyses the biosynthesis of S-adenosylmethionine (SAM), illustrates the initiation of this process. The *metK* sequence in the strain of *R. prowazekii* studied here has a termination codon within a region of the gene that is otherwise highly conserved among





bacterial species³⁵. However, a closely related strain does not have the termination codon. Many other defects, such as termination codons, insertions, and a preponderance of small deletions, have also been observed in the *metK* genes in several members of the spotted fever group *Rickettsia* (J.O.A. and S.G.E.A., unpublished observations). This random distribution of lethal mutations among some *metK* alleles from different *Rickettsia* species indicates that the gene may have just entered the extinction process. This distribution, and the identification of 11 more pseudogenes for carboxypeptidase (*ypwA*), penicillin-binding protein (*pbpC*), succinyl CoA-transferase (*scoB*), transposase (*tra3*), resolvase (*pin*), conjugative transfer protein (*taxB*), a hypothetical protein (*yfc1*) and four different fragmented open reading frames for (p)ppGpp 3'-pyrophosphohydrolase, indicates that the *R. prowazekii* genome continues to eliminate genes.

Genome sequences can be purged by a more abrupt mechanism. This consists of intrachromasomal recombination at duplicated sequences, which can result in the deletion of intervening sequences, the loss of a sequence duplication and the rearrangement of flanking



Figure 5 The organization and phylogenetic relationships of gene encoding ribosomal protein from *R. prowazekii* and the mitochondrial genome of *Reclinomonas americana*. **a**, The organization of ribosomal-protein genes. The S10, *spc* and α-operons are organized similarly in these two genomes, except that several ribosomal-protein genes³⁸ have been deleted from the mitochondrial genome of *Reclinomonas americana*. **b**, The phylogenetic relationships of mitochondria and bacteria were derived from the combined amino-acid sequences of ribosomal proteins S2, S3, S7, S10, S11, S12, S13, S14, S19, L5, L6 and L16. Neighbour-joining and maximum-parsimony methods gave identical topologies. Branch lengths are proportional to those reconstructed by using the neighbour-joining method. Values at nodes are bootstrap values indicating the degree of support for individual clusters under each method (neighbour-joining, maximum parsimony). Only bootstrap values >90% are shown.

sequences. Such a mechanism will account for the presence in *R. prowazekii* of one, unlinked copy of *rrs* and *rrl*, both of which are surrounded by new flanking sequences³⁶. Likewise, *R. prowazekii* has one *tuf* gene and one *fus* gene in atypical clusters that seem to have been created by intrachromosomal recombination between the two *tuf* genes that are normally found in Gram-negative bacteria³⁷. Indeed, rearranged gene operon structures encoding ribosomal proteins are characteristic of all members of the genus *Rickettsia* (H. Amiri, C.A. and S.G.E.A., unpublished observations).

Conserved operons that are found in free-living bacteria are often dispersed throughout the *Rickettsia* genome (see above). The *R. prowazekii* genome contains an unusually small fraction of repeat sequences (<10% of that observed in free-living bacteria). We suggest that the repeat sequences found in the ancestor to the *Rickettsia* have been 'consumed' by the intrachromosomal-recombination mechanism that generated some of the deletions and rearrangements seen in *R. prowazekii*. Such intrachromosomal recombinants arise at a substantial rate in bacteria growing in culture, but here they are eliminated from the populations by selection. That such remnants of intrachromosomal recombination are retained in *R. prowazekii* indicates that purifying selection has been attenuated in this organism.

Mitochondrial affinities

The reduction in genome size in mitochondria and *Rickettsia* is likely to have occurred independently in the two lineages. Most of



Figure 6 The organization and phylogenetic relationships of genes involved in ATP synthesis from *R. prowazekii* and the mitochondrial genome of *Reclinomonas americana*. **a**, The organization of bioenergetic genes. **b**, The phylogenetic relationships of mitochondria and bacteria were derived from the combined amino-acid sequences of NADH dehydrogenase I chains A, J, K, L, M and N, which are encoded by the genes *nuoA*, *J*, *K*, *L*, *M*, *N*. These genes are highlighted by asterisks in **a**. Neighbour-joining and maximum-parsimony methods gave identical topologies. Branch lengths are proportional to those reconstructed using the neighbour-joining method. Values at nodes are bootstrap values indicating the degree of support for individual clusters under each method (neighbour-joining, maximum parsimony). Only bootstrap values >90% are shown.

the genes supporting mitochondrial activities are nuclear. Many of the 300 proteins encoded in the nucleus of the yeast *Saccharomyces cerevisiae* but destined for service within the mitochondrion are close homologues of their counterparts in *R. prowazekii*. Nearly one-quarter of these proteins are required for bioenergetic processes and another one-third of them are required for the expression of the genes encoded in the mitochondrial genome. In total, more than 150 nucleus-encoded mitochondrial proteins share significant sequence homology with *R. prowazekii* proteins (Fig. 4).

Another group of 58 nucleus-encoded mitochondrial proteins represents components of the mitochondrial transport machinery and regulatory system (Fig. 4). These include proteins found in the mitochondrial outer membrane and others involved in splicing reactions. Such proteins have probably been secondarily recruited to mitochondria from genomes not necessarily related to that of the α proteobacterial ancestor.

The mitochondrial genome of the early diverging, freshwater protozoan Reclinomonas americana is more like that of a bacterium than any other mitochondrial genome sequenced so far³⁸. This genome contains 67 protein-coding genes, most of which provide components of genetic processes and the bioenergetic system³⁸. Several gene clusters in this mitochondrial genome are reminiscent of those in bacteria (Figs 5a, 6a). Most similarities represent retained, ancestral traits present in the common ancestor of bacteria and mitochondria. For example, the genes *rplKAJL* and *rpoBC* are identically organized in R. prowazekii and the mitochondrial genome of Reclinomonas americana. Likewise, the genes encoding the S10, spc and the α -ribosomal protein operons are organized similarly in the two genomes. The immediate proximity of these two clusters in the Reclinomonas americana mitochondrial DNA is reminiscent of the arrangement in free-living bacteria, whereas the physical separation of the two clusters in the R. prowazekii genome is atypical. A further rearrangement event is indicated by the fact that the *rpsLrpsGfus* cluster is located upstream of the rplKAJLrpoBC cluster in R. prowazekii, rather than downstream as it is in the Reclinomonas americana mtDNA. Phylogenetic reconstructions based on ribosomal proteins within each of these two clusters indicate that there is a close evolutionary relationship between R. prowazekii and mitochondria (Fig. 5b).

Mitochondria and *R. prowazekii* have a similar repertoire of proteins involved in ATP production and transport, including genes encoding components of the TCA cycle, the respiratorychain complexes, the ATP-synthase complexes and the ATP/ADP translocases. There are some similarities in the gene orders of some functional clusters (Fig. 6a). There are also some rearrangements of clusters that are specific to *Rickettsia*. One example is the inversion of segments corresponding to *nuoJKLM* and *nuoGHI*. Another is the scattered displacement of genes involved in the biogenesis of cytochrome *c*. Nevertheless, phylogenetic reconstructions based on components of the NADH dehydrogenase complexes indicate that there is a close evolutionary relationship between *R. prowazekii* and mitochondria (Fig. 6b).

We have identified as many as five genes coding for ATP/ADP transporters, all of which are expressed (R.M.P. *et al.*, unpublished observations). The *Rickettsia* ATP/ADP translocases are monomers with 12 transmembrane regions each, whereas the mitochondrial translocates are dimers with six transmembrane regions per dimer. We found no relationship between the primary structures of the mitochondrial and *Rickettsia* ATP/ADP translocases, indicating that these transport systems may have originated independently.

The study of the *R. prowazekii* genome sequence supports the idea that aerobic respiration in eukaryotes originated from an ancestor of the *Rickettsia*, as indicated previously by phylogenetic reconstructions based on the rRNA gene sequences^{7,9}. Phylogenetic analyses of the *petB* and *coxA* genes indicate that the respiration systems of *Rickettsia* and mitochondria diverged ~1,500–2,000 million years ago¹⁰, shortly after the amount of oxygen in the atmosphere began

to increase. The finding that the ATP/ADP translocases in *R. prowazekii* and mitochondria are of different evolutionary origin is problematic (R.M.P. *et al.*, unpublished observations). Free-living bacteria do not seem to have homologues of ATP/ADP translocases, which are found only in organelles and in two obligate intracellular parasites, *Rickettsia* and *Chlamydia*. Thus it is not known whether the original endosymbiont was capable of efficient exchange of adenosine nucleotides with its host cell. More detailed comparative analysis of the genomes of α -proteobacteria may refine our understanding of the origins of mitochondria.

Methods

Genome sequencing. We prepared genomic DNA from the Madrid E strain of *R. prowazekii*, which was originally isolated in Madrid from a patient who died in 1941 with epidemic typhus. We propagated *R. prowazekii* in the yolk sac of embryonated hen eggs and purified DNA according to standard procedures³⁹. We sequenced the *R. prowazekii* genome by a whole-genome shotgun approach in combination with shotgun sequencing of a selected set of clones from a cosmid library (A.Z. et al., unpublished observations). Genomic and cosmid DNA was sheared by nebulization to an average size of ~2 kb. The random fragments were cloned into a modified M13 vector using the double adaptor method⁴⁰. We collected 19,078 sequence reads during the random sequencing phase using Applied Biosystems 377 DNA sequencers (Perkin-Elmer).

The sequences were assembled and the consensus sequence was edited using the STADEN program⁴¹. We verified the structure of the assembled sequence by end-sequencing of 3-kb-insert λ Zap II clones³⁶, 10-kb λ clones and 30-kb cosmid clones. More than 97% of the genome was covered by clones from the three different libraries (A.Z. *et al.*, unpublished observations). Gaps between contigs were closed by direct sequencing of clones from the three libraries or of polymerase chain reaction (PCR) products. The final four gaps were closed by direct sequencing of PCR products generated with the Long Range PCR system (Gene Amp). Regions of ambiguity were identified by visual inspection of the assembly and resequenced. The final assembly contains ~20,000 sequences. The genome sequence has eightfold coverage on average and no single region has less than twofold coverage. We estimate the overall error frequency to be $< 1 \times 10^{-5}$.

Informatics. Sequence analysis and annotation was managed by CapDB (T.S.-P. *et al.*, unpublished observations). We identified open reading frames of more than 50 codons as genes on the basis of their characteristic patterns in nucleotide-frequency statistics¹⁴ using BioWish⁴². The identified genes were analysed using the program BLASTX⁴³ to search for sequence similarities in EMBL, TREMBL, SwissProt and in-house databases. We identified tRNA genes with the program tRNA scan-SE⁴⁴. Remaining frameshifts were considered to be authentic and annotated as pseudogenes. Families of paralogues were constructed using BLAST to search for sequence similarities within the *R. prowazekii* genome. Multiple alignments and phylogenetic trees for genes with significant sequence similarities to genes in the public databases were constructed automatically using CLUSTAL-W⁴⁵, Phylo_win⁴⁶ and GRS⁴⁷. The final annotation was based on manual inspection of the phylogenetic placement of *R. prowazekii* in the resulting gene trees.

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Table 1. Functional classification of Rickettsia prowazekii protein-coding genes. Gene numbers correspond to those in Fig. 2. Percentages represent per cent identitites.

| AMINO ACID METABOLISM | | | |
|----------------------------------|------------------------|---|--|
| RP743 | glyA | serine hydroxymethyl transferase (B-Mex, 60.9%) | |
| RP428 | ΪνΈ | branched-chain amino acid aminotransferase (B- Eco, 36.8%) | |
| RP091 RP618 | aatA pccA | aspartate aminotransferase (B- <i>Rme</i> , 55.6%) propionyl-CoA carboxylase α chain (E- <i>Rno</i> , | |
| RP619 | рссВ | 45.0%) propionyl-CoA carboxylase β chain (E- <i>Hsa</i> , 63.3%) | |
| RP449 | tdcB | threonine dehydratase (E-Yeast, 35.3%) | |
| BIOSYN | ITHESI | S OF COFACTORS25 | |
| Folic ac BP536 | id folC | folvloolvolutamate synthetase (B-Bsu 34.5%) | |
| RP515 RP383 | foID foIF | 46.3%) GTP cyclohydrolase I (B-Syn, 48.1%) | |
| | | | |
| RP841 | na porp hemA | delta-aminolevulinate synthase (B- <i>Bja</i> , 49.1%) | |
| RP539 RP466 | hemB | delta-aminolevulinate dehydratase (B-Bja, 53.3%) | |
| RP885 | hemE | uroporhyrinogen decarboxylase (B-Rca, 42.6%) | |
| RP884 | hemH | ferrochelatase (B-Syn, 40.4%) | |
| RP847 RP175 | hemK hemN | protoporphyrinogen oxidase (B- <i>Eco</i> , 44.3%) oxygen-independent coproporphyrinogen II (B- <i>Bsu</i> , 34.4%) | |
| <i>Lipoate</i> RP742 RP876 | lipA lipB | lipoic acid synthetase (B- <i>Hin</i> , 50.5%) lipoic acid ligase (B- <i>Mtu</i> , 35.6%) | |
| <i>Menaqu</i> RP190 | iinone a coq7 | <i>und ubiquinonens</i> ubiquinone biosynthesis prt Coq7 (E- <i>Rno</i> , | |
| RP479 | ispB | 36.9%) octaprenyl-diphosphate synthase (B- <i>Eco</i> , | |
| RP686 | ubiA | 4-hydroxybenzoate octaprenyltransferase (B- | |
| RP541 | ubiX | 3-octaprenyl-4-hydroxybenzoate carboxylase (B- Eco, 53.2%) | |
| RP680 | ubiE | ubiquinone biosynthesis methyltransferase (B- | |
| RP622 | ubiG | 3-demethylubiquinone methyltransferase (B- <i>Eco</i> , 39.1%) | |
| Thio- ar | nd gluta | redoxin | |
| RP204 RP745 | grxC1 grxC2 | glutaredoxin 3 (B- <i>Eco</i> , 50.0%) glutaredoxin 3 (B- <i>Syn</i> , 50.0%) | |
| RP327 RP002 | tdpX1 | thioredoxin-peroxidase (B-Hpy, 54.0%) | |
| RP445 | trxB1 | thioredoxin reductase (B-Hin, 52.0%) | |
| RP514 | trxB2 | thioredoxin reductase (B-Cpa, 28.4%) | |
| Diamino | pimela | ie | |
| RP316 | asd | aspartate-semialdehyde dehydrogenase (B-Vch, 43.3%) | |
| RP429 RP148 RP194 | dapA dapB dapD | dihydrodipicolinate synthase (A-Mja, 39.6%) dihydrodipicolinate reductase (B-Hpy, 37.7%) tetrahydrodipicolinate N-succinyltransferase (B- | |
| RP874 | dapE | Eco, 57.9%) succinyl-diaminopimelate desuccinylase (B-Hin, | |
| RP415 RP753 | dapF lysC | diaminopimelate epimerase (B- <i>Hin</i> , 35.0%) aspartokinase (B- <i>Bst</i> , 37.3%) | |
| <i>Membra</i> RP347 | anes an asmA | d lipoproteins outer membrane assembly protein (B-Eco, | |
| RP446 | lgtD | 19.3%) prolipoprotein diacylglyceryl transferase (B-Vch, | |
| RP366 BP300 | Int nInD | apolipoprotein N-acyltransferase (B-Hin, 29.1%) linoprotein (B-Hin, 22.4%) | |
| RP390 | ripA | rare lipoprotein A (B-Hin, 23.9%) | |
| RP048 | yidC | inner membrane protein, 60 kDa (B-Hin, 30.4%) | |
| Murein RP095 RP389 | sacculu air dacF | s alanine racemace (B-Hin, 29.5%) penicillin binding protein precursor (B-Bsu | |
| RP249 | ddiB | 33.8%) D-alanine:D-alanine ligase (B- <i>Hin</i> , 32.8%) | |
| RP595 | gimU mraY1 | (B-Hin, 34.3%) phospho-N-acetylmuramovl-pentapeptide-trans- | |
| RP825 | mraY2 | ferase (B-Hin, 49.9%) phospho-N-acetylmuramoyl-pentapeptide-trans- | |
| RP807 | mrcA | ferase (B-Sac, 22.0%) penicillin binding protein 1A (B-Eco, 35.6%) UDP-N-acetylolucosamine 1-carboxwinyltrans- | |
| RP248 | murB | ferase (B-Aca, 51.6%) UDP-N-acetylenolyruvoylglucosamine reductase | |
| RP247 | murC | (B-Bsu, 35.7%) UDP-N-acetylmuramoylalanine ligase (B-Hin, | |
| RP410 | murD | 41.5%) UDP-N-acetylmuramoylalanine-D-glutamate lig- aso (R-Hin 32.9%) | |
| RP597 | murE | UPD-MurNac-tripeptide synthetase (B-Bsu, 35.2%) | |
| RP596 | murF | UDP-MurNac-pentapeptide synthetase (B-Eco, 30.6%) | |
| RP412 | murG | UDP-MurNac-pentapeptide transferase (B-Bsu, 28.8%) | |
| пР565 RP567 | popA1 pbpA2 | penicillin binding protein (B- <i>Hin</i> , 34.3%) penicillin binding protein (B- <i>Bsu</i> , 30.7%) | |
| RP195 | pbpC* | penicillin-binding protein (B- <i>Eco</i> , 26.7%) | |
| RP400 | sit | lytic murein transglycosidase (B-Hin, 21.4%) | |
| Surface RP333 | polysa capD | ccnarides, lipopolysaccharides and antigens capsular polysaccharide biosynthesis protein CapD (B-Sau 34 6%) | |
| RP344 | capM1 | capsular polysaccharide biosynthesis protein | |
| RP414 | capM2 | capsular polysaccharide biosynthesis protein CapM prt (B-Sau, 23.7%) | |
| RP339 | ggaB | galactosamine-containing techoic acid biosyn- thesis (B-Bsu, 23.3%) | |
| | | | |

