主論文

ゲノム間比較に基づく遺伝子クラスターの解析

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要旨

現在、全ゲノム配列が同定された生物種は１０種を越え、同時に大量の配列データが蓄積されるようになった。データベースの種類も増加し、どのように生物学データベースを整理し統合するか、またどうやってこれらから新たに有効な情報を取り出すのかが問題となってきた。

分子間の反応やシグナル伝達の経路など、殆んどの生物学的現象は、その分子間に関連があるかないかだけに着目したリンク（関係）と言う概念で統一的に表わす事が可能である。このリンクを用いて生物学データベースを統合化しようと、著者は次のような基本構造を考案した。

1. あらゆる生物学データベースをエントリーのレベルで統合し、同じ検索方式で、どのエントリーにも現実的な時間内での検索が可能であること
2. エントリー間に情報となるリンクは全て抽出し、リンクを次々と辿ることで新たなリンクを生み出せるようにすること

これらの構造を基礎において、著者はDBGET/LinkDB統合データベース検索システムを作成した。リンク情報は、もともとデータベースに書かれてあるエントリー間の相互参照的なリンク（ファクトリンク）だけでなく、生物学的な現象として関連のあるエントリー間のリンク（生物学的リンク）や相同性検索の結果を結び付けたリンク（相同性リンク）を組み込んで統合的なリンク検索ができるようになっている。このうち、生物学的リンクは特に、KEGG（Kyoto Encyclopedia of Genes and Genomes）プロジェクトで進めているデータの蓄積に依るところが大きい。

この統合リンク検索に基づく有効な応用例として、ここでは１０生物種の全塩基配列が決定されたゲノムで、種内および種間で保存される遺伝子クラスターの解析を行った。ゲノム上で対応する遺伝子を抽出する過程ではこの統合リンク検索の手法が用いられている。

この解析の結果には、種間の違いを越えて保存されたクラスターの存在が確認されたことを始め、近縁種の *Mycoplasma pneumoniae* と *Mycoplasma genitalium* の比較により、ゲノム量の増幅が遺伝子クラスターの増加に起因していることが

多いことが示された。

また、*Escherichia coli* ゲノムとの比較から抽出したクラスターを Blattner らの予測したオペロンに照らし合わせたところ、抽出クラスター数の 20% しか完全にこのオペロンと一致しなかったが、オペロン内の遺伝子群と部分一致したクラスターでは 80% にまで達する生物種まで見られた。この部分一致度は相手のゲノムが小さいほど、また遠縁の種になるほど高い値を示す傾向があり、オペロン予測を行う上で重要な手掛かりを示した。

この結果から、遺伝子クラスターは小さなクラスターが集まって、次第に大きなクラスターを形成し、種によってクラスターを再編成するなど、遺伝子クラスターを階層的に定義することが重要であることがわかった。このデータを用いてオペロン予測を行うことは今後可能であり、そのステップとしてこの解析は重要な役割を果たしたと考えられる。

略語

生物種名の略語

- *Mja* : *Methanococcus jannaschii*
- *Mth* : *Methanobacterium thermoautotrophicum*
- *Eco* : *Escherichia coli*
- *Hin* : *Haemophilus influenzae*
- *Hpy* : *Helicobacter pylori*
- *Bsu* : *Bacillus subtilis*
- *Mge* : *Mycoplasma genitalium*
- *Mpn* : *Mycoplasma pneumoniae*
- *Syn* : *Synechocystis sp.*
- *Sce* : *Saccharomyces cerevisiae*

データベースの略語

- nr-nt : Non-redundant nucleic acid sequence database
- nr-aa : Non-redundant protein sequence database
- genbank : GenBank nucleic acid sequence database
- genbank-upd : Cumulative daily updates of GenBank since the latest release
- embl : EMBL nucleic acid sequence database
- embl-upd : Cumulative daily updates of EMBL since the latest release

- dbest : dbEST database of Expressed Sequence Tags
- dbsts : dbSTS database of Sequence Taged Sites
- swissprot : SWISS-PROT protein sequence database
- swissprot-upd : Cumulative daily updates of SWISS-PROT since the latest release
- pir : PIR protein sequence database
- prf : PRF protein sequence database
- genpept : Translated protein sequences from genbank
- genpept-upd : Translated protein sequences from genbank-upd
- pdb : Brookhaven Protein Data Bank
- pdb-upd : Cumulative daily updates of PDB since the latest release
- pdbstr : Re-organized Protein Data Bank
- pdbstr-upd ; Cumulative daily updates of PDBSTR since the latest release
- epd : Eukaryotic Promoter Database
- transfac : TRANSFAC database, Combination of TFFACTOR and TFSITE
- prosite : Dictionary of Protein Sites and Patterns
- prosdoc : PROSITE ducumentation file
- ligand : Ligand Chemical Database, Combination of ENZYME and COMPOUND
- pathway : KEGG Pathway Database
- genes : KEGG Genes Database
- pmd : Protein Mutant Database
- aaindex : Amino Acid Index Database, Combination of AAindex1 and AAindex2

- litdb : Literature Database compiled by PRF
- omim : Online Mendelian Inheritance in Man
- linkdb : Database of Link Information

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第1章　全体への序論

1.1　生物学におけるデータベース

生物学は基本的に経験を記述的に説明する学問であると言っても過言ではない。したがって知識の蓄積から新たな発見を見いだすことは稀ではない。かつてダーウィンが自然を直接観察することにより進化論を唱えたのは有名であるが、現代では分子生物学の発展により、生物が持つ機能の情報が分子というレベルで記述され、蓄積されるようになった。またさらにシーケンス技術の発展により、生物の持つ遺伝情報がDNAやRNAのヌクレオチドの並びで表現される時代へと変り、そこにはまさに大量情報の氾濫へと急速な転換期を向かえた生物学の姿がある。

この様な時代背景のもと1980年代に誕生したGenBankデータベースプロジェクト[12]は急激な勢いでその登録塩基配列数を伸ばし、今では分子生物学者には切り放すことのできない重要なデータベースへとその価値を高めた。また、近年シーケンス技術の革新的な進歩によって、小さなゲノムであれば、一生物種が持つ核酸配列を、僅か数ヵ月で丸ごと読み取れるようになり、これまでシーケンスプロジェクトだったものから、ゲノムサイエンス[42]と呼ばれる生物学での新しい分野にまで発展してきたことはまだ記憶に新しい。

1.2　全ゲノム配列の蓄積

1995年に比較的小さなゲノムを持つバクテリア *Haemophilus influenzae*Rd の全塩基配列が発表されて[16]以来、*Mycoplasma genitalium*[17]、*Methanococcus jannaschii*[11]の全ゲノム配列が続き、1998年の始めに至るまで、あっと言う間に１０種を越える生物種のゲノム配列が解読された[30, 26, 23, 51, 7, 46, 34, 33, 18]。まさにここ二、三年は、完全解読されたゲノムデータが次々とGenBankへと登録を開始した年であった。

同時に、蓄積する多量なゲノム配列を整理し、必要な情報をいつでも取り出せるようなシステム作りが世界各地で開始され、The Institute for Genome Research [1]を始め多種多様なゲノム関連データベースが作成されている[32]。著者の参加する別プロジェクトであるKEGG（Kyoto Encyclopedia of Genes and Genomes）

は、このようなデータベースのうちの一つであり、特に代謝系に重点を置き、構成されている[24, 28]。また、さらにKEGGにはシグナルパスウェイや細胞周期、発生制御と言った制御系のデータ面からも情報を蓄積中である[25, 31]。

1.3　従来のデータとの統合

ここで、生物学データベースの統合化について考えてみたいと思う。先に述べたが、GenBankが発足してから１０年以上の歳月を経ており、時間とともに様々な観点から作成された多種多様なデータベースが出現してきた。そこには、核酸や蛋白質の配列データを始め、構造のデータベース、文献、遺伝病、モチーフ配列、蛋白質ミューテーション、酵素反応、アミノ酸インデックス、転写因子とその結合サイトなどのデータがあり、これまでそれぞれのデータベースが一部の関連研究を行っている研究者によって利用されてきた傾向が強い。

ところが、大量のゲノム配列を扱うゲノムサイエンスの時代に入り、事態は変りつつある。例えば、大量にゲノムが放出されると、次は決まって各遺伝子へ機能の割り当てが行われる。この場合に、FASTA[41]などの相同性検索によってすでに実験でわかっている配列がどうかを確認するのと同時に、既存のデータと照らし合わせることで機能を割り振っていくことが常套手段となっている。

しかし、この機能割り当ては常にうまくいくとは限らない。理由の一つは、相同性検索で得た答のスコアが低い場合には、その情報の確信度が薄れてしまうことである。もう一つは、多機能な蛋白質などがあり、生物種によってその生物が生きているシステム全体の構成を考慮しないと機能の割り当てができない場合である。これはアイソザイムなどが当てはまる。

生物システム全体を眺めるのは容易ではない。そもそもシステム全体が完全に知られている生物種など無いと言うこともあるが、それ以前にも仮に全ての遺伝子の機能が解き明かされた生物種がいたとしても、それらの情報は、様々な観点に基づいて構築されたデータであり、それらを統合的に考察しながら、遺伝子の機能を割り当てることなど、人間の力だけでは到底不可能である。

この様な面からも計算機によるデータベースの統合化は必至のことであり、この統合化をいかに行うかでより有益な情報を既存データから抽出することが可能になる。著者はこの点にまず着目し、優れたデータベースが優れた解析を可能にすることを実現化することに着手した。

1.4 統合データベース検索システム

多種多様な生物学のデータベースを統合化するには、根底によりシンプルな共通概念が必要である。本稿では金久らによる IDEAS[54] を拡張した統合データベース検索システム DBGET/LinkDB について述べ、共通の検索方式と共通のデータベース間のエントリーの結び付き（リンク）によって、情報の洪水の中からいかに効率よく必要なデータを取り出すかについて記述する。そこでは、KEGG データベースとの共通接点でもある二項関係によるリンクが使用され、単純化によって異なる形式のデータベースが容易に結び付けられている。

1.5 ゲノム比較による遺伝子クラスターの解析

統合データベース検索から期待されるものは既存の情報が、新たな情報を生み出すかである。著者は、基礎となる論文 1 [19, 20] にあるように、これまで生命現象の中でも特に転写の制御系に興味を持ち、真核生物のプロモーターを特徴づける転写因子の結合サイト解析を行い、遺伝子発現の時期特異的、組織特異的なプロモーターの予測を行ってきた。これとの関連により、バクテリアでは転写単位はオペロンという形をとることが多く、統合データベース検索の解析としてオペロン予測を行うことを試みているところである。本稿においては、オペロン予測を行うためのアセスメント的解析である遺伝子クラスター解析を行った結果について報告した。それによると、オペロンがさらに小さな単位の遺伝子群の単位に分けることができ、それらが異なる集合形態をとることで生物種に特有のオペロン構造ができあがっていることや、遠縁の種間比較で共通に保存されている遺伝子クラスターは生物に基本的なクラスターであり、遺伝子が単独で振る舞うよりむしろクラスター単位で振る舞う事が存在する、などについての結果が得られてきている。これは、最近、よく耳にするようになった生物種間でのゲノムの水平移動（horizontal transfer）と関係した議論が興味を持たれるところである。

第2章　方法

2.1　生物学データベース統合の具体的方法

生物学データベースは実に様々な種類がある。しかしながら、それらには二つの共通の特徴がある。その第一は、ここで言うデータベースとはフラット形式のテキストデータであること、そして第二に、それぞれのデータベースは、エントリーと呼ばれる単位のデータの集合であること、である。それら以外の例えばエントリー内の項目については、データベースごとに異なっている。これを考慮してデータベースを統合化することを考えると、以下の二つの対極する考え方に分けることができる。