| | | 5 · · · · · · · | |
|---------------------|---------------|---|--|
| BP321 | loxB | Hri, 90.4%) lipid A disaccharide synthetase (B-Hin, 27.3%) | |
| RP254 | lpxC | UDP-3-O-acyl N-acetylglucosamine deacetylase | |
| BP009 | InxD | (B- <i>Eco</i> , 44.4%) UDP-3- <i>O</i> -(B-3-hydroxymyristoyl)-glucosamine N- | |
| | | acetyltransferase (B-Rri, 92.4%) | |
| RP062 | Kas A | 3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase (B-Pha. 45.1%) | |
| RP379 | kdsB | CTP:CMP-3-deoxy-manno-octulosonate-cytidylyl | |
| BP089 | kdtA | transferase (B-Hin, 34.8%) 3-deoxy-D-manno-octulosonic acid transferase | |
| | | (B- <i>Eco</i> , 28.9%) | |
| RP505 | kpsF | polysiliac acid capsule expression protein (B- | |
| RP833 | omp | cell surface antigen, 17 kD (B-Rty, 46.9%) | |
| RP160 | omp1 | OMP1 precursor (B-Bab, 29.5%) | |
| | μαι | 37.9%) | |
| RP476 | rfaJ | lipopolysaccharide 1,2-glucosyltransferase (B- | |
| RP004 | rfbA | O-antigen export system permease (B-Kpn, 22.3%) | |
| RP003 | rfbE | O-antigen ABC export system, ATP-binding pro- | |
| RP334 | rffE | UDP-N-acetvlolucosamine 2-epimerase (B-Bsu. | |
| | | 26.8%) | |
| HP018 BP081 | sca1 sca2 | cell surface antigen (B- <i>Hri</i> , 24.9%) cell surface antigen (B- <i>Bri</i> , 27.4%) | |
| RP451 | sca3 | cell surface antigen (B-Rri, 27.6%) | |
| HP498 BP704 | sca4 sca5 | cell surface antigen (B- <i>H</i> /a, 67.4%) cell surface antigen (B- <i>Bri</i> , 72.5%) | |
| RP779 | udg | UDP-glucose 6-dehydrogenase (B-Pae, 31.8%) | |
| | | | |
| CELLU | LAK PI | 10CESSES 44 | |
| Cell div | ision | | |
| HP251 RP043 | nsA ftsH | cell division protein FtsA (B-Hin, 29.5%) cell division protein FtsH (B-Eco. 54.0%) | |
| RP163 | ftsJ | cell division protein FtsJ (B-Eco, 44.4%) | |
| HP823 BP250 | ttsK fts⊖ | cell division protein FtsK (B-Cbu, 41.5%) cell division protein FtsQ (B-Hin 17.9%) | |
| RP411 | ftsW | cell division protein FtsW (B-Eco, 33.2%) | |
| RP775 | ftsY fts7 | cell division protein FtsY (B-Hin, 43.2%) | |
| RP056 | gidA | glucose inhibited division protein A (B-Eco, 48.8%) | |
| RP057 | gidB | glucose inhibited division protein (B-Ppu, 26.8%) | |
| RP042 | mesJ | cell cycle protein MesJ (B-Eco, 22,1%) | |
| RP768 | mreB | rod shape-determining protein (B-Eco, 60.5%) | |
| RP280 | rodA | rod shape-determining protein (B-Eco, 23.1%) rod shape-determining protein (B-Eco, 38.1%) | |
| | | ies on the second management (5 _ cot cot ret) | |
| Cell Killi BP555 | ng tivA | hemolysin (B-Thy 34.3%) | |
| RP740 | tiyC | hemolysin (B-Thy, 28.8%) | |
| Chanor | ones ar | ad stress-induced proteins | |
| RP670 | cspA | cold shock protein (B-Scl, 57.6%) | |
| RP816 | dksA dna l | DnaK suppressor protein (B-Hin, 38.8%) | |
| RP185 | dnaK | heat shock protein 70 (B-Rme, 72.7%) | |
| RP626 | groEL | heat shock protein GroEL (B-Rme, 69.4%) | |
| RP629 | grpE | heat shock protein GroEs (B-Ccr, 39.5%) | |
| RP200 | hscA | heat shock protein A (B-Hin, 39.6%) | |
| RP320 | nsiU hsiV | heat shock protein HsIU (B-Bsu, 54.8%) heat shock prt HsIV (B-Hin, 54.1%) | |
| RP273 | hsp22 | heat shock protein (E-Phy cp, 29.0%) | |
| HP840 | htpG | heat shock protein C62.5 (B- <i>Eco</i> , 43.1%) | |
| Detoxifi | cation | | |
| HP535 BP759 | sodB thdF | superoxide dismutase (B-Lpn, 53.4%) thiophene and furan oxidizer (B-Hin, 34.7%) | |
| | | | |
| Protein RP315 | and pe | ptide secretion | |
| 11-515 | арго | 40.0%) | |
| RP314 | aprE | protease secretion ATP-binding protein (B-Pae, | |
| RP173 | ffh | signal recognition particle receptor protein (B-Eco, | |
| DDOTE | 1 | 49.6%) | |
| RP116 | lepA lepB | signal peptidase (B-Stv. 37.3%) | |
| RP575 | secA | preprotein translocase SecA subunit (B-Rca, 51.8%) | |
| RP586 | secB secD | protein-export membrane protein (B- <i>Hin</i> , 30.7%) | |
| RP134 | secE | preprotein translocase SecE subunit (B-Bsu, 37.3%) | |
| HP114 RP079 | sec⊢ secG | protein-export membrane protein (B-Hin, 37.7%) protein-export membrane protein (B-Hnv 32-0%) | |
| RP639 | secY | preprotein translocase SecY subunit (B-Eco, 50.0%) | |
| HP842 | tig | trigger factor (B-Eco, 32.0%) | |
| ENERG | Y MET | ABOLISM 67 | |
| ATP-nm | oton me | tive force interconversion | |
| RP803 | atpA | ATP synthase F1 alpha subunit (B-Rru, 66.2%) | |
| RP023 | atpB atpC | ATP synthase F0 subunit a (B-Rru, 51.5%) ATP synthase F1 ensilon subunit (B-Rru, 24.5%) | |
| RP801 | atpD | ATP synthase F1 beta subunit (B-Rca, 77.0%) | |
| RP022 | atpE atpE | ATP synthase F0 subunit c (E-Ram mt, 43.2%) ATP synthase F0 subunit b (B-Ray 21.1%) | |
| RP802 | atpG | ATP synthase F1 gamma subunit (B-Rbl, 38.0%) | |
| RP804 | atpH atr¥ | ATP synthase F1 delta chain (E-Osi cp 26.4%) | |
| nrv21 | αψΛ | ATT synthase Fo subunit b (E-Malli IIII, 20.0%) | |
| Electron transport | | | |
| RP703 | ccmF | cytochrome c biogenesis protein (E-Ram mt, 33.6%) | |
| RP405 | COXA | cytochrome c oxidase subunit I (E-Mpo mt, 68.9%) | |
| RP191 | сохС сохС | cytochrome c oxidase subunit II (E-Mpo mt, 48.0%) | |
| RP257 | coxW | cytochrome c oxidase assemly (E-Sce, 35.2%) | |
| HP304 RP346 | cox11 ctaB | cytochrome c oxidase assembly (E-Ham mt, 42.9%) cytochrome c oxidase assembly factor (B-Pde | |
| DDOCC | | 40.6%) | |
| RP216 | cycM cydA | cytochrome c (B-Bja, 35.6%) cytochrome oxidase d subunit I (B-Avi. 34.0%) | |
| RP217 | cydB | cytochrome oxidase d subunit II (B-Eco, 30.0%) | |
| нг272 | TDCH | ubiquinoi cytochrome c oxidoreductase, cytochrome c1 subunit (B-Bia. 47.8%) | |
| RP829 | fdxA | ferredoxin (<i>Rca</i> , 57.5%) | |
| HP357 BP356 | nuoA nuoR | NAUH dehydrogenase I chain A (E-Pwimt, 64.6%) NADH dehydrogenase I chain B (E-Bammt 73.2%) | |
| RP355 | nuoC | NADH dehydrogenase I chain C (B-Pde, 42.1%) | |
| RP354 RP353 | nuoD nuoE | NADH dehydrogenase I chain D (E-Ram mt, 71.4%) | |
| | | | |