2.1.1　tight-coupling：強い統合方法

まず、具体的にデータベースを使うときの事を考えると、検索の効率を良くしたり、検索する部分を規定したりするのには、データベース中のエントリー内のフィールド部分にまで着目し、そのフィールドでなるべく共通部分を見いだすような方法が必要とされる。このような、エントリー内のフィールドを、データベースごとに全て拾い出し、そのフィールドに分けながらデータベースを再編成し、共通のフィールドは同じ概念で検索できるようにするものを「強い統合」と呼ぶことにする。これには既存の方法である関係データベースによる統合化[29]などが例として上げられる。強い統合化の利点は、しっかりとした検索能力であるが、その反面、余りの強固さに融通が効かず、エントリーのフィールド形式がわずかに変化しただけで全体を構成し直すことになりかねない点が弱点としてあげられる。

2.1.2　loose-coupling：緩い統合方法

次に強い統合とは全く対極である緩い統合とは、データベース中で唯一共通なエントリーという単位に着目し、エントリーとエントリーの関連性があるときはそのエントリー間を結ぶリンクを張る、という取り決めをすることである。この方式の基本概念は、米国 NCBI での Entrez[43] やヨーロッパの SRS[15] でも採

用されている。これにより、検索はエントリー単位でしか行えないというように、検索が粗くなってしまう難点があるが、反面、柔軟にエントリー形式の変更などにも耐えることができる。また、このリンクという概念は、情報学的に見ても最も高い単純化を行った関係付けであり、これにより、WWW 上での hypertext 形式での統合や、オブジェクト指向型言語との相性も良く、単純なゆえに利用価値も生まれやすいのが利点である。

2.1.3　著者の統合方法

著者は基礎となる論文2 [21] に記してあるように、この統合化に関して、弱い統合化をベースにした手法を用いた。但し、検索上のフィールドに条件をつけられないなどの難点を補うため、検索上どうしても必要になると想定されるフィールド数種のみを検索可能とし、その代わりにフィールドでの統合化は行わないようにエントリーレベルでの緩い統合化のみを行った。これにより、両統合法から必要な部分だけ組み入れることで、両者の弱点を排除できた統合化を行うことが可能になる。

2.2　リンク情報の概念

データベースを統合化するのに緩い統合化を用いたことにより、全てのデータベースはエントリーを単位として、または、エントリーと言う概念が当てはまりにくい様々な種類のファイルに対しても、次のようにデータベース名とその識別名だけで、

データベース名：識別名

とどんな場合でも一般的に表わすことができる様になる。

ここで、リンクとはそのように表わしたデータの集まりであると見做すことができ、リンクを式的に表現すれば、

データベース名１：識別名１ → データベース名２：識別名２

となる。この表現方法は、KEGG データベースにおいての二項関係の概念と共通で、従って DBGET/LinkDB と KEGG のデータとの間で相互にリンクを通しての情報のやりとりが効率よく行えるようになっている。

2.2.1 リンクの概要と種類

先ほどから、リンクと読んでいる関連付けも多様であり、ここではそのデータの保持の仕方の違いから、三種類にリンクの分類分けを行った。

ファクト（factual）リンク 実際に、データベースを眺めてみると、そのエントリーの作者などによって予め別のデータベースのエントリーへとリンクが埋め込まれていることが多々ある。これを、データベース中の事実に基づく、ファクトによるリンクであると見做して、ファクトリンクと呼ぶ。

相同性（similarity）リンク FASTA や BLAST[2] など相同性検索の結果によってもたらされる関係によるリンクでこれを相同性リンクと呼ぶ。

生物学的（biological）リンク KEGG データベース中に存在する酵素反応の経路や、シグナル伝達経路など、いわゆるパスウェイ上での繋がりによるリンクや、オペロンに属する遺伝子間の関連や、ゲノム上の位置での関連など一般の生物学の知識による関連付けを差すリンク。

一般に、ファクトリンクは、既存のものを使用するだけであり、SRS でも Entrez でも使用されるものであるが、相同性リンクは、Entrez によって先駆けて実現され、前もって全配列エントリーに対して、BLAST 検索をかけた結果を neighbor と呼ばれるものとして保存する形式をとっている。一方、生物学的リンクは著者のシステムで先駆けて導入された。

2.3 統合データベース検索システム

このような統合化とリンクの概念に基づいて著者は１７の既存データベースを統合した統合データベース検索システム DBGET/LinkDB を作成した。

この DBGET/LinkDB の統合的な検索能力を用いると一般的に図 2.1 の様なリンクのネットワークの中を辿ることで検索を行うことが可能である。図中で、エントリーは○でまた矢印はリンクとその方向を表わした。このようにリンクには方向性があり、正方向のオリジナルリンク、逆方向リンクが存在し、さらにリンクを辿ることで新たに生まれる間接的なリンク（図中太線で示した矢印）も存在する。

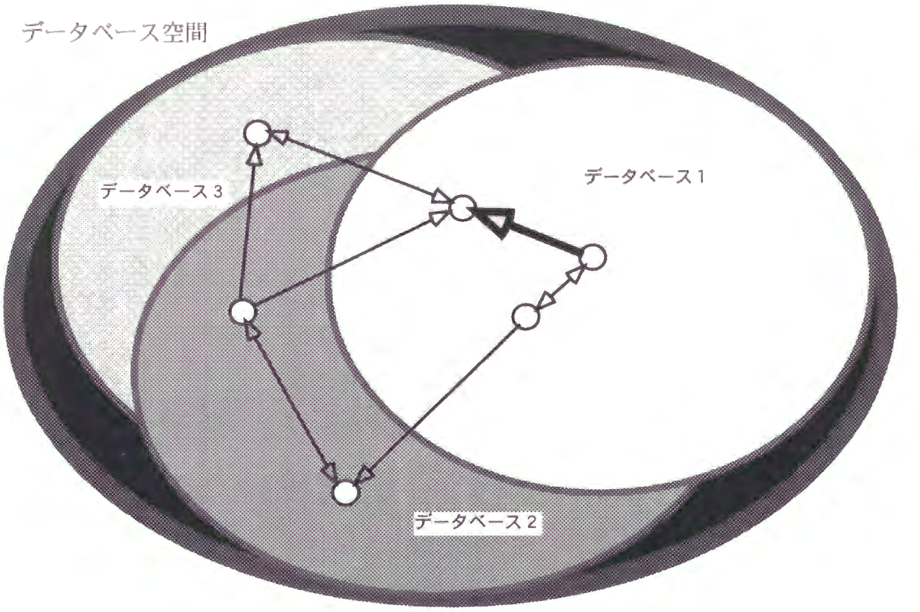


図 2.1: **DBGET/LinkDB 統合検索の概念図** 緩い統合を用いた検索により、データベース中のエントリーだけを単位として自由にリンクを辿ることができ、これによる柔軟な検索が可能となっている。図中の○はエントリーを、矢印はリンクとその方向を、また太線で書かれた矢印はリンクを辿ることで新たに生じるリンクを表わしている。