| DDHE | nun E | NADI Jahudrananan Lakain E (D. Oda. CO. 19/1) | | |
|---|---|---|--|--|
| RP797 | nuor nuoG | NADH denydrogenase I chain G (E- <i>Bta</i> mt, 49.3%) | | |
| RP796 | nuoH | NADH dehydrogenase I chain H (E-Ram mt, 63.5%) | | |
| RP795 | nuol nuol | NADH dehydrogenase I chain I (E-Ham mt, 71.4%) NADH dehydrogenase I chain I (E-Bam mt 42.3%) | | |
| RP791 | nuoK | NADH dehydrogenase I chain K (B-Pde, 61.4%) | | |
| RP792 | nuoL1 | NADH dehydrogenase I chain L (E-Ram mt, 45.5%) | | |
| RP282 | nuoL3 | NADH dehydrogenase I chain L (E-Ane mt, 17.0%) | | |
| RP793 | nuoM nuoM1 | NADH dehydrogenase I chain M (E-Ram mt, 46.6%) | | |
| RP284 | nuoN2 | NADH dehydrogenase I chain N (E-Ram mt, 34.0%) | | |
| RP270 | petA | Rieske-I iron sulphur protein (B- <i>Bja</i> , 58.3%) | | |
| RP863 | pntAA | NAD(P) transhydrogenase α subunit (B-Eco, 37.7%) | | |
| RP862 | pntAB | NAD(P) transhydrogenase α subunit (B-Hin, 44.7%) | | |
| 111-07-4 | рты | TVAD(F) transitydrogenase p suburnt (D-Fmil, 51.5%) | | |
| Fermen BP110 | tation ackA | acatata kinasa (R. Cts. 38.4%) | | |
| | | | | |
| Glycoly: BP492 | sis ppdK | pyruvate, orthophosphate dikinase (E-Etr. 48.8%) | | |
| | | p) | | |
| RP589 | ање рра | inorganic pyrophosphatase (B-Eco, 59.3%) | | |
| Durinet | o dohu | trogeneee | | |
| RP261 | pdhA | pyruvate dehydrogenase E1 component, α sub- | | |
| BP262 | ndhR | unit (E-Ath, 44.0%) | | |
| | pand | unit (E-Sce, 59.7%) | | |
| HP530 | panc | dihydrolipoamide acetyltransferase E2 compo- nent (E-Rno. 45.1%) | | |
| RP460 | pdhD | dihydrolipoamide dehydrogenase E3 component | | |
| RP805 | pdhD | (E-Psa, 54.7%) dihydrolipoamide dehydrogenase E3 component | | |
| TOA | - | (Zým, 51.1%) | | |
| RP799 | acnA | aconitate hydratase (B-Lpn, 59.1%) | | |
| RP665 | fumC | fumarate hydratase (B-Ror, 63.5%) | | |
| RP265 | icd | isocitrate dehydrogenase (B-Tth, 38.6%) | | |
| RP376 | mdh sdhA | malate dehydrogenase (B-Can, 51.5%) | | |
| 111 120 | Junia | (B-Bja, 70.0%) | | |
| RP044 | sdhB | succinate dehydrogenase, iron-sulphur protein (E- | | |
| RP126 | sdhC | succinate dehydrogenase, cytochrome b556 | | |
| BP127 | sdhD | subunit (E-Ram mt, 39.5%) succinate debydrogenase, subunit IV (E-Ram | | |
| | canz | mt, 25.6%) | | |
| RP180 RP179 | sucA sucB | 2-oxoglutarate dehydrogenase (B-Hin, 44.3%) dihydrolipoamide succinvltransferase (B-Eco, 48.7%) | | |
| RP433 | sucC | succinyl-CoA synthetase, β subunit (B- <i>Eco</i> , 52.1%) | | |
| HP432 | sucD | succinyi-CoA synthetase, α subunit (E-Ddi, 70.7%) | | |
| Sugars | | al and the second se | | |
| RP299 | lacA | galactosidase acetyltransferase (B-Mpn, 44.4%) | | |
| | | | | |
| FATTY ACID AND PHOSPHOLIPID METABOLISM25 | | | | |
| FATTY | ACID A | IND PHOSPHOLIPID METABOLISM25 | | |
| FATTY RP620 | acida | 2-acyl-glycerol-phosphate-ethanolamine (B- <i>Eco</i> , | | |
| RP620 BP038 | aas aco1 | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast 27.6%) | | |
| RP620 RP038 RP763 | aas aco1 acpP | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl cariter protein (B- <i>Lmu</i> , 52.6%) | | |
| FATTY RP620 RP038 RP763 RP577 BP533 | aas aco1 acpP acpS birA | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-carbo protein (B- <i>Lmu</i> , 52.6%) holo-facyl carrier protein (S-ynthase (B-Eco, 38.5%) biolina Ac-CoA carboxylase swithase (B- <i>Ero</i> , 33.6%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP523 RP424 | aas aco1 acpP acpS birA cdsA | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-carrier protein (B-Euru, 25.6%) holo-facyl carrier protein (3.50%) biotin Ac-CoA carboxylase synthase (B-Eco, 31.8%) phosphatidate cylidylyltransferase (B-Eco, 31.5%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 | aas aco1 acpP acpS birA cdsA fabD | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-coA desaturase (E-Yeast, 27.6%) acyl-carrier protein (B-Lmu, 52.6%) holor[acyl carrier protein] synthase (B-Eco, 38.5%) phosphatidate cytldyl/transferase (B-Eco, 31.5%) phosphatidate cytldyl/transferase (B-Eco, 31.5%) malonyl-CoA:Acyl carrier protein transacylase (B-Esu, 40.3%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP764 | aco1 aco1 acpP acpS birA cdsA fabD fabF | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-carrier protein (B- <i>Lmu</i> , 52.6%) holor[acyl carrier protein] synthase (B- <i>Eco</i> , 38.5%) phosphatidate cytldyl/transferase (B- <i>Eco</i> , 31.5%) phosphatidate cytldyl/transferase (B-Eco, 31.5%) malonyl-CoA:Acyl carrier protein transacylase (B-Bsu, 40.3%) 5-xoacyl-[acyl-carrier-protein] synthase II(B- | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP764 RP764 RP762 | aco1 acpP acpS birA cdsA fabD fabF fabG | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-Carler protein (B- <i>Imu</i> , 52.6%) holo-facyl carlory(ase synthase (B- <i>Pde</i> , 33.6%) phosphatidate cytidy(ylfransferase (B- <i>Pde</i> , 33.6%) phosphatidate cytidy(ylfransferase (B- <i>Eco</i> , 31.5%) malonyl-CoA:Acyl carler protein transacylase (B- <i>Ba</i> , 40.3%) 3-xxxacyl-facyl-carlier-protein] synthase II(B- <i>Eco</i> , 53.5%) 3-xxxacyl-facyl-carlier-protein] | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP764 RP764 RP762 | aco1 acpP acpS birA cdsA fabD fabF fabG | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) acyl-carrier protein (B- <i>Hm</i> , 52.6%) holo-facyl carrier protein] synthase (B- <i>Pde</i> , 33.6%) phosphatidate cytidylyltransferase (B- <i>Pde</i> , 33.6%) phosphatidate cytidylyltransferase (B- <i>Eco</i> , 31.5%) maionyt-CoA-Acyl carrier protein transacylase (B- <i>Bu</i> , 40.3%) -sowacyl-facyl-carrier-protein] synthase II(B- <i>Eco</i> , 53.5%) -sowacyl-facyl-carrier-protein] reductase (B- <i>Hme</i> , 54.3%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP764 RP762 RP762 RP772 | aas aco1 acpP acpS birA cdsA fabD fabF fabG fabH | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-carrier protein (B- <i>Hu</i> , 52.6%) holo-facyl carrier protein (B- <i>Pite</i> , 33.6%) phosphatidate cytidylyttransferase (B- <i>Eco</i> , 31.5%) malomy-Co-Acyl carrier protein transacylase (B-Bsu, 40.3%) 3-oxoacyl-[acyl-carrier-protein] synthase II(B- Eco, 53.5%) 3-axoacyl-[acyl-carrier-protein] reductase (B- <i>Hme</i> , 54.4%) 3-oxoacyl-(acyl-carrier-protein] synthase (B- <i>Rac</i> , 47.3%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP424 RP735 RP764 RP762 RP762 RP762 RP772 | aas aco1 acpP acpS birA cdsA fabD fabF fabG fabH fabI fabI | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-carier protein (B- <i>Lmu</i> , 52.6%) holo-facyl carrier protein (B- <i>Pde</i> , 33.6%) phosphatidate cytidylyltransferase (B- <i>Pde</i> , 33.6%) phosphatidate cytidylyltransferase (B- <i>Eco</i> , 31.5%) malonyl-CoA:Acyl carrier protein transacylase (B- <i>Bsu</i> , 40.3%) 3-oxoacyl-facyl-carrier-protein) synthase II(B- Eco, 53.5%) 3-oxoacyl-facyl-carrier-protein] reductase (B- <i>Rme</i> , 54.3%) 3-oxoacyl-facyl-carrier-protein] synthase (B- Rca, 47.3%) B-hydrogrowynistoni acyl carrier protein facultase (B- <i>Rca</i> , 47.3%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP424 RP762 RP762 RP762 RP762 RP772 | aas aco1 acpP acpS birA fabD fabF fabG fabH fabI fabI | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) biolin Ac-CoA desaturase (B-File, 33.6%) phosphatidate cytidylytiransferase (B-File, 33.6%) phosphatidate cytidylytiransferase (B-File, 33.6%) malonyl-CoA:Acyl carrier protein transacylase (B-Bau, 40.3%) 3-xoxacyl-(acyl-carrier-protein) synthase II(B- Eco, 53.5%) 3-xoxacyl-(acyl-carrier-protein) reductase (B- Rme, 54.8%) 3-xoxacyl-(acyl-carrier-protein) synthase (B- Rca, 47.3%) enoyl-facyl-carrier-protein) reductase (B-Asp, 49.0%) 3R-hydroxymyristoyl acyl carrier protein dehy dratase (B-Rf, 91.7%). | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP753 RP424 RP764 RP764 RP762 RP764 RP762 RP762 RP772 RP365 RP008 RP736 RP038 | aco1 acpP acpS birA cdsA fabD fabF fabG fabH fabI fabZ fadA fadB | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) biolin Ac-CoA carboxylase synthase (B-Pdr, 33.6%) phosphatidate cytidylyltransferase (B-Pdr, 33.6%) phosphatidate cytidylyltransferase (B-Eco, 31.5%) malonyl-CoA/Acyl carrier protein transacylase (B-Bat, 40.3%) 3-xxxacyl-(acyl-carrier-protein) synthase II(B- Eco, 53.5%) 3-xxxacyl-(acyl-carrier-protein) reductase (B- Rme, 54.8%) 3-xxxacyl-(acyl-carrier-protein) synthase (B- Rca, 47.3%) 9-Article (B-Age, 40.0%) 3-R-hydroxymyristoyl acyl carrier protein dehy dratase (B-Rr, 91.7%) acetyl-CoA acetyltransferase (B-Pde, 54.5%) [atty xxidation complex a subunit (F-Cd, 30.6%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP764 RP764 RP764 RP762 RP762 RP772 RP365 RP008 RP737 RP5600 RP442 | ACID A acp acpP acpS birA cdsA fabD fabF fabG fabH fabH fabI fabZ fadA fadB gpsA | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) bolot-Ac-CoA desaturase (B-Zea, 33.6%) phosphatidate cytidylyttansferase (B-Zea, 33.6%) phosphatidate cytidylyttansferase (B-Eco, 31.5%) malonyl-CoA:Acyl carrier protein transacylase (B-Bat, 40.3%) 3-xxxacyl-(acyl-carrier-protein) synthase II(B- Eco, 53.5%) 3-xxxacyl-(acyl-carrier-protein) synthase II(B- Eco, 53.5%) 3-xxxacyl-(acyl-carrier-protein) synthase (B- Rma, 64.3%) 3-xxxacyl-(acyl-carrier-protein) synthase (B- Rca, 47.3%) 3-xxxacyl-(acyl-carrier-protein) synthase (B- Rca, 47.3 | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP424 RP762 RP762 RP772 RP365 RP008 RP777 RP560 RP737 RP560 RP442 RP046 | ACID A acp acpP acpS birA cdsA fabD fabF fabG fabH fabI fabI fabZ fadB gpsA lqt | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-carrier protein (B- <i>Imu</i> , 52.6%) holo-facyl carrier protein] synthase (B- <i>Eca</i> , 33.6%) phosphatidate cytidylyltransferase (B- <i>Eca</i> , 31.5%) malomy-CoA-Acyl carrier protein transacylase (B- <i>Bu</i> , 40.3%) -xoxacyl-facyl-carrier-protein] synthase II(B- <i>Eca</i> , 53.5%) -xoxacyl-facyl-carrier-protein] synthase (B- <i>Rma</i> , 54.4%) 3-xoxacyl-facyl-carrier-protein] synthase (B- <i>Rac</i> , 47.3%) -acyl-carrier-protein] synthase (B- <i>Rac</i> , 47.3%) -acyl-CoA-carrier-protein] synthase (B- <i>Rac</i> , 47.3%) -acyl-CoA-carrier-protein] coluctase (B- <i>Asp</i> , 49.0%) B-hydroxymyristoyl acyl carrier protein dehy dratase (B- <i>Rri</i> , 91.7%) accyl-CoA acylitansferase (B- <i>Pde</i> , 54.5%) fatty oxidation complex a subuni (E- <i>Cel</i> , 30.6%) glycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) | | |
| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP424 RP762 RP762 RP772 RP762 RP772 RP365 RP008 RP737 RP560 RP442 RP046 RP035 RP035 | aco1 acpP acpS birA cdsA fabD fabF fabG fabH fabI fabI fabZ fadA fadB gpsA lgt phbB | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) acyl-Carrier protein (B- <i>Imu</i> , 52.6%) holo-facyl carrier protein (B- <i>Eco</i> , 33.6%) phosphatidate cytidylytiransferase (B- <i>Eco</i> , 31.5%) malomy-CoA-Acyl carrier protein transacylase (B-Bat, 40.3%) 3-oxoacyl-facyl-carrier-protein] synthase II(B- Eco, 53.5%) 5-oxoacyl-facyl-carrier-protein] synthase II(B- Eco, 53.5%) 6-3oxoacyl-facyl-carrier-protein] synthase II(B- Eco, 53.5%) 6-3oxoacyl-facyl-carrier-protein] synthase (B- <i>Rac</i> , 47.3%) 6-3oxoacyl-facyl-carrier-protein] synthase (B- Rac, 47.7%) accell+coA-carrier-protein] facuctase (B- <i>Asp</i> , 49.0%) 5-hydroxymyristoyl acyl carrier protein dely dratase (B- <i>Rri</i> , 91.7%) accell+coA-coltitamsferase (B- <i>Pde</i> , 54.5%) fatty oxidation complex a subunit (E- <i>Cel</i> , 30.6%) glycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) prolipoprotein diacylglycerol (B- <i>Eco</i> , 39.1%) acelcacetyl/CoA reductase (B- <i>Zra</i> , 52.9%) | | |
| FATTY RP620 RP763 RP577 RP533 RP424 RP735 RP764 RP762 RP762 RP762 RP772 RP365 RP008 RP737 RP560 RP442 RP468 RP442 RP046 RP035 RP738 | ACID P aas acco1 accpP birA accpS birA cdsA fabD fabF fabG fabH fabI fabI fabI fabI fabI fabI fabB fabB fabB fabB fabB fabB | Auto Procent LapJ MeT AboLLSM | | |
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| FATTY RP620 RP038 RP763 RP577 RP533 RP424 RP735 RP764 RP762 RP772 RP762 RP772 RP560 RP442 RP046 RP046 RP035 RP738 RP738 RP730 RP500 RP442 | ACID P aas acco1 accpP birA cdsA fabD fabF fabG fabH fabB fabB gpsA igt phbB phbC01 phbC02 pgpA | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) acyl-Carler protein (B- <i>Lmu</i> , 52.6%) holo-facyl carrier protein (B- <i>Eco</i> , 33.5%) phosphatidate cytidylyftransferase (B- <i>Eco</i> , 31.5%) malonyl-CoA:Acyl carrier protein transacylase (B- <i>Bat</i> , 40.3%) 3-xxxacyl-(acyl-carrier-protein) synthase II(B- <i>Eco</i> , 53.5%) 3-xxxacyl-(acyl-carrier-protein) synthase (B- <i>Rme</i> , 54.8%) 3-xxxacyl-(acyl-carrier-protein) synthase (B- <i>Rac</i> , 47.3%) 3-R-hydroxymyristoyi acyl carrier protein dehy dratase (B- <i>Rif</i> , 91.7%) acetyl-CoA acetyltransferase (B- <i>Pa</i> , 54.5%) fatty cottation complex a subunit (E- <i>Cel</i> , 30.6%) glycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) prolipoprotein diacylglycerol (B- <i>Eco</i> , 39.1%) acetoacetyl-CoA raductase (B- <i>Zra</i> , 52.9%) poly-beta-hydroxyburytrate polymerase (B- <i>Cwl</i> , 22.7%) poly-beta-hydroxyburytrate polymerase (B- <i>Ma</i> , 37.4%) | | |
| FATTY RP620 RP038 RP757 RP577 RP573 RP424 RP735 RP424 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP760 RP442 RP37 RP560 RP49 RP035 RP738 RP035 RP738 RP035 RP738 RP035 RP738 RP035 RP738 RP036 RP036 RP036 RP750 RP049 | actor a acpS birA cdsA fabD fabF fabG fabH fabG fabH fabJ fabB gpsA ggsA ggt phbB phbC2 pgpA pgsA | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-Carler protein (B- <i>Imu</i> , 26.6%) holo-facyl carler protein (B- <i>Eco</i> , 33.6%) phosphatidate cytidylyftansferase (B- <i>Eco</i> , 33.5%) malonyi-CoA-Acyl carlier protein transacylase (B- <i>Bu</i> , 40.3%) 3-xxxacyl-facyl-carlier-protein] synthase II(B- <i>Eco</i> , 53.5%) 5-xxxacyl-facyl-carlier-protein] synthase II(B- <i>Eco</i> , 53.5%) 5-xxxacyl-facyl-carlier-protein] synthase (B- <i>Rm</i> , 64.8%) 5-xxxacyl-facyl-carlier-protein] reductase (B- <i>Rm</i> , 64.8%) 5-xxxacyl-facyl-carlier-protein] synthase (B- <i>Rd</i> , 47.7%) acetyl-CoA acetyltransferase (B- <i>Pale</i> , 54.5%) fatty oxidation complex a subunit (E- <i>Cel</i> , 30.6%) glycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) prolipoprotein diacylglycerol (B- <i>Eco</i> , 39.1%) acetoacetyl-CoA reductase (B- <i>Zrd</i> , 52.9%) poly-beta-hydroxybutyrate polymerase (B- <i>Mx</i> , 37.4%) phosphatidylglycerophosphates A (B- <i>Hm</i> , 31.9%) phosphatidylglycerophosphates synthase (B- <i>Bsu</i> , 40.1%) | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP764 RP735 RP424 RP735 RP424 RP742 RP464 RP762 RP500 RP442 RP500 RP442 RP500 RP449 RP509 RP469 | ACID P aas accp2 birA cdsA fabD fabF fabG fabH fabI fabB fabB fabB gpsA gpsA glt phbB phbBC1 pgpA pgsA plsC | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Yeast, 27.6%) acyl-Cartier protein (B- <i>Hw</i> , 52.6%) holo-facyl cartier protein) synthase (B- <i>Eco</i> , 33.6%) phosphatidate cytidylyltransferase (B- <i>Eco</i> , 31.5%) malomy-CoA-Acyl cartier protein transacylase (B- <i>Bu</i> , 40.3%) 3-oxoacyl-(acyl-cartier-protein) synthase II(B- <i>Eco</i> , 53.5%) 3-oxoacyl-(acyl-cartier-protein) reductase (B- <i>Hm</i> , 54.3%) 3-oxoacyl-(acyl-cartier-protein) synthase (B- <i>Ra</i> , 47.3%) 3-oxoacyl-(acyl-cartier-protein) synthase (B- <i>Ra</i> , 47.3%) acethace(Hr, 91.7%) acethace(Hr, 91.7 | | |
| FATTY RP620 RP038 RP763 RP763 RP772 RP424 RP735 RP424 RP735 RP424 RP742 RP424 RP742 RP464 RP464 RP469 RP549 RP549 RP549 RP549 RP549 | ACID A aas accp2 accp2 birA fabD fabF fabG fabH fabB fadA fadB gpsA lgt phbC2 pgpA pgsA plsC psSA | Auto Procent Lip/D METABOLISM | | |