2.4 遺伝子クラスター解析

DBGET/LinkDB 統合検索システムを用いた解析として、既にゲノム配列がわかっている１０種類の生物について遺伝子クラスター解析を行った。使用した１０生物種は、DBGET/LinkDB の Genes データベースに既に全ゲノムが登録されているものに限り、古細菌から *Methanococcus jannaschii (Mja)*、*Methanobacterium thermoautotrophicum (Mth)* の二種、グラム陰性菌から *Escherichia coli (Eco)*、*Haemophilus influenzae (Hin)*、*Helicobacter pylori (Hpy)* の三種、グラム陽性菌から *Bacillus subtilis (Bsu)*、*Mycoplasma genitalium (Mge)*、*Mycoplasma pneumoniae (Mpn)*、シアノバクテリア *Synechocystis sp. (Syn)* 一種、真核生物酵母菌として、*Saccharomyces cerevisiae (Sce)* を用いた。

それぞれのゲノムの特徴を表2.1 に示す。

2.4.1 遺伝子クラスターの抽出

これらのゲノム間で、遺伝子クラスターを探すには、FASTA による総当たりの similarity link サーチを行い、ここでは経験的にスコアが 80 以上のものだけを残す

生物種		主な染色体数	ゲノムサイズ (nt)	ORF 数	RNA 数
古細菌	*Mja*	1（環状）	1,664,987	1,735	43
	Mth	〃	1,751,377	1,871	47
グラム陰性細菌	*Eco*	〃	4,639,221	4,289	108
	Hin	〃	1,830,135	1,717	74
	Hpy	〃	1,667,867	1,566	43
グラム陽性細菌	*Bsu*	〃	4,214,814	4,100	121
	Mge	〃	580,073	467	36
	Mpn	〃	816,394	677	33
シアノバクテリア	*Syn*	〃	3,573,470	3,166	49
酵母菌	*Sce*	16（線状）	12,069,313	6,064	262

表 2.1: １０生物種のゲノムサイズとその特徴

ようにセレクションをかけ、さらにそれらをゲノム上の位置データから biological link に基づいてゲノム上で隣り合うようなエントリーのリンクを延ばせるだけ延ばす方法でクラスターを抽出した（図 2.2)。但し、Orthologue 遺伝子を探すときのような双方向からスコアの最高値をとる相同性検索を行ったわけではなく、単純にどちらかから相同性があるものを抽出している。抽出したクラスターは種間ごとに抽出数や含まれる遺伝子の数の分布をとった。

2.4.2　大腸菌オペロンとのマッチング

オペロン予測へ向けて、ここでは Blattner らの論文 [7] に基づいて図から読み取ったオペロンデータとここで抽出した遺伝子クラスターがどの程度マッチしているのかを調べた。その時、オペロン内に含まれる遺伝子が全て一致した「完全マッチ」および、オペロン内の連続遺伝子がマッチした場合の「部分マッチ」の両方から解析を行った。

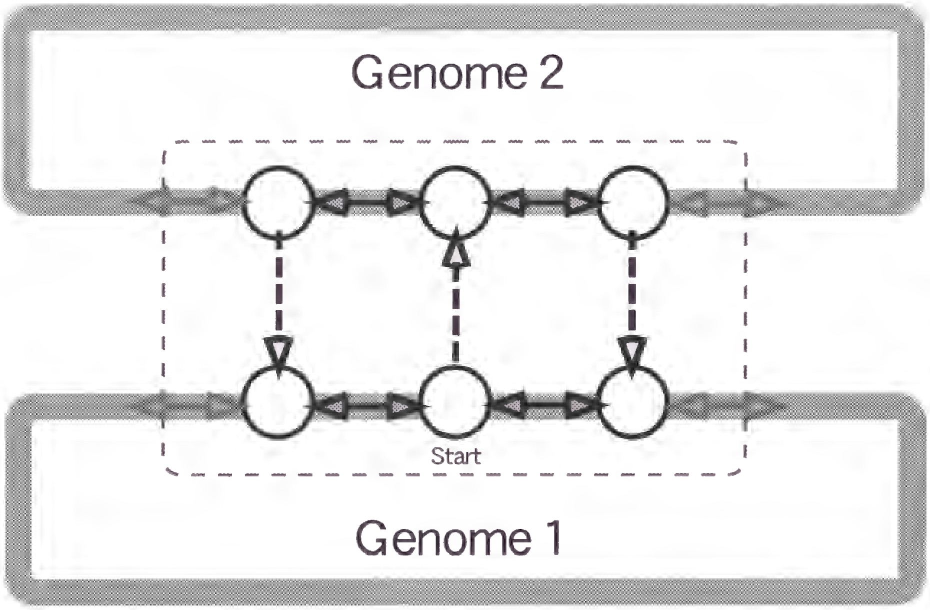


図 2.2: **統合 Link サーチによる遺伝子クラスターの検索** ○が遺伝子を表わし、点線の矢印が similarity link、それ以外の矢印が biological link を表わしている。Genome1 の中央の遺伝子から出発して、similarity link で Genome2 で対応する遺伝子を探し、そこから両方のゲノム上を左右に移動してまた similarity link で対応を探る。この時、出発遺伝子の biological link になっていれば遺伝子クラスター（点線枠）として抽出した。