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| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP763 RP764 RP737 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP785 RP787 RP808 RP499 RP469 RP749 RP469 RP503 RP503 RP503 | ACUD P aas acopP acopP acopS birA fabD fabF fabG fabH fabJ fabJ fabJ fabJ fabJ fabJ fabJ fabJ | Auto Procent Lip/D Me1 AboLLSM | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP764 RP735 RP764 RP776 RP762 RP776 RP762 RP762 RP762 RP762 RP764 RP765 RP908 RP737 RP560 RP494 RP494 RP469 RP469 RP469 RP469 RP469 RP469 RP469 RP503 RP573 | ACUD <i>P</i> aas acopP acopP acopS birA fabD fabF fabG fabH fabB fabB phbBC1 phbBC1 phbBC2 pgpA pgsA plsC pgsA plsC pgsA plsC pssA psSC pssA psSC pssA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSC psSA psSA psSA psS psSA psS psSA psS psS psS psS psS psS psS psS psS psS | 2-acyl-glycerol-phosphate-ethanolamine (B- <i>Eco</i> , 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-Carler protein (B- <i>Lmu</i> , 52.6%) holo-facyl carlier protein (B- <i>Eco</i> , 33.5%) phosphatidate cytidylytransferase (B- <i>Eco</i> , 31.5%) malomyl-CoA-Acyl carlier protein transacylase (B- <i>Bu</i> , 40.3%) -xoxacyl-(acyl-carlier-protein) synthase II(B- <i>Eco</i> , 53.5%) -xoxacyl-(acyl-carlier-protein) synthase II(B- <i>Eco</i> , 53.5%) -xoxacyl-(acyl-carlier-protein) synthase (B- <i>Rma</i> , 64.3%) -xoxacyl-(acyl-carlier-protein) synthase (B- <i>Rma</i> , 64.3%) -acotacyl-(acyl-carlier-protein) synthase (B- <i>Rma</i> , 47.3%) encyl-(acyl-carlier-protein) synthase (B- <i>Rma</i> , 47.3%) phosphatidyleycerol (B- <i>Eco</i> , 39.1%) acetoacetyl-CoA reductase (B- <i>Zra</i> , 52.9%) phosphatidyleycerophosphate acyltransferase (B- <i>Cwl</i> , 22.7%) phosphatidyleycerophosphate acyltransferase (B- <i>Ma</i> , 37.4%) phosphatidyleycerophosphate acyltransferase (E- <i>Su</i> , 37.4%) phosphatidyleycerophosphate acyltransferase (E- <i>Su</i> , 37.4%) phosphatidyleycerophosphate acyltransferase (E- <i>Su</i> , 37.4%) phosphatidyleycerophosphate acyltransferase (E- <i>Su</i> , 27.5%) phosphatidyleycerophosphate acyltransferase (E- <i>S</i> | | |
| FATTY RP620 RP038 RP533 RP424 RP735 RP424 RP735 RP764 RP737 RP764 RP762 RP762 RP764 RP776 RP762 RP764 RP776 RP762 RP764 RP705 RP708 RP708 RP409 RP400 RP400 RP400 RP400 RP400 RP400 RP400 RP400 RP400 | ACUD # aacs accpP accpS birA accpS birA cdsA fabD fabF fabG fabH fabl fabB gpsA gpsA phbB phbB phbB phbC2 pgpA pssA time vacus ssA time vacus time vacus ssA time vacus time vacus time vacus time vacus time vacus time vacus time vacus time vacus time time vacus time | 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl-CoA desaturase (B-Fec, 33.6%) biolin Ac-CoA carboxylase synthase (B-Fde, 33.6%) phosphatidate cytidylyltransferase (B-Eco, 31.5%) malonyi-CoA-Acyl carrier protein transacylase (B-Edu, 40.3%) -xoxacyl-facyl-carrier-protein] synthase II(B-Eco, 53.5%) -xoxacyl-facyl-carrier-protein] reductase (B-Rm, 64.8%) -xoxacyl-facyl-carrier-protein] reductase (B-Rm, 64.8%) -xoxacyl-facyl-carrier-protein] synthase (B-Rd, 47.5%) acotacyl-facyl-carrier-protein] synthase (B-Rd, 47.5%) acotacyl-facyl-carrier-protein] for the synthase (B-Rd, 47.5%) acotacyl-facyl-carrier-protein] synthase (B-Rd, 47.5%) acotacetyl-facyl-carrier-protein] synthase (B-Rd, 47.5%) acetyl-CoA redyltransferase (B-Pde, 54.5%) fatty oxidation complex a subunit (E-Ccl, 30.6%) glycerol-3-phosphate delydrogenase (B-Cdv, 22.7%) poly-beta-flydroxybutyrate polymerase (B-Max, 37.4%) phosphatidylglycerophosphates and (B-Hm, 31.9%) phosphatidylserine synthase (B-Hz, 28.8%) malic enzyme (B-Hin, 45.5%) vacl lipoprotein precursor (B-Stl, 33.8%) subDINES | | |
| FATTY RP620 RP038 RP533 RP533 RP424 RP753 RP754 RP752 RP764 RP762 RP772 RP762 RP762 RP772 RP764 RP762 RP772 RP764 RP762 RP765 RP764 RP569 RP409 RP669 RP409 RP669 RP669 | acus a acop acops acops acops dacops das fabo fab f fab fab fab fab fab fab fab fab fab fab | Aug. Proceedings 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-cold desaturase (E-Yeast, 27.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) phosphatidate cytidylytransferase (B-Eco, 31.5%) malonyl-CoArAcyl carrier protein transacylase (B- <i>But</i> , 40.3%) 3-coxacyl-(acyl-carrier-protein) synthase II(B-Eco, 53.5%) 3-coxacyl-(acyl-carrier-protein) reductase (B- <i>Rme</i> , 47.3%) acroacyl-(acyl-carrier-protein) reductase (B- <i>Rse</i> , 49.0%) SR-Hydroxymyristoyl acyl carrier protein drahy dratase (B- <i>R</i> , 19.1%) acetalv-(CoA acetyltransferase (B- <i>Pde</i> , 54.5%) tatty oxidation complex a subunit (E-Cc4, 30.6%) glycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) proliportein diacylglycerol (B- <i>Eco</i> , 39.1%) acetaacetyl-CoA reductase (B- <i>Zra</i> , 52.9%) poly-bata-hydroxybutyrate polymerase (B- <i>Cvi</i> , 22.7%) poly-bata-hydroxybutyrate polymerase (B- <i>Mex</i> , 37.4%) phosphatidylglycerophosphates acyltransferase (E- <i>Soc</i> , 23.6%) poly-bata-hydroxybutyrate polymerase (B- <i>Bsu</i> , 40.1%) phosphatidylylycerophosphates cyltransferase (E- <i>Soc</i> , 23.6%) | | |
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| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP764 RP764 RP764 RP764 RP764 RP766 RP762 RP764 RP764 RP765 RP708 RP787 RP820 RP49 RP442 RP469 RP749 RP469 RP503 RP503 RP503 RP509 RP264 RP703 RP509 RP604 RP703 RP509 RP604 RP703 | actor A actor A actor A actor A actor A actor A fab D fab D | Aug. Proscription Met Aboldsmith, 23 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-cohd desaturase (E-Yeast, 27.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) biolin Ac-Cock carboxylase synthase (B- <i>Pote</i> , 33.6%) phosphatidate cylidylyltansferase (B- <i>Eco</i> , 31.5%) malonyl-Cock-Acyl carrier protein transacylase (B- <i>But</i> , 40.3%) -xoxacyl-qacyl-carrier-protein] synthase II(B-Eco, 53.5%) -xoxacyl-qacyl-carrier-protein] reductase (B- <i>Rme</i> , 54.8%) -xoxacyl-qacyl-carrier-protein] synthase (B- <i>Rca</i> , 47.3%) -acyl-facyl-carrier-protein reductase (B-Asp, 49.0%) 3R-hydroxymyristoyl acyl carrier protein dehy dratase (B- <i>Ri</i> , 91.7%) acelyl-coA acelyltransferase (B- <i>Pdc</i> , 54.5%) glyperot-B-phosphate dehydrogenase (B-Eco, 32.1%) prolipoprotein diazylglycerol (B-Eco, 39.1%) acelstacyl-CoA raductase (B-Zra, 52.9%) poly-beta-hydroxybulyrate polymerase (B- <i>Mex</i> , 37.4%) phosphatidylglycerophosphates acyltransferase (E- <i>Cu</i> , 22.7%) prolophotein diazylglycerol (B-Eco, 39.1%) acelstacyl-CoA raductase (B- <i>Har</i> , 31.9%) phosphatidylglycerophosphates acyltransferase (E- <i>Sco</i> , 23.6%) phosphatidylglycerophosphates acyltransferase (E- <i>Sco</i> , 28.5%) | | |
| FATTY RP620 RP038 RP573 RP763 RP533 RP424 RP735 RP764 RP762 RP764 RP762 RP764 RP762 RP764 RP764 RP764 RP765 RP760 RP498 RP489 RP489 RP489 RP489 RP499 | Acut p aasa acop acopS acopS acopS trab fab fab fab fab fab fab fab fab fab f | Aug Prosperiod Process 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-carie protein (B- <i>Lmu</i> , 52.6%) acyl carier protein (B- <i>Lmu</i> , 52.6%) acyl carier protein (B- <i>Lmu</i> , 52.6%) biotin Ac-Cock carboxylase synthase (B- <i>Pcte</i> , 33.6%) phosphatidate cytidylytransferase (B- <i>Eco</i> , 31.5%) malonyl-Cock-Acyl carrier protein transacylase (B-Bau, 40.3%) >-xoxacyl-(acyl-carrier-protein) synthase II(B-Eco, 53.5%) >-xoxacyl-(acyl-carrier-protein) reductase (B-Rm, 54.8%) >-xoxacyl-(acyl-carrier-protein) synthase (B-Ra, 49.0%) SR-map(-lacyl-carrier-protein) reductase (B-Agg, 49.0%) SR-inyl-corrier-protein reductase (B-Agg, 49.0%) ratie on yme (B-Agg, 49.0%) scell-cork acelyltransferase (B-Agg, 49.0%) scell-cork acelyltran | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP764 RP735 RP764 RP736 RP762 RP762 RP762 RP762 RP762 RP762 RP764 RP763 RP764 RP049 RP469 RP469 RP049 | actor A actor A actor A actor A actor A data fab G fab | Aug. Prosperiod Lip/D Me1 Abold SM 2-acyl-giycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-CoA desaturase (E-Yeast, 27.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) phosphatidate cytidylytransferase (B- <i>Pate</i> , 33.6%) phosphatidate cytidylytransferase (B- <i>Eco</i> , 31.5%) malonyl-CoA/cayl carrier protein transacylase (B- <i>Bau</i> , 40.3%) 3-coxacyl-(acyl-carrier-protein) synthase II(B- <i>Eco</i> , 53.5%) 3-coxacyl-(acyl-carrier-protein) reductase (B- <i>Rma</i> , 47.3%) aromolyl-(acyl-carrier-protein) reductase (B- <i>Ra</i> , 47.3%) arolyl-(acyl-carrier-protein) reductase (B- <i>Ra</i> , 47.3%) arolyl-(acyl-carrier-protein) reductase (B- <i>Asp</i> , 49.0%) 3R-hydroxymyristoyl acyl carrier protein dans/glycerol activ complex a suburit (E-Ccl, 30.6%) giycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) prolipoprotein diacylglycerol (B- <i>Eco</i> , 39.1%) acetacet/b-CoA reductase (B- <i>Zra</i> , 52.9%) poly-bata-hydroxybulyrate polymerase (B- <i>Mex</i> , 37.4%) phosphatidylgverophosphate synthase (B- <i>Hun</i> , 31.9%) phosphatidylycerophosphate synthase (B- <i>Su</i> , 40.1%) actacet/b-CoA reductase the synthase (B- <i>Su</i> , 40.4%) yactalipoprotein synthase (B- <i>Hy</i> , 28.8%) | | |
| FATTY RP620 RP038 RP533 RP763 RP763 RP753 RP753 RP754 RP752 RP764 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP763 RP763 RP764 RP069 RP669 RP664 RP513 RP513 RP513 RP513 RP513 | actor A action according accord according accord according accord according fabD fabD fabD fabD fabD fabD fabD gpsA phoB phoB phoB phoB phoB phoB phoB phoB | Aug Prosendulp/D Mel AdoutsMinume (B-Eco, 39.9%) 2-acyl-giycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-cold desaturase (E-Yeast, 27.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) malonyl-CoA: carboxylase synthase (B- <i>Pole</i> , 33.6%) phosphatidate cytidylytransferase (B-Eco, 31.5%) malonyl-CoA: Acyl carrier protein transau/lase (B- <i>But</i> , 40.3%) -xoxacyl-(acyl-carrier-protein) synthase II(B-Eco, 53.5%) -xoxacyl-(acyl-carrier-protein) reductase (B- <i>Rme</i> , 47.3%) enolyl-facyl-carrier-protein] reductase (B- <i>Asp</i> , 49.0%) SR-hydroxymyristoyl acyl carrier protein dansydrydroxymyristoyl acyl carrier protein dansydrydrogenase (B- <i>Eco</i> , 32.1%) glocerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) proliportein dlacyldylcerol (B- <i>Eco</i> , 39.1%) acetacetyl-CoA reductase (B-Zra, 52.9%) poly-bata-hydroxybutyrate polymerase (B- <i>Max</i> , 37.4%) phosphatidylgylcerophosphates acyltransferase (B- <i>Su</i> , 22.7%) poly-bata-hydroxybutyrate polymerase (B- <i>Lany</i> , 31.9%) phosphatidylgylceroph | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP742 RP735 RP744 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP762 RP763 RP763 RP764 RP905 RP644 RP399 RP644 RP399 RP644 RP399 | acus a acon acopP acopS acopS fabD fabD fabD fabD fabD fabD fabD fabD fabD fabD fabD fabD phoB phoB phoB phoB phoB phoB phoB pscA time cosc pscA time time cosc pscA time time cosc pscA time time cosc pscA time time time cosc pscA time | acyl-giycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-carlier protein (B- <i>Lmu</i> , 52.6%) acyl carlier protein (B- <i>Lmu</i> , 52.6%) phosphatidate cytidylytransferase (B- <i>Eco</i> , 33.5%) phosphatidate cytidylytransferase (B- <i>Line</i> , 33.6%) phosphatidate cytidylytransferase (B- <i>Line</i> , 31.5%) malonyl-CoAX-cyt carlier protein transacylase (B- <i>Bu</i> , 40.3%) -xoxacyl-(acyl-carlier-protein) synthase (IB- -xoxacyl-(acyl-carlier-protein) reductase (B- <i>Ra</i> , 47.3%) -acvbacyl-carlier-protein) reductase (B-Asp, 49.0%) 3R-hydroxymyristoyl acyl carlier protein dehy dratase (B- <i>Hi</i> , 91.7%) acetbacet/LoA acetyltransferase (B- <i>Line</i> , 30.6%) giycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) proliporotein diacylghycerol (B- <i>Eco</i> , 39.1%) acetbacet/LoA acetyltransferase (B- <i>Hine</i> , 31.9%) poly-bata-hydroxybutyrate polymerase (B- <i>Max</i> , 37.4%) phosphatidylghycerophosphatase A (B- <i>Hin</i> , 31.9%) phosphatidylghycerophosphatase A (B- <i>Hin</i> , 31.9%) phosphatidylghycerophosphatase (B- <i>Hasu</i> , 40.1%) yatage | | |
| FATTY RP620 RP033 RP763 RP763 RP763 RP763 RP763 RP763 RP764 RP762 RP764 RP762 RP764 RP762 RP762 RP764 RP39 RP39 RP492 RP492 RP494 RP494 RP494 RP393 RP503 RP503 RP504 RP509 RP504 RP509 RP604 RP509 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP509 RP604 RP509 RP509 RP509 RP509 RP604 RP509 RP509 RP509 RP509 RP604 RP509 RP509 RP604 RP509 RP509 RP509 RP604 RP509 RP509 RP604 RP509 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP604 RP509 RP50 | actor A actor A actor A actor A actor A actor A fab D fab D | AND PROSPHOLIPID MET ABOLISM | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP763 RP764 RP737 RP764 RP762 RP762 RP762 RP762 RP762 RP764 RP764 RP785 RP785 RP499 RP499 RP499 RP499 RP499 RP499 RP499 RP499 RP499 RP505 RP513 RP513 RP513 RP514 RP301 RP514 RP301 RP514 RP314 | Acut P aaas acop acopS acopS acopS fab fab fab fab fab fab fab fab fab fab | Aug - Proservolupin Mer Aebultsminner (B-Eco, 39.9%) 2-acyl-giycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl-carier protein (B- <i>Lmu</i> , 52.6%) acyl carier protein (B- <i>Lmu</i> , 52.6%) acyl carier protein (B- <i>Lmu</i> , 52.6%) biolta Ac-CoA carboxylase synthase (B- <i>Pate</i> , 33.6%) phosphatidate cylidylyltransferase (B- <i>Eco</i> , 31.5%) malonyl-CoAX-cyl carier protein transacylase (B-Bau, 40.3%) >-xoxacyl-(acyl-carier-protein) synthase II(B- Eco, 53.5%) >-xoxacyl-(acyl-carier-protein) reductase (B- <i>Rme</i> , 54.8%) >-xoxacyl-(acyl-carier-protein) synthase (B- Rca, 47.3%) = anoyl-facyl-carier-protein reductase (B-Asp, 49.0%) SR-inydroxymyristoyl acyl carier protein dehy dratase (B-Ri, 19.17%) acetyl-CoA acetyltransferase (B-Zde, 54.6%) fatty oxidation complex a subunit (E-Cel, 30.6%) giycerol-3-phosphate dehydrogenase (B- <i>Eco</i> , 32.1%) prolipoprotein diacylgiycerol (B- <i>Eco</i> , 39.1%) acetoacetyl-CoA reductase (B-Zra, 52.9%) poly-beta-hydroxyburytra polymerase (B- <i>Cul</i> , 22.7%) poly-beta-hydroxyburytra polymerase (B- <i>Cul</i> , 22.7%) poly-beta-hydroxyburytra polymerase (B- <i>Su</i> , 40.1%) 1-acyl-giycerol-3-phosphate acyltransferase (E- <i>Sce</i> , 23.6%) phosphatidylglycerophosphates synthase (B- <i>Ha</i> , 31.9%) < | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP764 RP737 RP764 RP762 RP764 RP762 RP764 RP765 RP764 RP365 RP469 | Acut P aaas acop acopS acopS fabD fabF fabG fabH fabB fabB fabB gpsA gpsA gpsA gpsA phbB gphB phbB gphB phbB gphB gpsA gpsA gpsA gpsA gpsA gpsA gpsA gpsA | AND PROSPHOLIPID MET ABOLISM | | |
| FATTY RP620 RP038 RP533 RP533 RP424 RP753 RP754 RP752 RP752 RP764 RP762 RP762 RP762 RP762 RP762 RP764 RP762 RP765 RP737 RP764 RP059 RP649 RP513 RP512 RP513 RP514 | actor A action accord accpS accpS facbD fabD fabD fabD fabD fabD fabD fabD fa | Aug Prosence (LPC) MeT Abol LSM 23 2-acyl-glycerol-phosphate-ethanolamine (B-Eco, 39.9%) 39%) acyl-cold desaturase (E-Yeast, 27.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) acyl carrier protein (B- <i>Lmu</i> , 52.6%) 30%) malony-CoA-cartoxylase synthase (B- <i>Pote</i> , 33.6%) phosphatidate cytidylytransferase (B- <i>Eco</i> , 31.5%) malony-CoA-Acyl carrier protein transaviase (B- <i>Eco</i> , 53.5%) -xoxacyl-(acyl-carrier-protein) synthase II(B-Eco, 53.5%) | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP763 RP735 RP735 RP744 RP782 RP782 RP782 RP782 RP787 RP | actor A action accord accpS accpS facbD fabD fabD fabD fabD fabD fabD fabD fa | Aug - Prosendulary Mark Aboldsmine (B-Eco, 39.9%) 2-acyl-giycerol-phosphate-ethanolamine (B-Eco, 39.9%) acyl cartier protein (B- <i>Lmu</i> , 52.6%) phosphatidate cytidylytiransferase (B-Eco, 33.5%) phosphatidate cytidylytiransferase (B-Eco, 31.5%) malonyl-CoAX-dyl cartier protein transacylase (B-Ecu, 40.3%) 3-coxacyl-(acyl-cartier-protein) synthase (IIB-Eco, 53.5%) 3-coxacyl-(acyl-cartier-protein) reductase (B-Rm, 64.8%) 3-coxacyl-(acyl-cartier-protein) reductase (B-Asp, 49.0%) 3R-hydroxymyristoyl acyl cartier protein dehy dratase (B-Ri, 91.7%) acetale-CoA acelyltransferase (B-Pde, 54.5%) fatty oxidation complex a subunit (E-Cci, 30.6%) giycerol-3-phosphate dehydrogenase (B-Eco, 32.1%) proliportein diacylghycerol (B-Eco, 39.1%) acetacet/-OA reductase (B-Zra, 52.9%) poly-bata-hydroxybutyrate polymerase (B-Max, 37.4%) phosphatidylghycerophosphatase A (B-Hin, 31.9%) phosphatidylghycerophosphatase (B-Hox, 28.8%) malio anzyme (B-Hin, 45.5%) Yazuliporotein precursor (B-Sti, 33.8%) RIMDINES 14 volde metabolism | | |
| FATTY RP620 RP038 RP763 RP763 RP763 RP763 RP763 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP764 RP38 RP442 RP442 RP442 RP442 RP442 RP442 RP442 RP442 RP442 RP444 RP750 RP499 RP444 RP599 RP644 RP399 RP665 RP509 RP644 RP399 RP664 RP509 RP644 RP399 RP664 RP509 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP644 RP709 RP645 RP709 RP655 RP709 RP655 RP709 RP655 RP709 RP655 RP709 RP655 RP709 RP655 RP709 RP655 RP709 RP655 RP709 RP700 R | A cub <i>A</i> aaas acopP acopS dacpS fabD fabD fabD fabD fabD fabd fabd gpsA gpsA gpbB phbB phbB phbB phbC psSA tme vacJ SS, PYF bonucle dcd dcd dcd dcd dcd dcd dcd dcd dcd dc | AND PROSPHOLIPID MET ABOLISM | | |