第3章　結果１：DBGET/LinkDB 統合データベース検索システム

3.1　序論

DBGET は二つの基本コマンドである *bget* と *bfind* を用いてエントリーの取得とキーワードによるデータベース検索ができるシンプルなシステムである。他にもデータベースの情報を知りたい場合には *binfo* や *bman* といったコマンドが用意されてある。また、データベース間のリンクデータベースである LinkDB を検索するのには、*blink* というコマンドが利用できる。DBGET は pre-GenBank project のために Los Alamos 配列解析システム [27] として開発されたのを出発点とした IDEAS (Integrated Database and Extended Analysis System for nucleic acids and protein)[54] を拡張したものとして位置づけられる。

DBGET/LinkDB は概念的に三つの階層から組み立てられている。まず、データベースを利用するだけの DBGETclient、データベースサーバー機能を備えた DBGETserver、そしてサーバーに WWW からのアクセスを可能にするサーバー機能を拡張した WebDBGETserver である。ローカルに置かれたデータベースをシステムに組み入れたり更新するには *seqnew* と呼ばれるプログラムが実行されることが必要である。現在、DBGET/LinkDB は Web を通じてゲノムネットサービスの根幹をなしているものであり、Web の特徴である hyperlink を通じて LinkDB の情報を一段と利用しやすくなっている。

3.2　特徴

図 3.1 にシステム全体の概念図を示した。DBGET/LinkDB には以下のような特徴が備わっている。

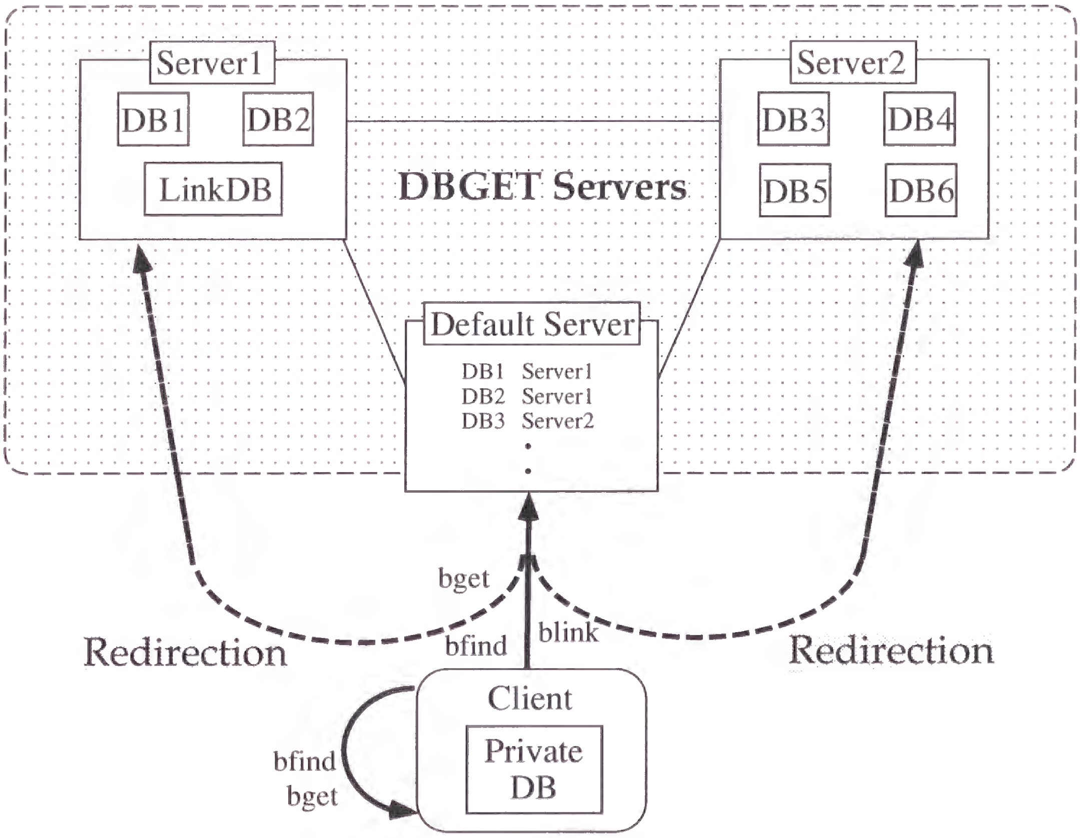


図 3.1: **DBGET/LinkDB システム全体の概念図** クライアント側からはデフォルトのサーバー以外は特に意識することなく、リダイレクション機能によって自動的にネットワーク分散型のデータベースサーバー全体にアクセスでき、統合検索が可能である。

分散データベースシステム　DBGET はネットワークを通じて利用でき、データベースも複数のサーバーに分けて存在させたものを同時に使用することができる分散環境をとることができる。しかし、クライアントからはサーバー全体を特に意識することなく、デフォルトサーバーからのリダイレクションによって、自動的に全体のデータベースにアクセスするようになっている。

緩い統合化によるシンプルなシステム　DBGET/LinkDB はデータベースのエントリー単位での緩い統合化しか行っていないために、データベースの形式などの変更に対して非常に柔軟である。このことは、世界中で日時更新されるデータベースを収集し、一日のうちに検索可能な形へと置き換えることを容易にしている。

ユーザーに対し開かれた技術　DBGET/LinkDB システムの利用者は自分の保持するデータベースを公共のデータベース群に組み入れることが比較的容易にでき、自分だけの統合環境を構築することが可能な開かれたシステム技術を提供している。

複数インターフェースによる利用　コマンドによるデータベース検索の他、Web版による統合検索も提供している。またサーバーを持たず、以前は NetDBget と呼ばれていた DBGETclient プログラムも別に配布し、異なる環境においても何らかの形でデータベースにアクセスできるようになっている。

3.3 データベースのインデックス化

緩い統合化による検索機能の弱点を補うには、必要とされる範囲のフィールドに限り、検索機能を追加することである。DBGET ではデータベースに対してエントリー名、アクセッション名、タイトル行、リファレンス行、著者行の5つのフィールドに限り、データベースの索引を持つことで細かな検索を可能にしている。また、リンクについては各データベースからのファクトリンクは抽出したのと逆向きのリンクとしても利用できるため、データベースごとにオリジナル、逆方向の両方の索引を持つようになっている。これらの索引付けは *seqnew* と呼ばれるプログラムを実行することで行われる。表3.1に、*seqnew* コマンドによって、データベースのインデックス化（索引付け）を行ったときにできるファイルの一覧を示した。

普通、様々な形式のデータベースからキーワードやフィールドを取り出すには、文法構造解読ルーチンがそれぞれのデータベースに対して必要となるが、この *seqnew* プログラムのコーディングには C++ の特徴を利用し、Class ライブラリーを用いることで、パージングには基底クラスの継承などによって、コードの再利用を図っている。そのため、データベース間の共通の特徴はライブラリーに収納され、そこからの派生部分だけを付け足すような構成で、どんな形式のデータベースにも柔軟に対応でき、将来性のある設計となっている。

さらに、表3.2にこれらのファイルを作成するのにかかる実際の CPU 時間を三つの代表的なデータベースについて測定してみた結果を示す。

このようにデータベースに対して八種類の付属ファイルを作成するだけで本体のファイルには全く手をつけずそのまま利用することで、領域的にも大幅な節約になるのが特徴である。

ファイル名	ファイル形式	内容
db.pag	dbm	エントリーとアクセッションをキーにしたエントリー位置のオフセットとバイトサイズを与えるハッシュテーブル
db.acc	flat	第二アクセッション以降も含めてアクセッションとエントリーとの対応を表記したファイル
db.tit	flat	エントリーのタイトル行やデフィニション行を抜き出したファイル
db.tit.pag	dbm	db.tit ファイルに対してエントリーおよびアクセッションをキーにして作ったハッシュテーブル
db.ref	flat	エントリーのリファレンス行を抜き出したファイル
db.aut	flat	エントリーの著者行を抜き出したファイル
db.lnk+.pag	dbm	オリジナルリンクをハッシュ化して格納したファイル
db.lnk–.pag	dbm	オリジナルリンクを逆向きにしてハッシュ化して格納したファイル

表 3.1: *seqnew* で作成されるインデックスファイル

データベース	サイズ	*seqnew* 時間	インデックスファイルサイズ
(Release)	**(KB)**	**(CPU time)**	**(KB)**
GenBank(103.0)	5,394,788	7:51:42	1,104,928
GenBank-upd(103.0+)	905,164	1:06:11	146,052
EMBL(52)	3,999,668	10:07:24	1,202,552
EMBL-upd(52+)	1,076,800	1:29:33	259,760
SWISS-PROT(34.0)	109,617	25:14	57,756
SWISS-PROT-upd(34.0+)	55,148	7:20	4,436

表 3.2: インデックス化にかかる時間とファイルサイズ

3.4 データベースの検索

3.4.1 ネットワークからの利用

図3.1に示したように、DBGETのデータベースはネットワークを通じて利用されるようになっている。このネットワークコンフィグレーションは *dbtab* ファイルによって定義することができる。例えば、表3.3のように、

database	dbtype	dbsite
genbank	genbank	@dbget.genome.ad.jp
embl	embl	@123.456.78.9:1111
mydb	genbank	/usr/local/db

表3.3: *dbtab* によるネットワークコンフィグレーションとローカルデータベースの統合化

と定義すると、genbank形式のgenbankデータベースはdbget.genome.ad.jpサーバーへリダイレクト接続し、embl形式のemblデータベースはIPアドレスで123.456.78.9のサーバーへport番号1111から接続する。

さらに、DBGETの持つ優れた特徴に、自分のデータベースを公共のデータベースと統合して、同時に使用できる点である。ここでは、genbank形式だが、mydbと言う名前の自分のデータベースがこのマシンに存在していて、ディレクトリ名/usr/local/dbでアクセスすると言う指定である。

3.4.2 alias および複合データベース

次に、DBGETが可能とした、データベースのalias機能について、表3.4に示した。

ここでは、genbankのalias名であるgbや、emblのalias名embが登録され、さらに、gbとembを合わせたものがdnaデータベースであると複合データベース形式の指定がなされている。このように、別名を指定できることは、長い名前のデータベースを簡略化して表記できるだけでなく、さらにその下の行の例のように、genbankのリリース分と、さらにそのリリースから日時更新によって増加した分だけのgenbank-updデータベースを合わせてgenbank-todayと呼ぶなど、仮想データベースが指定でき、その利用価値は高い。また、巨大化するデータベースを幾つかのモジュールに分けることで、ディスクの使用効率をよくすることが

database	dbtype	dbsite	mnemonic
genbank	genbank	/bio/db/genbank	gb
gb	alias	genbank	
embl	embl	/bio/db/embl	emb
emb	alias	embl	
dna	alias	gb+emb	
genbank-upd	genbank	/bio/db/genbank-upd	gbu
gbu	alias	genbank-upd	
genbank-today	alias	genbank-upd+genbank	
gbt	alias	genbank-today	

表 3.4: **DBGET が持つ alias 機能と複合データベース**

でき、さらに、部分的な修正を可能にし、*seqnew* プロセスをかける時間も無駄を省くことが可能である。

3.4.3 サポート可能なデータベース

DBGET/LinkDB がサポートできるデータベースは現在１７種類である。その一覧を表3.5に示した。

さらにデータ検索はできないが、医学生物学関連の文献データベースであるMedLine(PubMed) へのリンクも WebDBGET 上では実装されている。ここで、PATHWAY, LIGAND, GENES のデータベースは KEGG プロジェクトからの産物であり、LIGAND は ENZYME と COMPOUND データベースの複合データベースである。アスタリスクで示してあるのは、殆んどがデイリー更新により、最新のデータベースを検索できるようにしてあるもので、それらには、genbank-upd、embl-upd、swissprot-upd、pdbstr-upd、pdb-upd と言ったリリースからの増分のみを含むものと、ligand、pathway、omim、genes データベースの様に全体を作り直すものとに分けることができる。

3.4.4 FASTA/BLAST 形式ファイル

DBGET でサポートしているデータベースのうち、配列を含むものは FASTA や BLAST 検索の対象となり、相同性リンクなどで使用される。表?? での六種類の配列データベースがそのまま FASTA/BLAST 検索には使用できる以外にも、epd、