RP155 pyrH uridylate kinase (B-Syn, 53.3%)

| DEOLI | ATOD14 | |
|--|--|---|
| RP229 | barA | histidine kinase sensor protein (B-Eco, 23.2%) |
| RP071 | czcR | transcriptional activator protein (B-Aeu, 35.1%) |
| RP426 | envZ | histidine kinase osmolarity sensor protein (B- |
| BP294 | appA | pppGpp phosphohydrolase (B-Hpy, 23.3%) |
| RP011 | nifR3 | transcriptional activator nitrogen assimilation |
| DDC14 | ntrV | protein (B-Abr, 59.0%) |
| HF014 | nur | 30.6%) |
| RP562 | ntr X | transcriptional activator nitrogen assimilation |
| BP427 | omnR | protein (B-Aca, 45.2%) transcriptional activator protein OmpB (B-Bca |
| 115427 | ompri | 42.9%) |
| RP465 | phoR | histidine kinase phosphatase synthesis sensor |
| BP312 | snoT* | protein (B-Bsu, 24.4%) (n)nnGnn 3'-nvronhosphohydrolase (B-Eco, 29.9%) |
| RP624 | spor* | (p)ppGpp 3'-pyrophosphohydrolase (B-Leo, 28.8%) |
| RP625 | spoT* | (p)ppGpp 3'-pyrophosphohydrolase (B-Eco, 48.7%) |
| HP705 BP517 | spo I * vhhH | (p)ppGpp 3 -pyrophosphohydrolase (B-Eco, 31.7%) sigma 54 modulation protein (B-Bia, 26.2%) |
| | | |
| REPLIC | CATION | |
| Degrad | ation of | DNA |
| RP734 RP260 | addA xthA1 | Al P-dependent nuclease (B-Bsu, 23.7%) exodeoxyribonuclease III (B-Eco, 30.1%) |
| RP676 | xthA2 | exodeoxyribonuclease III (B-Eco, 33.2%) |
| RP675 | xseA | exodeoxyribonuclease large subunit (B-Eco, 31.7%) |
| HP350 | xseB | exodeoxyribonuclease small subunit (B-Eco, 32.5%) |
| DNA re | plicatior | n, restriction, modification, recombination and repair |
| RP601 | dnaA | chromosomal replication initiation protein DnaA (B- |
| RP542 | dnaB | DNA helicase (E-Osi cp. 40.9%) |
| RP778 | dnaE | DNA polymerase III alpha subunit (B-Sty, 37.2%) |
| HP859 | dnaG dnaN | DNA primase (B-Sity, 29.0%) DNA polymorece III bete cubunit (P. Poy. 20.0%) |
| RP732 | dnaQ | DNA polymerase III epsilon subunit (B-Stv. 46.7%) |
| RP865 | dnaX | DNA polymerase III gamma chain (B-Eco, 31.4%) |
| RP206 | gyrA | DNA gyrase A subunit (B-Rsp, 49.4%) |
| nr/22/ RP580 | gyr£1 avrPo | DNA gyrase b suburit (B-SCI, 42.0%) DNA gyrase B suburit (B-Pnu 51.5%) |
| RP172 | holB | DNA polymerase III, delta prime subunit (B-Pae, |
| | | 22.3%) |
| HP171 | hupA lic | UNA binding protein HU (B-Vpr, 47.8%) |
| BP777 | metK* | S-adenosylmethionine synthetase (B-Eco. 66.3%) |
| RP598 | mfd | transcription-repair coupling factor (B-Hin, 33.9%) |
| RP351 | mpg | DNA-3-methyladenine glycosidase (E-Hsa, 29.7%) |
| HP880 | mutL | DNA mismatch repair protein MutL (B-Spn, 35.4%) |
| RP746 | nth | endonuclease III (B-Eco, 50.7%) |
| RP067 | parC | DNA topoisomerase IV subunit A (B-Hin, 39.0%) |
| RP711 | pin* | invertase/recombinase (B-Eco, 38.0%) |
| BP540 | poiA | primosomal protein replication factor (B-Bru 39.7%) |
| RP546 | radA | DNA repair (B- <i>Bsu</i> , 46.5%) |
| RP761 | recA | recombination protein RecA (B-Pde, 71.2%) |
| HP029 | recr | 30.4%) |
| RP593 | recG | ATP-dependent DNA helicase (B-Eco, 34.1%) |
| RP528 | recJ | single-stranded DNA-specific exonuclease (B-Eco, |
| RP182 | recN | recombination protein RecN (B-Hin, 31.6%) |
| RP438 | recR | recombination protein RecR (B-Bsu, 36.9%) |
| RP385 | ruvA | Holliday junction DNA helicase (B-Pae, 35.0%) |
| BP119 | ruvC | Holliday junction ondedeepwritepueleese (P.E.e. |
| | | Tolliday unclion endodeoxynbonuclease (D-Lco, |
| DDooe | cch | 36.1%) |
| RP836 RP326 | ssb topA | 36.1%) single-stranded binding protein (B- <i>Bab</i> , 52.6%) DNA topoisomerase I (B- <i>Bsu</i> , 44.9%) |
| RP836 RP326 RP835 | ssb topA uvrA | Sol. 1%) single-stranded binding protein (B- <i>Bab</i> , 52.6%) DNA topoisomerase I (B- <i>Bsu</i> , 44.9%) repair excision nuclease subunit A (B- <i>Eco</i> , 57.7%) |
| RP836 RP326 RP835 RP203 | ssb topA uvrA uvrB | Financial junction encode xymosi nuclease (LP-Eco, 36.1%) single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase I (B-Bsu, 44.9%) repair excision nuclease subunit B (B-Hin, 56.0%) repair excision nuclease subunit B (B-Hin, 56.0%) repair excision nuclease subunit B (B-Hin, 56.0%) |
| RP836 RP326 RP835 RP203 RP572 RP572 RP447 | ssb topA uvrA uvrB uvrC uvrD | Findagy junction endodexymon nuclease (D*Lc), 36.1%) single-stranded binding protein (B-Bab, 52.6%) DNA topoisomerase (I <i>B</i> -Bay, 44.9%) repair excision nuclease subunit A (B- <i>L</i> co, 57.7%) repair excision nuclease subunit C (B- <i>P</i> fl, 56.9%) DNA belionese (R-Say, 42.5%). |
| RP836 RP326 RP835 RP203 RP572 RP447 RP817 | ssb topA uvrA uvrB uvrC uvrD xerC | Financey junction endoced synchronized (D=2c), 36.1%) single-stranded binding protein (B-Bab, 52.6%) DNA topoisomerase (I (B-8u, 44.9%) repair excision nuclease subunit A (B-Fin, 56.0%) repair excision nuclease subunit A (B-Fin, 56.0%) repair excision nuclease subunit C (B-Fin, 36.9%) DNA helicase (B-8au, 43.5%) integrase/recombinase (B-8au, 43.5%) |
| RP836 RP326 RP835 RP203 RP572 RP447 RP447 RP817 RP361 | ssb topA uvrA uvrB uvrC uvrD xerC xerD | Nonces Januard en does yn ochoesta (D-Loc, 36, %) single-stade binding profein (B-Bab, 52,6%) DNA topolsomerase (B-Bsu, 44,9%) repair excision nuclease subunit C (B- <i>Hn</i> , 56,0%) repair excision nuclease subunit C (B- <i>Hn</i> , 56,0%) DNA helicase (B-Sau, 43,5%) DNA helicase (B-Sau, 43,5%) DNA helicase (B-Sau, 43,5%) integrase/recombinase (B- <i>Esc</i> , 37,6%) |
| RP836 RP326 RP835 RP203 RP572 RP447 RP817 RP817 RP361 TRANS | ssb topA uvrA uvrB uvrC uvrD xerC xerD | Namosy Januard en does yn ochoesta (D-Loc, 36,1%) single-stranded binding profein (B-Bab, 52,6%) DNA topolsomerase ((B-Bau, 44,9%) repair excision nuclease subunit A (B-Eoo, 57,7%) repair excision nuclease subunit C (B-P/f, 56,0%) DNA helicase (B-Bau, 43,2%) integrase/recombinase (B-Bau, 32,2%) integrase/recombinase (B-Bau, 32,7%) ON |
| RP836 RP326 RP835 RP203 RP572 RP447 RP817 RP361 TRANS Degrad | ssb topA uvrA uvrB uvrC uvrD xerC xerD CRIPTI ation of | S6.1%) S6.1%) S6.1%) S6.1%) S6.1%) S6.1%) S6.1%) S6.1%) S6.1%) S6.1% S6.1%) S6.1% S |
| RP836 RP326 RP835 RP203 RP572 RP477 RP817 RP361 TRANS Degrad. RP504 | ssb topA uvrA uvrB uvrC uvrD xerC xerD cCRIPTI ation of pnp | Nontoxy (Initial encoded synchrotic locates) (D=Lc), 36.1%) \$86.1%) \$86.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase 1 (B-Bau, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pil, 50.9%) DNA helicase (B-Sau, 43.5%) integrase/recombinase (B-Sau, 32.2%) integrase/recombinase (B-Eco, 37.6%) ON 20 RNA polytioonucleotide nucleotidyltransferase (B-Eco, polytion |
| RP836 RP326 RP835 RP203 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 | ssb topA uvrA uvrB uvrC uvrD XerC XerD CCRIPTI ation of pnp | Nontasy junction encodes/ynconcleases (D=Ecc, 36.1%) Sin Téch Sin Téch Sin Téch DNA topoisomerase (I=Bsu, 44.9%) DNA topoisom nuclease subunit A (B=Ecc, 57.7%) repair excision nuclease subunit A (B=Ecc, 57.7%) repair excision nuclease subunit C (B=PH, 56.0%) DNA helicase (B=Sau, 43.5%) Integraser/ecombinase (B=Bsu, 32.2%) Integraser/ecombinase (B=Ecc, 37.6%) ON 20 RNA polyribonucleotide nucleotidyltransferase (B=Eco, 48.9%) Thomagene III (B=Eru, 40.2%) |
| RP836 RP326 RP326 RP203 RP572 RP447 RP361 TRANS <i>Degrad.</i> RP504 RP117 RP462 | ssb topA uvrA uvrB uvrC xerC xerD ccRIPTI ation of pnp rnc rnd | Tionicasy (Initial encodes/ynocinclease (D=Lc), 36.1%) Single-stranded binding profein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%) repair excision nuclease subunit A (B-Eoo, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helicase (B-Bau, 43.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) NN |
| RP836 RP326 RP835 RP203 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP256 | ssb topA uvrA uvrB uvrC uvrD xerC xerD cCRIPTI ation of pnp rnc rnd rne | Noncost plantal of encoded synchronic deals (D=Ecc, 36.1%) S6.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-P/II, 56.0%) DNA helicase (B-Sau, 43.5%) integrase/recombinase (B-Sau, 32.2%) integrase/recombinase (B-Ecc, 37.6%) ON 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 48.9%) Tibonuclease III (B-Hpy, 40.2%) ribonuclease (B-Eco, 28.5%) ribonuclease (B-Eco, 28.5%) |
| RP836 RP326 RP835 RP203 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP256 RP726 RP726 RP726 | ssb topA uvrA uvrB uvrC uvrD xerC xerD cCRIPTI ation of pnp rnc rnd rne rnh | Financey Junction encodes/ynconcloseds (D=Ecc, 36.1%) S6.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topoisomerase 1 (B-Bau, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit A (B-Fin, 56.0%) DNA helicitiese (B-Sau, 43.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Eco, 37.6%) ON ON Dividuelentiation (B-Hight) Philipsingle Integrase/recombinase (B-Eco, 37.6%) ON 20 RNA polytibonucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-Higy, 40.2%) ribonuclease III (B-Higy, 40.2%) ribonuclease III (B-Hight, 47.9%) ribonuclease III (B-Hight, 47.9%) |
| RP836 RP326 RP203 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP504 RP504 RP504 RP514 RP107 RP462 RP526 RP726 RP726 RP726 RP726 RP7202 RP611 | ssb topA uvrA uvrB uvrC uvrD xerC xerD cCRIPTI ation of pnp rnc rnd rne rnhA rnhA rnhA | Tionicasy (Initial encodes/ynocinclease (D=Lc), 36.1%) Single-stranded binding profein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helicase (B-Bau, 32.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Eco, 37.6%) DN 20 RNA polyitionucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-Hpy, 40.2%) ribonuclease III (B-Hpy, 40.2%) ribonuclease III (B-Eco, 34.7%) ribonuclease III (B-Eco, 34.7%) ribonuclease III (B-Eco, 44.7%) ribonuclease P (B-Mca, 28.4%) |
| RP836 RP326 RP835 RP203 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP504 RP504 RP117 RP462 RP266 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP726 RP727 RP7777 RP7777 RP7777 RP7777 RP7777 RP7777 RP7777 RP77777 RP77777 RP7777 RP77777777 | ssb topA uvrA uvrB uvrC uvrD xerC xerD cCRIPTI fation of pnp rnc rnd rne rnhA rnhA rnhA rnpA rph | Noncode y lanctick encoded synchronic locates (D=Ecc, 36.1%) S6.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit (B (E-Inf, 56.0%)) DNA helicities (B-Sau, 43.5%) repair excision nuclease subunit (B (E-Inf, 56.0%)) DNA helicities (B-Sau, 43.5%) integrase/recombinase (B-Sau, 32.2%) integrase/recombinase (B-Ecc, 37.6%) ON All Methods Polyribonucleotide nucleotidyltransferase (B-Ecc, 48.9%) ribonuclease E (B (B-Eco, 28.5%)) ribonuclease E (B (B-Eco, 28.4%)) ribonuclease E (B (B-Eco, 28.4%)) ribonuclease P (B-Mar, 42.4%) ribonuclease P (B-Har, 75.05%) |
| RP836 RP326 RP326 RP447 RP572 RP447 RP817 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP256 RP202 RP611 RP628 <i>ENA</i> str | ssb topA uvrA uvrB uvrD xerC xerD cCRIPTI ation of pnp rnc rnd rnhA rnhA rnhA rnhA rnhA rnhA | Finitesy (Initial encoded synchrotinuesias (D=Lc), 36.1%) Sin Tégi Single-stranded binding protein (B-Bab, 52.6%) DNA topolosmon nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pil, 36.9%) DNA helicase (B-Sau, 43.5%) integrase/recombinase (B-Sau, 32.2%) integrase/recombinase (B-Sau, 32.2%) ON 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 43.9%) DN-locase III (B-Hpy, 40.2%) ribonuclease II (B-Hpy, 40.2%) ribonuclease III (B-Kpy, 44.7%) ribonuclease P (B-Mca, 28.4%) ribonuclease P (B-Hax, 32.4%) ribonuclease P (B-Hax, 50.5%) and modification |
| RP836 RP326 RP326 RP47 RP47 RP47 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP504 RP117 RP462 RP266 RP726 RP726 RP202 RP611 RP628 <i>RNA sy</i> RP861 | ssb topA uvrA uvrB uvrD xerC xerD ccRIPTI ation of pnp rnc rnd rne rnhA rnhB rnpA rph rnthesis greA | Tionicasy (Initial encodes/ynocinclease (D=Lc), 36.1%) Single-stranded binding profein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helicase (B-Bau, 32.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Eco, 37.6%) DN 20 RNA polyitionucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-Hpy, 40.2%) ribonuclease III (B-Hpy, 40.2%) ribonuclease III (B-Eco, 44.7%) ribonuclease PH (B-Eco, 35.6%) ribonuclease PH (B-Eco, 43.7%) ribonuclease PH (B-Km, 43.4%) ribonuclease PH (B-Hm, 55.05%) and modification transcription elongation factor GreA (B-Hin, 61.4%) |
| RP836 RP326 RP326 RP47 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP507 RP | ssb topA uvrA uvrB uvrD xerC xerD ccRIPTI ation of pnp rnc rnd rnhA rnhB rnhA rnhB rnpA rph rnthesis greA nusA | Rinkay Bit |
| RP836 RP326 RP326 RP47 RP817 RP817 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP266 RP726 RP202 RP611 RP628 <i>RNA sy</i> RP861 RP553 RP463 RP463 RP463 | ssb topA uvrA uvrB xerD ccRIPTI ation of pnp rnc rnhB rnhB rnhB rnhA rnhB rnhA rnhB rnpA rnhB | Finited Processing (Initial Process |
| RP836 RP326 RP326 RP407 RP407 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP256 RP202 RP611 RP628 <i>RNA sy</i> RP861 RP553 RP162 | ssb topA uvrA uvrB uvrC uvrD xerC xerC roccePTI ation of pnp rnc rnh rnh rnh rnh rnh rnh rnh rnh rnh rnh | Tionicasy (Initial encodes/ynocinclease (D=Lc), 36.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolsomerase ((B-Bau, 44.9%)) repair excision nuclease subunit C (B-Pin, 56.0%) repair excision nuclease subunit C (B-Pin, 56.0%) DNA helicase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase (B (B-Co, 35.9%) P) |
| RP836 RP326 RP326 RP203 RP572 RP447 RP361 TRANS <i>Degrad</i> RP504 RP117 RP462 RP504 RP117 RP462 RP266 RP726 RP202 RP611 RP628 <i>RNA sy</i> RP8611 RP553 RP162 RP162 RP135 | ssb topA uvrA uvrB uvrD uvrD uvrD cRIPTI ation of rnc rnd rne rnhA rnhB rnpA rnba greA nusA nusB nusG | RANA S0.1%) S0.1%) S0.1%) S0.1%) S0.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) IPpair excision nuclease subunit (B (B-Inf, 50.0%)) repair excision nuclease subunit (B (B-Inf, 50.0%)) IPDA hericase (B-Bau, 43.5%) repair excision nuclease subunit (B (B-Inf, 50.0%)) Integrase/recombinase (B-Bau, 34.5%) repair excision nuclease subunit C (B-Inf, 36.9%) ON 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-Hp, 40.2%) ribonuclease (B-Eco, 35.9%) ribonuclease PI (B-Eco, 34.5%) ribonuclease PI (B-Eco, 43.4%) ribonuclease PI (B-Eco, 44.7%) ribonuclease PI (B-Ar, 43.4%) ribonuclease PI (B-Hin, 55.05%) and modification and modification termination factor GreA (B-Hin, 61.4%) transcription elongation factor NusA (B-Eco, 32.9%) ribonuclease PH transcription termination factor NusA (B-Eco, 32.9%) |
| RP836 RP836 RP326 RP326 RP326 RP522 RP447 RP572 RP462 RP361 RP564 RP256 RP726 RP462 RP462 RP462 RP462 RP462 RP462 RP462 RP462 RP462 RP462 RP462 RP463 RP464 RP553 RP464 RP553 RP465 | ssb topA uvrA uvrB uvrD uvrD uvrD vrC uvrD cRIPTI ation of rnd rnha rnha rnhB rnpA rnhB rnpA nusB nusB nusG | Financey (Initial encoded synchrotinuoeds) (D-Ecc, 36.1%) Sin (%) Sin (%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit (B (-Hin, 56.0%)) DNA heliciase (B-Sau, 43.5%) repair excision nuclease subunit (B (-Hin, 56.0%)) DNA heliciase (B-Sau, 43.5%) integrase/recombinase (B-Sau, 32.2%) integrase/recombinase (B-Ecc, 37.6%) ON CN polyribonucleotide nucleotidyltransferase (B-Ecc, 48.9%) Tibonuclease III (B-Hpy, 40.2%) ribonuclease [B (Ecc, 35.9%) ribonuclease [B (Ecc, 35.9%) ribonuclease [B (Ecc, 35.9%) ribonuclease [B (B-Ecc, 35.9%) |
| RP836 RP836 RP836 RP836 RP536 RP536 RP536 RP447 RP447 RP447 RP442 RP442 RP548 RP442 RP548 RP442 RP442 RP442 RP442 RP442 RP442 RP442 RP443 RP442 RP443 RP444 RP553 RP162 RP155 RP162 RP155 RP162 RP155 RP156 RP155 RP156 RP155 RP156 RP156 RP156 RP156 RP156 RP156 RP157 | ssb topA uvrA uvrB uvrC uvrD xerC xerD cCRIPTI ation of pnp rnc rnh rnh rnh rnh greA nusA nusB nusA | Tionicasy (Initial encodes/ynocinclease (D=Ecc, 36.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Eca, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helicase (B-Sau, 43.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Eca, 37.6%) ON 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 48.9%) Tioonuclease III (B-Hipy, 40.2%) ribonuclease II (B-Eco, 35.6%) ribonuclease II (B-Eco, 34.7%) ribonuclease II (B-Eco, 34.7%) ribonuclease II (B-Kipy, 40.2%) ribonuc |