カテゴリー	データベース名
nucleic acid sequences	*GenBank [5], *EMBL [47]
protein sequences	*SWISS-PROT [3], PIR [22], PRF, *PDBSTR
3D structures	*PDB [6]
sequence motifs	PROSITE [4], EPD [10], TRANSFAC [53]
enzyme reactions	*LIGAND [48]
metabolic pathways	*PATHWAY [24]
amino acid mutations	PMD [38]
amino acid indices	AAindex [37]
genetic diseases	*OMIM [40]
literature	LITDB
genes and genomes	*GENES

*印のものはデイリーまたは週ごとに更新されている

表 3.5: **DBGET/LinkDB がサポートするデータベース一覧**

genes の配列への検索や、genpept と言う genbank のアミノ酸への翻訳配列、また dbest、dbsts と言ったタグ配列データベースも検索できる。

さらに、利用者にとってはこの様な配列データベースを一括に検索したい場合があるが、そのような時に利用できるのが、nr-nt および nr-aa データベースである。これらは、幾つかのデータベースを合わせて冗長性を除いた non-redundant データベースある。しかも、これらはデイリー更新の対象でもある。例えば、nr-nt は、genbank、genbank-upd、embl の合成であり、nr-aa は swissprot、pir、prf、genpept、genpept-upd からの合成データベースである。

3.4.5 bget,bfind

データベースのエントリー取得に用いる *bget* コマンドの単純な使い方は、

bget データベース名：識別名

のように指定するのみである。これにより、先ほどのハッシュ化されたインデックスファイルをまずサーチし、そこからエントリーに対する全ファイル中のオフセット位置と大きさの情報を得た後、実際のファイル中を見て、中から必要なエントリーを抜き出すものである。

また、エントリーのキーワード検索は、*bfind* コマンドによって以下のような書式で行われる。

bfind データベース名 キーワード

ここで、通常キーワード検索はエントリー名またはアクセッション名、タイトル行かまたはデフィニション行の文字列に対して行われる。また、もう少し複雑な検索を行いたい場合には、リファレンス行、著者行、第二アクセッション番号などを指定し、また単に文字列が合うだけでなく、単語検索としての指定を行うこともできる。指定できる属性値は、以下のようになっており、「属性：キーワード」の形式で検索を行わせることができる。

T	title or definition field (default)
R	reference field; e.g., R:"Science 269"
A	author names; e.g., A:smith
N	primary and secondary accession numbers
E	entry names for partial matching; e.g., E:hum
W	indicates word matching; e.g., AW:smith

さらに、これらはブール代数のオペレーターによる *AND* 検索や *OR* 検索、*NOT* などの指定により、複数のキーワードによる複雑な検索も行えるようになっている。

3.5 リンク検索

3.5.1 リンク計算の定義

LinkDB はデータベースから抽出した factual リンクによるオリジナルリンクと、それを逆にした逆リンク、そして計算によって求められる間接リンクを含んでいる。それらは、データベースごとによって違い、どのリンクを使用するかを *linktab* という名前のファイルに次の表3.6の様に記述する。

genbank	+genbank
	+embl
	+embl:+swissprot
	–pir
	+enzyme
	+enzyme:-prf

表 3.6: *linktab* によるリンク経路の指定

ここで、オリジナルリンクは + で、逆リンクは – で示されている。例えば、この表

は genbank からのリンクを表わし、オリジナルリンク（genbank, embl, enzyme)、逆リンク（pir)、間接的リンク（swissprot, prf）を表わしている。

3.5.2 blink

データベースから抽出したファクトリンクは *blink* コマンドを用いて検索することができる。また、オリジナルのリンクの逆は逆方向リンクとして、さらにリンクのリンクは間接的リンクとして同時に検索可能である。*blink* の一般的書式は、

blink -ori データベース名：エントリー名

であり、-o がオリジナルリンク、-r が逆リンク、そして -i が間接的リンクを特定して表示するオプションである。

現在、データベース中から抜き出しているリンクを模式的に示したのが図 3.2 である。図でリンクの貼ってあるところを線で表わし、全体のリンクのネットワーク

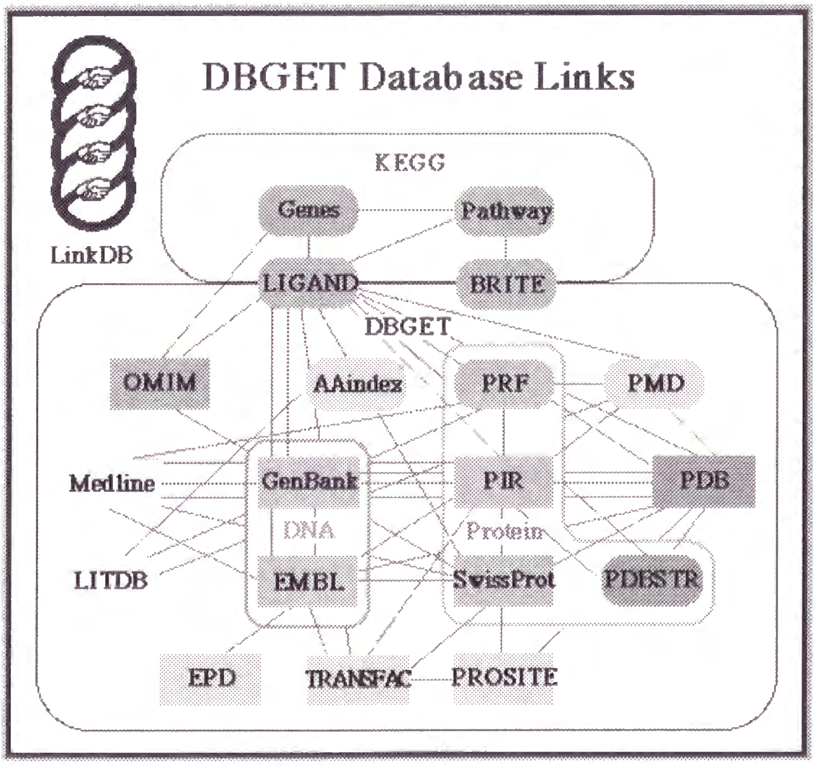


図 3.2: **DBGET/LinkDB によるデータベース間のリンクダイアグラム** リンクのネットワークの中を辿ることでほぼどのデータベースからどのデータベースへのリンクも間接リンクとして検索することが可能である。