| RP836 RP326 RP326 RP326 RP523 RP523 RP523 RP447 RP447 RP447 RP447 RP447 RP447 RP447 RP447 RP447 RP543 RP543 RP553 RP162 RP458 RP458 RP458 RP458 RP553 | ssb topA uvrA uvrB uvrC xerC cxerD rnc rnd rne rnpA rnbA greA nusB nusB nusB nusB nusB nusB | RNA S0.7%) S0.7%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-P/II, 56.0%) DNA hericase (B-Bau, 43.5%) repair excision nuclease subunit C (B-P/II, 56.0%) DNA hericase (B-Bau, 43.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Eco, 37.6%) ON 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-H/IP, 40.2%) ribonuclease D (B-Eco, 28.5%) ribonuclease PI (B-Eco, 34.5%) ribonuclease PI (B-Eco, 44.7%) ribonuclease PI (B-H/II, 55.05%) and modification transcription elongation factor GreA (B-H/II, 61.4%) transcription termination factor NusA (B-Eco, 38.9%) ribonuclease PI (B-Mar, 85.05%) and modification transcription termination factor NusA (B-Eco, 38.9%) ribonuclease (B-Eco, 42.2%) ribonuclease (B-Eco, 42.2%) ribonuclease (B-Eco, 42.2%) ribonuclease (B-Eco, 42.2%) poly (A) polymerase 1 (B-Esu, 26.3% |
| RP836 RP836 RP836 RP836 RP532 RP532 RP532 RP447 RP447 RP447 RP447 RP447 RP447 RP447 RP447 RP447 RP461 RP563 RP461 RP563 RP462 RP462 RP464 | ssb topA uvrA uvrB uvrC uvrD xerC rent rnp rnc rnh rnpA rnbasis greA nusA nusB nusB nusB | Noncode Synchronitolesky (D-Loc), 36.1%) Sin (%) DNA topolocomerase ((%) DNA topolocomerase (%) DNA topolocomerase (%) DNA topolocomerase (%) DNA helicase subunit (%) Tepair excision nuclease subunit (%) DNA helicase (%) Single (%) DNA helicase (%) Polyribonucleotide nucleotidyltransferase (%) ribonuclease (%) |
| RP836 RP326 RP326 RP326 RP523 RP572 RP47 RP47 RP47 RP47 RP47 RP47 RP47 RP47 | ssb topA uvrA uvrB uvrC cRIPTI ation of pnp rnc rnhA rph mthesis greA nusB pcnB rhiE rho rpoA pcnB rhiE rho rpoA | Tionicasy (Initial encodes/ynocinclease (D=Ecc, 36.1%) Single-stranded binding profein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helicase (B-Bau, 43.5%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Bau, 32.2%) integrase/recombinase (B-Eco, 37.6%) DN 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-H/p, 40.2%) ribonuclease III (B-H/p, 40.2%) ribonuclease FI (B-Eco, 35.6%) ribonuclease FI (B-Eco, 35.6%) ribonuclease PH (B-H/m, 43.4%) ribonuclease PH (B-H/m, 55.05%) and modification transcription termination factor GreA (B-H/m, 61.4%) transcription termination factor NusB (B-Eco, 42.2%) poly (A) polymerase (I-B-Bau, 26.3%) ribonuclease (B-Eco, 42.2%) Na polymerase apha subunit (B-Ero, 42.2%) RNA polymerase apha subunit (B-Ero, 42.2%) RNA polymerase apha subunit (B-F/m, 87.4%) ribonuclease PH (B-K/m, 81.4%) transcription termination factor ReA (B-H/m, 61.4%) transcription termination factor NusB (B-Eco, 42.2%) RNA polymerase apha subunit (B-F/m, 87.4%) RNA polymerase phas subunit (B-F/m, 87.4%) RNA polymerase |
| RP836 RP236 RP236 RP237 RP237 RP247 RP37 RP37 RP37 RP37 RP37 RP37 RP37 RP3 | ssb topA uvrA uvrB uvrC xerC cRIPTI ation of pnp rnc rnhA rnhB musA nusB nusA pcnB pcnB pcnB pcnB pcnB pcnC pcP rhIE rho rpoA | Tionicasy (Initial encodes/ynconclease (D=Ecc, 36.1%) Single-stranded binding profein (B-Bab, 52.6%) DNA topolsomerase ((B-Su, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-F/fi, 56.0%) DNA helicase (B-Su, 43.5%) integrase/recombinase (B-Su, 32.2%) integrase/recombinase (B-Su, 32.2%) integrase/recombinase (B-Eco, 37.6%) DN 20 RNA polyribonucleotide nucleotidyltransferase (B-Eco, 48.9%) ribonuclease III (B-H/gy, 40.2%) ribonuclease (B-Eco, 38.5%) ribonuclease (B-Eco, 38.5%) ribonuclease (B-Eco, 34.5%) ribonuclease (B-Eco, 34.5%) ribonuclease (B-Eco, 34.5%) ribonuclease PH (B-H/gy, 40.2%) ribonuclease PH (B-K/gy, 40.2%) ribonuclease (B-Eco, 34.5%) ribonuclease PH (B-K/gy, 40.2%) ribonuclease (B-Eco, 34.5%) ribonuclease (B-Eco, 34.5%) ribonuclease (B-Eco, 44.7%) ribonuclease (B-Eco, 44.7%) ribonuclease PH (B-K/gy, 40.2%) ribonuclease PH (B-K/gy, 40.2%) ribonuclease (B-Eco, 34.5%) ribonuclease (B-Eco, 34.5%) ribonuclease (B-Eco, 44.7%) ribonuclease (B-Eco, 45.5%) and modification termination factor NusA (B-Eco, 32.9%) ATP-dependent RNA helicase (B-Eco, 38.3%) RNA polymerase beta subunit (B-Rg, 74.2%) RNA polymerase segima 32 tator (B-K/gy, 26.0%) |
| RP836 RP236 RP236 RP237 RP835 RP247 RP817 RP877 RP817 RP877 RP877 RP877 RP877 RP452 RP145 RP452 RP452 RP452 RP452 RP451 RP553 RP615 RP556 RP553 RP556 RP140 RP145 RP553 RP140 RP553 RP140 RP553 RP140 RP553 RP140 RP553 RP140 RP553 RP140 RP553 RP554 RP554 RP555 | ssb topA uvrA uvrB uvrC xerC cRIPTI ation of rnc rnh rnh rnh rnh rnh rnh rnh rnh rnh rnh | Names Januard encodes ynocholedas (D-Eco, 38.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolsomerase (<i>IB-Su</i>, 44.9%) repair excision nuclease subunit A (<i>B-Eco</i>, 57.7%) repair excision nuclease subunit A (<i>B-Eco</i>, 57.7%) repair excision nuclease subunit A (<i>B-Hin</i>, 56.0%) DNA hericase (<i>B-Su</i>, 43.5%) integrase/recombinase (<i>B-Su</i>, 32.2%) integrase/recombinase (<i>B-Su</i>, 32.2%) integrase/recombinase (<i>B-Eco</i>, 37.6%) ON |
| RP836 RP236 RP235 RP355 RP447 RP817 RP817 RP817 RP817 RP504 RP504 RP504 RP504 RP504 RP452 | ssb topA uvrB uvrC uvrC uvrC uvrC vrC creation of pnp rnc rnd rnha rnhB rnb rnpA rnh mthasis greA nusB nusB nusB nusB nusB rhE rpoH rpoD | Handsy Januard Products yn conducts (D-Lcc, 38.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase (<i>B-Su</i>, 44.9%) repair excision nuclease subunit A (<i>B-Eco</i>, 57.7%) repair excision nuclease subunit A (<i>B-Eco</i>, 57.7%) repair excision nuclease subunit C (<i>B-Pil</i>, 36.9%) DNA helicase (<i>B-Su</i>, 43.5%) integrase/recombinase (<i>B-Su</i>, 32.2%) integrase/recombinase (<i>B-Su</i>, 32.2%) integrase/recombinase (<i>B-Eco</i>, 37.6%) ON |
| RP836 RP236 RP235 RP247 RP572 RP477 RP361 TRANS Degrada RP504 RP504 RP504 RP504 RP504 RP504 RP504 RP266 RP266 RP266 RP401 RP553 RP162 RP162 RP162 RP162 RP162 RP163 RP163 RP164 RP569 RP56 | ssb topA uvrB uvrC uvrB xerC cRIPTI ation of pnp rnc rnd rnhA rnhB rnpA nusB nusA nusB nusA pcnB rhC rpoH rpoB rpoF rpoF rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc rpoH roc roc rpoH roc roc roc roc roc roc roc roc roc roc | Noncode Synchrodiced (D=Ecc), 38.1%) Sin (%) |
| RP836 RP236 RP235 RP247 RP572 RP447 RP572 RP447 RP572 RP447 RP572 RP447 RP504 RP504 RP462 RP462 RP462 RP462 RP462 RP462 RP462 RP463 RP463 RP464 RP465 RP464 RP465 RP464 RP465 | ssb topA uvrB uvrB vrC uvrD vrC uvrD ccRIPTI ation of pnp rnc rnh rnh rnh rnh rnh rnh rnh rnh rnh rnh | Financey Junction encodes/ynconclease (D=Ecc, 36.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) integrase/recombinase (B-Bau, 32.5%) Integrase/recombinase (B-Bau, 32.5%) ON 20 <i>RNA</i> polytionucleotide nucleotidyltransferase (B-Eco, 48.9%) Tribonuclease III (B-H/py, 40.2%) ribonuclease III (B-H/py, 40.2%) ribonuclease (B-Eco, 35.8%) ribonuclease D (B-Eco, 28.5%) ribonuclease PH (B-Km, 43.4%) ribonuclease PH (B-Km, 43.4%) ribonuclease PH (B-H/m, 55.05%) and modification transcription termination factor GreA (B-H/m, 61.4%) transcription etrimination factor NusB (B-Eco, 42.2%) poly (A) polymerase (B-Bca, 28.3%) Transcription antitermination protein NusG (B-Eco, 42.2%) Polymerase alpha subunit (B-B-ph, 87.4%) RNA polymerase alpha subunit (B-FAR, 72.5%) RNA polymerase bal subunit (B-FAR, 72.5%) RNA polymerase bal subunit (B-FAR, 50.5%) A synthetases aaryu-FINA symthetase (B-Bba, 52.7%) |
| RP836 RP236 RP236 RP237 RP835 RP247 RP817 RP817 RP817 RP31 TRANS <i>Degrad</i> RP524 RP264 RP264 RP264 RP264 RP265 RP462 RP462 RP462 RP462 RP464 RP563 RP462 RP464 RP563 RP464 RP563 RP464 RP564 RP564 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP162 RP565 RP165 RP565 RP165 RP565 RP165 RP565 RP165 RP565 RP165 RP565 RP165 RP565 RP165 RP565 RP165 RP | ssb topA uvrB uvrC uvrC uvrC uvrC cellpTil ation of ppp rnc rnd rnh ation of ppp rnc rnd rnh rnh rnh rnh rnh rnh rnh rnh rnh rnh | Financey Junction encodes/ynconcloseds (D=Ecc, 36.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase (IB-Su, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-P/II, 36.9%) DNA helicase (B-Su, 32.5%) riboruclease (B-Su, 32.5%) riboruclease BII (B-H/py, 40.2%) riboruclease D (B-Eco, 28.5%) riboruclease D (B-Eco, 28.5%) riboruclease D (B-Eco, 28.5%) riboruclease D (B-Eco, 28.5%) riboruclease D (B-Eco, 28.6%) Riva polymerase 1 (B-Bsu, 26.3%) ATP-dependent RNA helicase (B-Eco, 28.3%) RNA polymerase beta subunit (B-B, 47.2%) RNA polymerase beta subunit (B-B, 47.2%) RNA polymerase beta subunit (B-B, 47.2%) RNA polymerase sigma-70 factor (B-Rae, 50.5%) A anyt-IRNA synthetase (B-Bca, 52.7%) argint/I-BNA synthetase (B-Eco, 30.6%) argint/I-BNA synthetase (B-Eco, 30.6%) |
| RP836 RP236 RP235 RP247 RP447 RP572 RP447 RP572 RP447 RP572 RP467 RP572 RP462 RP462 RP462 RP462 RP462 RP462 RP461 RP553 RP461 RP553 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP162 RP155 RP165 | ssb topA uvrB uvrC uvrD ccRIPTI ation of pnp rnd rnha rnha rnha rnha rnha rnha sraf nusA nusA nusA nusA nusA nusA nusA nusA | Tantagy Junction encodesky modification (B-Bab, 52.6%) DNA topolscimerase ((B-Bau, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) Tepair excision nuclease subunit C (B-Pit, 56.0%) Tepair excision nuclease subunit C (B-Pit, 56.0%) Tepair excision nuclease subunit C (B-Pit, 56.0%) Tibona (B-Bab, 52.6%) Tibona (B-Bab, 52.6%) Tibona (B-Bab, 50.2%) Tibona (B-Bab, 74.2%) Tibona (B-Bab, 74.2%) |
| RP836 RP236 RP235 RP247 RP847 RP572 RP447 RP572 RP447 RP572 RP572 RP572 RP572 RP572 RP452 | ssb topA uvrB uvrB vrC uvrD vrC vrC vrD rnc rnd rnh rnh rnh rnh rnh rnh rnh rnh rnh rnh | Tionizey (Initial encodes/ynocinclease (D=Lot, 36.1%) Single-standed binding profein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helicase (B-Bau, 43.9%) Tionaclease (B-Bau, 35.9%) DNA helicase (B-Bau, 35.9%) DNA helicase (B-Bau, 35.9%) DN |
| RP836 RP236 RP236 RP237 RP835 RP247 RP817 RP817 RP817 RP31 RP31 RP31 RP31 RP422 RP236 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP422 RP43 | ssb topA uvrB uvrC uvrC uvrC uvrC cellpTil ation of ppp rnc rnd rnh rnh rnh rnh rnh rnh rnh rnh rnh rnh | Hondess (Januard en doubles yn bondess (D=Lot, 36,1%) Single-stranded binding protein (B-Bab, 52,6%) DNA topolosomerase ((B-Su, 44,9%)) repair excision nuclease subunit (B-Eco, 57,7%) repair excision nuclease subunit (B-Eco, 57,7%) repair excision nuclease subunit (B-F/H, 76,0%) ToNA hericase (B-Su, 43,5%) Tintegrase/recombinase (B-Su, 32,2%) integrase/recombinase (B-Su, 32,2%) integrase/recombinase (B-Eco, 37,6%) ON |
| RP836 RP236 RP235 RP247 RP477 RP361 TRANS Degradd RP572 RP477 RP361 TRANS Degradd RP572 RP462 RP462 RP462 RP462 RP462 RP462 RP463 RP463 RP464 RP553 RP162 RP463 RP464 RP553 RP162 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP563 RP464 RP573 RP573 RP | ssb topA uvrB uvrB vorC vorC vorC vorC pnp rnc rnc rnc rnc rnc rnc rnc rnc rnc rnc | Financey Joint Of encodes/ynconclease (DFLc), 36, %) Single-stranded binding protein (B-Bab, 52.6%) DNA topolscomerase ((B-Ec), 44.9%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helpolscomerase (B-Sau, 44.9%) DNA helpolscomerase (B-Sau, 45.5%) repair excision nuclease subunit C (B-Pit, 56.0%) DNA helpolscomerase (B-Sau, 45.5%) repair excision nuclease subunit C (B-Pit, 56.0%) Integrase/recombinase (B-Eco, 37.6%) ON 20 RNA polytionucleotide nucleotidyltransferase (B-Eco, 44.9%) ribonuclease III (B-H/py, 40.2%) ribonuclease III (B-H/py, 40.2%) ribonuclease III (B-K, 35.0%) ribonuclease III (B-K, 34.7%) ribonuclease III (B-K, 34.7%) ribonuclease P (B-Eco, 34.6%) ribonuclease P (B-Eco, 34.7%) ribonuclease P (B-Kaz, 34.4%) ribonuclease P (B-Kaz, 44.7%) ribonuclease P (B-Kaz, 42.7%) RNA polymerase ablasituati |
| RP836 RP236 RP236 RP237 RP247 RP847 RP572 RP447 RP572 RP447 RP572 RP457 RP457 RP457 RP457 RP452 RP452 RP452 RP452 RP452 RP452 RP452 RP452 RP451 RP553 RP461 RP553 | ssb topA uvrB uvrB vrC uvrD vrC uvrD ccRIPTI ation of pnp rnc rnd rnh rnh grpA nusA nusB nusB nusB nusB nusB nusB nusB nusB | Financey Junction encodes/ynconcloseds (DFLc), 36.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Bau, 44.9%)) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit A (B-Eco, 57.7%) repair excision nuclease subunit C (B-P/II, 56.0%) DNA helicase (B-Sau, 43.5%) integrase/recombinase (B-Bau, 32.5%) integrase/recombinase (B-Bau, 32.5%) ON 20 <i>RNA</i> polytonucleotide nucleotidyltransferase (B-Eco, 48.9%) Tribonuclease III (B-H/py, 40.2%) ribonuclease III (B-H/py, 40.2%) ribonuclease (B-Eco, 35.9%) ribonuclease (B-Eco, 35.9%) ribonuclease D (B-Eco, 28.5%) ribonuclease D (B-Eco, 28.5%) ribonuclease PH (B-H/n, 53.05%) and modification transcription elongation factor GreA (B-H/II, 61.4%) transcription elongation factor SreA (B-Eco, 42.2%) poly (A) polymerase (B-Bau, 28.3%) transcription antifermination protein NusG (B-Eco, 42.2%) provent RNA helpase (B-Eco, 38.9%) transcription antifermination factor GreA (B-H/II, 61.4%) transcription antifermination factor GreA (B-H/II, 61.4%) transcription antifermination factor GreA (B-H/II, 61.4%) transcription antifermination factor GreA (B-Eco, 42.2%) POV (A) polymerase beta subunit (B-Eco, 58.7%) RNA polymerase sigma-70 factor (B-Rca, 50.5%) A synthetase (B-H/II, 43.3%) cysteinyl-fINA synthetase (B-H/II, 40.3%) glutamyl-fINA synthetase (B-Eco, 33.3%) transcription termination (B-Eco, 58.7%) RNA polymerase sigma-70 factor (B-Rca, 50.5%) A synthetase (B-H/II, 43.3%) cysteinyl-fINA synthetase (B-H/II, 40.3%) </td |
| RP836 RP236 RP236 RP237 RP357 RP447 RP817 RP447 RP572 RP447 RP572 RP457 RP457 RP457 RP457 RP457 RP452 | ssb topA uvrB uvrB vrC torR pnp rnc rnd rnbasis greA nusA nusA nusA nusA nusA nusA nusA nus | Hondess (Januard) encloses/procinclease (D=Lot, 36.1%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolosomerase ((B-Su, 44.9%)) repair excision nuclease subunit (B-Eco, 57.7%) repair excision nuclease subunit (B-Fl/n, 56.0%) DNA hericase (B-Su, 43.5%) repair excision nuclease subunit (B-P/I, 78.9%) DNA hericase (B-Su, 43.5%) integrase/recombinase (B-Su, 32.2%) integrase/recombinase (B-Su, 32.2%) integrase/recombinase (B-Eco, 37.6%) ON |
| RP836 RP236 RP235 RP247 RP477 RP361 TRANS Degradd RP572 RP477 RP361 TRANS Degradd RP572 RP462 RP462 RP462 RP462 RP462 RP462 RP463 RP464 RP553 RP553 RP | ssb topA uvrB uvrB vorC uvrD cRIPTI ation of pnp rnd rna rnhB rnb rnhB rnb rnhB rnb rnhB rnb rnb rnb rnb rnb rnb rnb rnb rnb rnb | Financey Jonation encodes/ynocholes/set (DFLoC, 36.7%) Single-stranded binding protein (B-Bab, 52.6%) DNA topolscomerase ((B-Bau, 44.9%)) repair excision nuclease subunit C (B-Fin, 56.0%) Terpair excision nuclease subunit C (B-Fin, 56.0%) Tilonuclease (B-Eco, 37.6%) ON 20 <i>RNA</i> poly(A) (D-K) Poly (A) (D-K) Tibonuclease D (B-Eco, 28.5%) Tibonuclease D (B-Hin, 55.05%) and modification transcription termination factor GreA (B-Hin, 61.4%) transcription termination factor NusB (B-Eco, 39.9%) transcription termination factor NusB (B-Eco, 42.2%) Poly (A) polymerase 1 (B-Esu, 26.3%) ATP-dependent RNA helicase (B-Eco, 38.3%) transcription termination factor Rea (B-Riz, 72.5%) RNA polymerase bela' subunit (B-Rig, 72.7%) RNA polymerase bela' subunit (B-Rig, 72.7%) RNA polymerase bela' subunit (B-Eco, 42.7%) RNA polymeras |

| 10.9421 | ieuo | leucy-u inva synulleuase (D-Lco, 45.576) |
|---------|------|--|
| RP371 | lysS | lysyl-tRNA synthetase (B-Bbu, 26.3%) |
| RP683 | metS | methionyl-tRNA synthetase (B-Bsu, 46.9%) |
| RP417 | pheS | phenylalanyl-tRNA synthetase alpha sub (B-Hin, |
| | | 49.2%) |

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| | | 33.9%) |
|---|--|--|
| RP384 BP783 | proS serS | proline-tRNA synthetase (B-Zmo, 51.8%) servl-tBNA synthetase (B-Chu, 47.2%) |
| RP221 | thrS | threonyl-tRNA synthetase (B-Hin, 50.6%) |
| HP468 RP556 | trpS tvrS | tryptophanyl-tHNA synthetase (B-Syn, 48.5%) tyrosyl-tRNA synthetase (B-Bca, 38.7%) |
| RP687 | valS | valyI-tRNA synthetase (A- <i>Mja</i> , 38.3%) |
| tRNA a | nd amir | no acvl-tRNA modification |
| RP208 | def | methionyl-tRNA deformylase (B-Eco, 49.4%) |
| RP152 | imi gatA | glutamyl-tRNA (GIn) amidotransferase subunit A (B- |
| DDICI | | Mca, 48.6%) |
| HP151 | gaiB | Mca, 46.9%) |
| RP153 | gatC | glutamyl-tRNA (GIn) amidotransferase subunit C (B- |
| RP672 | ksqA | dimethyladenosine transferase (B-Bsu, 35.7%) |
| RP510 | miaA | tRNA delta-2-isopentenylpyrophosphate (IPP) trans |
| RP605 | pth | peptidyl-tRNA hydrolase (B-Hin, 40.5%) |
| RP213 | queA | S-adenosylmethionine:tRNA ribosyltransferase-iso |
| RP721 | tgt | tRNA-guanine transglycosylase (B-Zmo, 61.2%) |
| RP111 | <i>trmD</i> | tRNA (guanine-N1)-methyltransferase (B-Eco, |
| RP857 | truA | pseudouridylate synthase I (B-Eco, 40.1%) |
| RP501 | truB | tRNA pseudouridine 5S synthase (B-Hin, 37.6%) |
| Degrad | ation of | proteins, peptides and glycopeptides |
| RP036 | clpB | ATP-dependent protease, ATP binding subunit (B- |
| RP520 | clpP | ATP-dependent Clp protease (B-Yen, 67%) |
| RP692 | clpX | ATP-dependent protease, ATPase subunit (B-Eco, 62.8%) |
| RP228 | ctp | tail-specific protease precursor (B-Bba, 42.6%) |
| RP037 | gcp httc | sialoglycoprotein endopeptidase (B-Hin, 42.2%) |
| RP122 | hflK | lambda cli stability-governing protein (B-220, 33.9%) |
| BP124 | htrA | 30.3%) serine protease (B-Bhe 37.7%) |
| RP186 | htrA | protease DO (E-Sce, 26.7%) |
| RP450 | lon len A | ATP-dependent protease LA (B-Ccr, 53.1%) |
| RP824 | map | methionyl aminopeptidase (B-Sty, 55.3%) |
| RP219 | mpp | mitochondrial protease (B-Bsu, 35.4%) |
| RP174 | рөрд ррсЕ | peptidase II (B-Rsn, 32.5%) |
| RP281 | ptrB sohB | protease II (B-Eco, 34.2%) |
| RP525 | sppA | protease IV (B-Hin, 27.6%) |
| Protein | modific | ation and translation factors |
| RP238 | efp | elongation factor P (B-Bsu, 39.5%) |
| RP132 | fusA | elongation factor G (B-Atu, 68.7%) |
| RP552 | infB | initiation factor IF-2 (B-Hin, 42.6%) |
| RP531 | infC | initiation factor IF-3 (B-Pvu, 47.7%) |
| RP274 | prfB | peptide chain release factor RF-2 (B-Eco, 50.4%) |
| RP435 | rbfA | ribosome binding factor A (B-Bsu, 31.6%) |
| nP093 | TIIIIJ | 23.2%) |
| | | |
| HP154 | rrt tip A | ribosome recycling factor (B-Hin, 43.3%) |
| RP397 RP661 | rrt tipA tuf | ribosome recycling factor (B- <i>Hin</i> , 43.3%) thiol:disulphide interchange protein (B- <i>Bja</i> , 27.4%) elongation factor Tu (B- <i>Tcu</i> , 81.5%) |
| RP397 RP661 RP087 | rrf tipA tuf tsf | ribosome recycling factor (B- <i>Hin</i> , 43.3%) thiol:disulphide interchange protein (B- <i>Bja</i> , 27.4%) elongation factor Tu (B- <i>Tcu</i> , 81.5%) elongation factor Ts (B- <i>Sci</i> , 40.7%) |
| RP397 RP661 RP087 <i>Ribosor</i> | rrf tlpA tuf tsf nal proi | ribosome recycling factor (B-Hin, 43.3%) thiol:disulphide interchange protein (B-Bja, 27.4%) elongation factor Tu (B-Tzu, 81.5%) elongation factor Ts (B-Sci, 40.7%) teins; synthesis and modification |
| RP154 RP397 RP661 RP087 <i>Ribosor</i> RP137 RP137 | rrf tlpA tuf tsf mal prot rplA rplP | ribosome recycling tactor (B-H/in, 43.3%) thiodisulphile interchange protein (B-BJa, 27.4%) elongation tactor Tu (B-Tou, 81.5%) elongation tactor Ts (B-Sol, 40.7%) elons: synthesis and modification ribosomal protein L1 (B-Ggr, 50.2%) theorem encode to L1 (B-Ggr, 50.2%) |
| RP154 RP397 RP661 RP087 <i>Ribosor</i> RP137 RP656 RP659 | rrf tipA tuf tsf nal prot rpIA rpIB rpIC | ribosoma recycling tactor (B-H/in, 43.3%) thiotidisulphile interchange protein (B-Bja, 27.4%) elongation factor Tu (B-Tcu, 81.5%) elongation factor Ts (B-Sci, 40.7%) fei/ns; synthesis and modification ribosomal protein L1 (B-Cgr, 50.2%) ribosomal protein L2 (E-Ram mt, 61.5%) ribosomal protein L3 (E-Sce, 44.1%) |
| RP154 RP397 RP661 RP087 RP087 RP137 RP656 RP659 RP658 RP658 | rrf tipA tuf tsf rpIA rpIB rpIC rpID rpID | ribosoma recycling tactor (B-Hin, 43.3%) thiodisulphile interchange protein (B-Bja, 27.4%) elongation factor Tu (B-Tou, 81.5%) elongation factor Ts (B-Soi, 40.7%) telors; synthesis and modification ribosomal protein L1 (B-Cgr, 50.2%) ribosomal protein L2 (E-Cgr, 50.2%) ribosomal protein L3 (E-Sce, 44.1%) ribosomal protein L3 (E-Sce, 44.1%) ribosomal protein L3 (E-Sce, 44.1%) ribosomal protein L4 (B-Bst, 39.3%) |
| RP154 RP397 RP661 RP087 RP137 RP656 RP659 RP658 RP658 RP647 RP644 | rrf tlpA tuf tsf rpIA rpIB rpIC rpID rpIE rpIF | ribosoma provint Lebra (B-H/in, 43.3%) thiodistulphile interchange protein (B-Bja, 27.4%) elongation factor Tis (B-Sci, 40.7%) teins; synthesis and modification ribosomal protein L1 (B-Car, 50.2%) ribosomal protein L2 (E-Ram mt, 61.5%) ribosomal protein L3 (E-Sce, 44.1%) ribosomal protein L3 (E-Sce, 43.1%) ribosomal protein L4 (B-Bst, 39.3%) ribosomal protein L5 (B-Aco, 53.6%) ribosomal protein L6 (B-Aco, 53.6%) ribosomal protein L6 (B-Aco, 53.6%) ribosomal protein L6 (B-Aco, 53.6%) |
| RP154 RP397 RP661 RP087 RP137 RP656 RP659 RP658 RP647 RP644 RP644 RP644 RP041 | rrf tipA tuf tsf rpIA rpIB rpID rpIE rpII rpII rpII | ribosoma protein L5 (<i>B-Aco</i> , 53.6%) ribosoma protein (<i>B-Ba</i> , 27.4%) elongation factor Tu (<i>B-Tou</i> , 81.5%) elongation factor Ts (<i>B-Sci</i> , 40.7%) elongation factor Ts (<i>B-Sci</i> , 40.7%) elons, synthesis and modification ribosomal protein L1 (<i>B-Car</i> , 50.2%) ribosomal protein L2 (<i>B-Car</i> , 50.2%) ribosomal protein L3 (<i>B-Sci</i> , 50.3%) ribosomal protein L4 (<i>B-Sci</i> , 50.3%) ribosomal protein L4 (<i>B-Sci</i> , 50.3%) ribosomal protein L5 (<i>B-Aco</i> , 53.6%) ribosomal protein L5 (<i>B-Aco</i> , 53.6%) ribosomal protein L5 (<i>B-Car</i> , 56.7%) |
| HP154 RP397 RP661 RP087 RP087 RP087 RP656 RP659 RP658 RP647 RP644 RP041 RP041 RP138 RP136 | rrf tipA tuf tsf rpIA rpIB rpIC rpID rpIE rpII rpIJ rpIJ rpIK | ribosome recycling tactor (B-H/in, 43.3%) thiodisulphile interchange protein (B-Bja, 27.4%) elongation tactor Tu (B-Tou, 81.5%) elongation tactor Ts (B-Sci, 40.7%) elongation tactor Ts (B-Sci, 40.7%) ribosomal protein L1 (B-Cgr, 50.2%) ribosomal protein L2 (E-Ram mt, 61.5%) ribosomal protein L3 (E-Sci, 44.1%) ribosomal protein L3 (B-Sci, 39.3%) ribosomal protein L5 (B-Bcs, 53.8%) ribosomal protein L5 (B-Bcs, 53.8%) ribosomal protein L5 (B-Bcs, 53.8%) ribosomal protein L5 (B-Bcs, 75.8%) ribosomal protein L5 (B-Bcs, 75.8%) ribosomal protein L5 (B-Bcs, 75.8%) ribosomal protein L5 (B-Bcs, 75.8%) |
| HP154 RP397 RP661 RP087 RP087 RP659 RP659 RP659 RP658 RP644 RP041 RP138 RP644 RP041 RP138 RP136 RP139 RP233 | rrf tipA tuf tsf rpIA rpIB rpIC rpID rpIE rpIF rpII rpIK rpIM | ribosoma proving tactor (B-Hin, 43.3%) thiodisulphile interchange protein (B-Bja, 27.4%) elongation factor Tu (B-Tou, 81.5%) elongation factor Ts (B-Sol, 40.7%) elongation factor Ts (B-Sol, 40.7%) fibosomal protein L1 (B-Ggr, 50.2%) ribosomal protein L2 (E-Ram mt, 61.5%) ribosomal protein L3 (E-Soc, 44.1%) ribosomal protein L3 (E-Soc, 53.6%) ribosomal protein L5 (B-Aco, 54.5%) ribosomal protein L5 (B-Aco, 54.5%) |
| HP154 RP397 RP661 RP087 RP087 RP087 RP656 RP659 RP658 RP659 RP658 RP647 RP644 RP041 RP138 RP136 RP139 RP233 RP233 RP249 | rrf tipA tuf tsf rpIA rpIB rpIC rpID rpIF rpII rpIK rpIL rpIM rpIN | ribosome recycling tactor (B-H/in, 43.3%) thiotidisulphile interchange protein (B-Bja, 27.4%) elongation factor Tu (B-Tcu, 81.5%) elongation factor Ts (B-Scl, 40.7%) fei/sr; synthesis and modification ribosomal protein L1 (B-Cgr, 50.2%) ribosomal protein L2 (E-Ram mt, 61.5%) ribosomal protein L3 (E-Sce, 44.1%) ribosomal protein L3 (B-Bst, 39.3%) ribosomal protein L5 (B-Asc, 53.6%) ribosomal protein L5 (B-Asc, 53.6%) ribosomal protein L5 (B-Asc, 53.6%) ribosomal protein L5 (B-Asc, 53.6%) ribosomal protein L10 (B-Laf, 36.7%) ribosomal protein L10 (B-Laf, 36.7%) ribosomal protein L10 (B-Bab, 66.9%) ribosomal protein L110 (B-Bab, 66.9%) ribosomal protein L13 (B-Sca, 52.8%) ribosomal protein L14 (B-Sca, 56.8%) |
| HP154 RP397 RP661 RP087 RP087 RP637 RP656 RP659 RP659 RP658 RP647 RP644 RP041 RP138 RP139 RP233 RP649 RP640 RP640 RP640 | rrf tipA tuf tsf rpIA rpIB rpIC rpIE rpIF rpII rpIN rpIN rpIN rpIN rpIN | ribosome recycling tactor (B-H/in, 43.3%) thiotidisulphile interchange protein (B-B)a, 27.4%) elongation tactor Tu (B-Tou, 81.5%) elongation tactor Ts (B-Soi, 40.7%) taloss, synthesis and modification ribosomal protein L1 (B-Car, 50.2%) ribosomal protein L2 (E-Ram mt, 61.5%) ribosomal protein L3 (E-Soc, 43.1%) ribosomal protein L3 (E-Soc, 43.1%) ribosomal protein L3 (E-Soc, 43.1%) ribosomal protein L3 (E-Soc, 43.1%) ribosomal protein L3 (E-Soc, 45.3%) ribosomal protein L3 (E-Rac, 45.4%) ribosomal protein L3 (E-Rac, 53.6%) ribosomal protein L3 (E-Rac, 45.4%) ribosomal protein L1 (E-Ram mt, 45.5%) ribosomal protein L1 (E-Ram mt, 45.5%) ribosomal protein L1 (1.2, B-Bab, 68.9%) ribosomal protein L1 (1.3) ribosomal protein L1 (1.4) ribosomal protein L1 (1.5) ribosomal pro |
| HP154 RP397 RP661 RP087 RP137 RP656 RP659 RP658 RP644 RP041 RP041 RP041 RP041 RP041 RP138 RP136 RP139 RP639 RP640 RP652 RP652 RP652 | rrf tipA tuf tsf rpIA rpIB rpIC rpID rpID rpID rpIJ rpIN rpIN rpIN rpIN rpID rpIP rpIQ | ribosome recycling tactor (B-H/in, 43.3%) thiodisulphile interchange protein (B-B)a, 27.4%) elongation tactor Tu (B-Tou, 81.5%) teiongation tactor Ts (B-Sci, 40.7%) teions; synthesis and modification ribosomal protein L2 (E-Am mt, 61.5%) ribosomal protein L2 (E-Am mt, 61.5%) ribosomal protein L3 (B-Aco, 53.6%) ribosomal protein L5 (B-Aco, 53.6%) ribosomal protein L5 (B-Aco, 53.6%) ribosomal protein L5 (B-Aco, 53.6%) ribosomal protein L9 (E-By to, 23.6%) ribosomal protein L9 (E-By to, 23.6%) ribosomal protein L10 (B-Lat, 36.7%) ribosomal protein L10 (B-Lat, 36.7%) ribosomal protein L11 (E-Bab, 66.9%) ribosomal protein L14 (B-Eco, 69.6%) ribosomal protein L16 (B-Aak, 54.3%) ribosomal protein L16 (B-Aak, 54.5%) ribosomal protein L16 (B-Aak, 55.5%) |
| HP154 RP397 RP661 RP087 RP137 RP656 RP659 RP658 RP647 RP644 RP041 RP041 RP041 RP138 RP138 RP139 RP649 RP649 RP642 RP652 RP643 RP643 RP119 | rrf tipA tuf tsf rpIB rpIC rpIB rpIC rpIE rpII rpII rpIK rpIN rpIQ rpIQ rpIQ rpIQ rpIQ rpIQ rpIQ rpIQ | ribosome recycling tactor (B-H/in, 43.3%) thiodisulphile interchange protein (B-B)a, 27.4%) elongation tactor Tu (B-Tou, 81.5%) elongation tactor Ts (B-Sol, 40.7%) elongation tactor Ts (B-Sol, 40.7%) ribosomal protein L3 (E-Soc, 44.1%) ribosomal protein L3 (E-Soc, 44.1%) ribosomal protein L3 (E-Soc, 44.1%) ribosomal protein L5 (B-Boc, 53.6%) ribosomal protein L1 (B-Bah, 60.9%) ribosomal protein L1 (B-Bah, 60.57.5%) ribosomal protein L1 (B-Bah, 60.57.5%) ribosomal protein L1 (B-Bah, 60.57.5%) ribosomal protein L1 (B-Bah, 60.57.5%) |
| HP154 RP397 RP6561 RP087 RP6566 RP659 RP658 RP647 RP658 RP647 RP644 RP041 RP138 RP647 RP648 RP649 RP640 RP642 RP643 RP643 RP112 RP603 | rrf tipA tuf tsf rpiA rpiB rpiD rpiB rpiB rpiB rpiB rpiB rpiN rpiN rpiN rpiN rpiQ rpiR rpiR rpiP rpiR rpiP rpiR rpiD rpiN rpiN rpiN rpiD rpiD rpiD rpiD rpiD rpiD rpiD rpiD | ribosoma protein L1 (B -Ba, 23.3%) tiobosoma protein (B -Ba, 27.4%) elongation factor Tu (B -Tou, 81.5%) elongation factor Ts (B -Sol, 40.7%) elongation factor Ts (B -Sol, 40.7%) fibosomal protein L1 (B -Cgr, 50.2%) ribosomal protein L2 (E -Rar m1, 61.5%) ribosomal protein L3 (E -Soc, 44.1%) ribosomal protein L3 (E -Soc, 44.1%) ribosomal protein L5 (B -Bot, 53.6%) ribosomal protein L6 (B -Bot, 63.6%) ribosomal protein L6 (B -Bot, 63.6%) ribosomal protein L1 (B -Bat, 63.7%) ribosomal protein L1 (B -Bat, 64.9%) ribosomal protein L1 (B -Bat, 66.9%) ribosomal protein L1 (B -Bat, 65.5%) ribosomal protein L1 (B -Bat, 55.9%) ribosomal protein L1 (B -Bat, 55.9%) ribosomal protein L1 (B -Bat, 55.8%) ribosomal protein L1 (B -Bat, 55.8%) ribosomal protein L1 (B -Bat, 55.8%) |
| HP154 RP397 RP6561 RP087 RP6566 RP659 RP658 RP647 RP658 RP647 RP644 RP041 RP138 RP647 RP648 RP643 RP643 RP643 RP112 RP603 RP643 RP112 RP603 RP6751 RP655 | rrf tipA tuf tsf rpiA rpiB rpiC rpiB rpiB rpiB rpiB rpiB rpiB rpiB rpiN rpiN rpiN rpiN rpiN rpiN rpiN rpiN | ribosome recycling tactor (B-H/in, 43.3%) thiotidisulphile interchange protein (B-B)a, 27.4%) elongation tactor Tu (B-Tou, 81.5%) elongation tactor Tu (B-Tou, 81.5%) tibosomal protein L1 (B-Car, 50.2%) ribosomal protein L2 (E-Tam mt, 61.5%) ribosomal protein L2 (E-Tam mt, 61.5%) ribosomal protein L3 (E-Sce, 44.1%) ribosomal protein L3 (E-Sce, 45.4%) ribosomal protein L3 (E-Sce, 45.4%) ribosomal protein L3 (E-Sce, 45.4%) ribosomal protein L3 (E-Sce, 45.4%) ribosomal protein L3 (E-Sce, 56.3%) ribosomal protein L3 (E-Sce, 56.3%) ribosomal protein L3 (E-Sce, 56.3%) ribosomal protein L3 (E-Sce, 56.5%) ribosomal protein L3 (E-Sce, 56.5%) |
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| HP154 RP397 RP697 RP397 RP696 RP087 RP656 RP658 RP644 RP041 RP138 RP138 RP138 RP139 RP649 RP652 RP634 RP614 RP652 RP637 RP649 RP521 RP649 RP652 RP637 RP649 RP521 RP649 RP549 RP540 RP | rtf tipA tuf tuf tuf tuf tal procession phane pha | ribosome recycling tactor (B-Hin, 43.3%) thichdisulphile interchange protein (B-Bja, 27.4%) elongation tactor Ts (B-Sci, 40.7%) teinsgiant factor Ts (B-Sci, 40.7%) teinsgiant factor Ts (B-Sci, 40.7%) tibosomal protein L2 (E-Ram mt, 61.5%) tibosomal protein L2 (E-Ram mt, 61.5%) tibosomal protein L3 (E-Ram ts, 45.4%) tibosomal protein L3 (E-Ram ts, 45.4%) tibosomal protein L4 (B-Bst, 45.4%) tibosomal protein L6 (B-st, 45.4%) tibosomal protein L6 (B-st, 45.4%) tibosomal protein L7 (E-Ram mt, 45.5%) tibosomal protein L1 (E-Ram ts, 45.5%) tibosomal protein L1 (B-Bst, 46.5%) tibosomal protein L1 (B-Bst, 46.5%) tibosomal protein L1 (B-Bst, 46.5%) tibosomal protein L1 (B-Bst, 46.5%) tibosomal protein L1 (B-Cst, 55.8%) tibosomal protein L1 (B-Cst, 55.9%) tibosomal protein L1 (B-Cst, 55.9%) tibosomal protein L2 (B-Kst, 55.9%) tibosomal protein L3 (B-Kst, 55.9%) tibosomal protein S (B-Kst, 48.8%) tibosomal protein S (B-Kst, 48.8%) tibosomal protein S (B-Kst, 48.8%) tibosomal protein S (B- |

RP060 *abcT*1 ABC transporter, ATP-binding protein (B-*Hin*, 55.7%) RP508 *abcT*2 ABC transporter, ATP-binding protein (B-*Rme*,

| RP214 | abcT3 | 48.8%) ABC transporter, ATP-binding protein (B-Hin, |
|----------------------------------|------------------------|--|
| RP387 | msbA1 | ABC transporter, ATP-binding protein (B-Eco, |
| RP696 | msbA2 | 26.2%) ABC transporter, ATP-binding protein (B- <i>Eco</i> , 28.2%) |
| <i>Amino a</i> RP307 RP129 | acids atrc1 glnP | cationic amino acid transporter (E-Mmu, 29.7%) glutamine transport system permease (B-Bsu, |
| RP700 | gInQ1 | 48.6%) glutamine ABC transporter, ATP-binding protein (B- |
| RP868 | alnQ2 | Eco, 39.1%) alutamine ABC transporter, ATP-binding protein (B- |
| BP176 | altP | Bst, 51.0%) |
| RP483 RP369 | potE potG | putrescine-ornithine transporter (B- <i>Hin</i> , 26.9%) putrescine-ornithine transporter (B- <i>Hin</i> , 26.9%) putrescine ABC transporter, ATP-binding protein (B- <i>Mpn</i> , 29.2%) |
| RP313 | proP1 proP2 | proline/betain transporter (B-Eco, 26.7%) proline/betain transporter (B-Eco, 24.9%) |
| RP375 BP685 | proP3 proP4 | proline/betain transporter (B-Eco, 21.2%) |
| RP755 | proP5 | proline/betain transporter (B-Eco, 27.8%) |
| RP881 | proP7 | proline/betain transporter (B-Eco, 34.8%) |
| HP150 | yqiX | amino acid ABC transporter (B-Bsu, 32.4%) |
| Nucleos RP097 RP053 | ides an mki tic1 | <pre>id nucleotides ribonucleotide ABC transporter, ATP-binding protein (B-Mie, 36.2%) ATP(ADE translocase (B-Ctr. 43.3%)</pre> |
| RP377 | tic2 | ATP/ADP translocase (B-Ctr, 35.2%) |
| RP500 | tic3 | ATP/ADP translocase (B-Ctr, 39.6%) ATP/ADP translocase (B-Ctr, 36.3%) |
| RP739 | tlc5 | ATP/ADP translocase (B-Ctr, 34.7%) |
| Carbohy RP054 | /drates, glpT | organic alcohols and acids glycerol-3-phosphate permease (B-Bsu, 37.1%) |
| RP834 | afuC | iron ABC transporter, ATP-binding protein (B-Eco, |
| RP810 | kefB | 33.9%) glutathionine-regulated potassium-efflux system pro |
| BP583 | matE | tein (B-Eco, 33.9%) magnesium transporter (B-Sun, 27.0%) |
| Other | | |
| RP205 | atm1 | mitochondrial ABC transporter, ATP-binding protein |
| RP794 | ccmA | (E-Sce, 43.3%) haem ABC transporter A, ATP-binding protein (B- |
| RP268 | ccmB | Hin, 35.5%) haem exporter protein B (E-Ram mt. 20.9%) |
| RP830 | ccmC | haem exporter protein C (B-Bja, 43.7%) |
| RP630 | perM | permease PerM homologue (B-Hin, 25.0%) |
| RP374 RP576 | sec7 prsA | transport protein Sec7 (B-Hsa, 29.6%) protein export (B-Bsu, 28.9%) |
| OTHER | CATEO | OBIES 52 |
| Adapted | ione te | |
| RP708 | himA | integration host factor α (B- <i>Eco</i> , 29.5%) |
| RP236 RP590 | invA mviN | invasion protein A (B- <i>Bba</i> , 42.8%) virulence factor Mvin protein (B-Sty, 32.4%) |
| RP717 BP286 | taxB* trhG | conjugative DNA processing (B-Eco, 33.5%) |
| RP103 | virB4 | virulence protein VIRB4 (B-Atu, 30.9%) |
| RP287 | virB8 | virulence protein VIRB8 (B-Atu, 20.3%) |
| RP290 RP291 | virB9 virB10 | virulence protein VIRB9 (B-Atu, 24.8%) virulence protein VIRB10 (B-Atu, 20.3%) |
| RP292 RP293 | virB11 virD4 | virulence protein VIRB11 (B-Atu, 29.6%) virulence protein VIBD4 (B-Atu, 31.3%) |
| Drug or | d anala | |
| RP170 | acrD | acriflavin resistance protein D (B-Eco, 31.3%) |
| RP668 | ampG1 | AMPG protein (B- <i>Eco</i> , 31.4%) 2AMPG prt (B- <i>Eco</i> , 26.3%) |
| RP781 RP603 | ampG3 bcr1 | BAMPG prt (B- <i>Eco</i> , 27.6%) bicyclomycin resistance (B- <i>Eco</i> , 21.7%) |
| RP698 RP243 | bcr2 emrA | bicyclomycin resistance (B- <i>Eco</i> , 18.8%) multidrug resistance protein A (B- <i>Eco</i> , 26.9%) |
| RP157 | emrB torC | multidrug resistance protein B (B-Hin, 29.3%) tollurite resistance protein (B-Eco. 35.3%) |
| 0.00 | | functions |
| RP302 | tolB | colicin tolerance protein (B-Hin, 29.8%) |
| нР309 RP310 | tolQ tolR | inner membrane protein (B- <i>Eco</i> , 39.7%) inner membrane protein (B- <i>Pae</i> , 40.1%) |
| Uncated | orized | |
| RP493 BP199 | addA adx1 | adducin alpha subunit (E- <i>Hsa</i> , 32.6%) adrenodoxin precursor (E- <i>Sno</i> , 57.1%) |
| RP714 | ank2 | ankyrin (E-Hsa, 32.7%) |
| RP181 | ctaQ* | thermostable carboxypeptidase (B-Pho, 29.1%) |
| RP297 RP323 | cysQ cyaY | sulphite synthesis pathway protein (B-Eco, 31.2%) CyaY protein (B-Ech, 31.1%) |
| RP118 RP063 | era hesB1 | GTP binding protein Era (B- <i>Bsu</i> , 33.6%) HesB protein (B- <i>Ava</i> , 37.0%) |
| RP484 | hesB2 | HesB protein (B-Pbo, 40.2%) |
| RP485 | nifU | nitrogen fixation protein (B-Avi, 43.0%) |
| RP602 | p34 pat1 | patatin B1 precursor protein (E-Stu, 22.9%) |
| RP317 RP109 | pkci ptb | protein kinase C inhibitor (B-Abr, 38.6%) phosphate buturyltransferase (B-Cab, 36.4%) |
| RP594 | scoB* | succinyl-CoA:3-ketoacid-CoA transferase subunit B |
| RP031 | sco2 | Sco yeast precursor protein (E-Sce, 32.6%) |
| пР587 RP846 | sco2 sfhB | Sco yeast precursor protein (E-Sce, 36.6%) SfhB protein (E-Zmo, 40.6%) |
| HP430 RP058 | smpB soj | small protein (B-Syn, 46.7%) SOJ protein (B-Bsu, 50.4%) |
| RP486 RP487 | spi1 spi1 | tRNA splicing protein (E-Cal, 58.9%) tBNA splicing protein (E-Cal, 32.3%) |
| RP059 | spo0J | sporulation protein (B-Bsu, 40.4%) |
| RP733 | sunB surf1 | SurF1 protein (E-Hsa, 23.9%) |
| нн/10 | tra3* | transposase (B-Hme, 34.0%) |
| HYPOT Integral | HETICA membra | AL PHOTEINS |
| | | |

NO SIMLARITY 208 Integral membrane proteins 21