がワイヤーダイヤグラムで示されている。しかし、このダイヤグラムではリンクの向きまでは表わされていない。例えば、OMIM は内部リンクしかもたず、外部のデータベースへは出ていけないが、SWISS-PROT が OMIM にリンクを持ち、さらにそれ以外の EMBL、PROSITE、PIR、PDB などにリンクを持っているために、SWISS-PROT の逆リンクを利用することで OMIM からその他へのデータベースへの間接的リンク検索が可能になる。

また、核酸配列のデータベースを DNA、またアミノ酸配列データベースを Protein と表わしてあるが、これは DBGET のもう一つの特徴である複合データベースの一括検索ができることを示している。すなわち、データベースに DNA と指定すれば GenBank と EMBL を同時に検索し、また、Protein と指定すれば PRF、PIR、SWISSPROT、PDBSTR の4種を同時に検索するものである。

これらから、オリジナルリンク、逆リンク、間接的リンクの種別に分けて一覧にしたものが、表3.7に示してある。

	To																		
From	gb	emb	sp	pir	prf	str	pdb	ps	epd	tff	tfs	ec	cpd	path	pmd	aax	mim	lit	med	kegg
gb	o	o	i	r	i	i	r	i	i	i	i	o	-	i	i	-	i	-	o	-
emb	o	o	o	r	i	i	r	i	o	r	o	o	-	i	i	-	i	-	o	-
sp	i	o	i	o	i	i	o	o	-	o	-	o	-	i	i	-	o	-	o	r
pir	o	o	r	i	r	i	o	i	-	r	-	o	-	i	r	-	i	-	o	r
prf	i	i	i	o	-	i	o	i	-	i	-	o	-	i	r	-	i	o	o	-
str	i	i	i	i	i	-	o	i	-	-	-	o	-	i	i	-	i	-	i	-
pdb	o	o	o	o	r	r	o	r	-	-	-	o	-	i	r	-	i	-	o	-
ps	i	i	o	i	-	-	o	-	-	-	-	r	-	i	-	-	i	-	i	-
epd	i	o	i	-	-	-	i	i	-	i	i	i	-	i	-	-	i	-	i	-
tff	-	o	o	o	-	-	i	i	-	o	o	-	-	-	-	-	i	-	i	-
tfs	-	o	-	-	-	-	i	i	-	o	-	-	-	-	-	-	i	-	i	-
ec	r	r	r	r	r	r	o	o	-	-	-	o	o	o	r	-	o	-	i	o
cpd	-	-	-	-	-	-	-	-	-	-	-	o	-	o	-	-	-	-	-	-
path	i	i	i	i	-	i	i	i	-	-	-	o	r	-	i	-	i	-	-	-
pmd	i	i	i	o	o	i	o	i	-	-	-	o	-	i	-	-	i	o	i	-
aax	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	o	-	o	-	-
mim	i	i	r	i	i	i	i	i	-	-	-	r	-	-	i	-	o	-	i	r
lit	i	i	i	i	r	-	i	-	-	-	-	i	-	-	r	r	-	-	-	-
med	r	r	r	r	r	i	r	i	-	-	-	i	-	-	i	-	i	-	-	-
kegg	-	-	o	o	-	-	-	-	-	-	-	o	-	-	-	-	o	-	-	-

表 3.7: １７種のデータベースおよび **MedLine** 間のファクトおよび生物学的リンク（**o**：オリジナルリンク、**r**：逆リンク、**i**：間接的リンク） gb:genbank, emb:embl, sp:swissprot, str:pdbstr, ps:prosite, tff: factor data of transfac, tfs:site data of transfac, ec:enzyme data of ligand, cmd: compound data of ligand, path:pathway, aax:aaindex, mim:omim, lit:litdb, med:medline.

この様に、データベース空間の中を自由にリンクを辿ることで、必要な情報を抽出することが可能である。どのデータベースからどのデータベースへ到達可能かは、グラフ理論の推移的閉包を求める問題に帰着し、Warshall のアルゴリズム [44] によって、行列の n 乗を求めてみると、理論的には全データベース間で到達可能となる。しかし、実際には検索上意味のないリンクや、データベース間のリンクはあってもエントリー単位で見ると途切れてしまう場合もあり、経験的に、有効な範囲でのみ Link 検索を行うようにすると、表3.7の様になる。

3.5.3 実際に検索される経路

さらに、どのような経路でどのデータベースからどのデータベースへ到達しているのかは表3.7を見ただけでは間接的リンクについてはわからない。経路情報を factual リンク、similarity リンク、biological リンクに分けて次の表3.8に記した。

表 3.8: **LinkDB** で実際に検索される経路

LinkDB 検索によるデータベースの経路一覧
* Factual Links
AAindex ↔ AAindex
AAindex → LITDB
* Factual Links
COMPOUND ↔ ENZYME
COMPOUND → ENZYME ← E.coli
COMPOUND → ENZYME ← H.influenzae
COMPOUND → ENZYME ← B.subtilis
COMPOUND → ENZYME ← M.genitalium
COMPOUND → ENZYME ← M.pneumoniae
COMPOUND → ENZYME ← M.jannaschii
COMPOUND → ENZYME ← Synechocystis
COMPOUND → ENZYME ← S.cerevisiae
COMPOUND → ENZYME ← H.sapiens
* Factual Links
EMBL ↔ GenBank
EMBL ↔ SWISS-PROT
EMBL ← PIR
EMBL ← PIR ← PRF
EMBL ← PDB
EMBL → SWISS-PROT → PDB
EMBL ← PDB ← PDBSTR
EMBL → SWISS-PROT → PDB ← PDBSTR
EMBL ↔ EPD
EMBL ↔ TFSITE
EMBL ← TFFACTOR
EMBL ← TFFACTOR ← TFMATRIX
EMBL → SWISS-PROT → PROSITE ← TFCLASS
EMBL → SWISS-PROT → PROSITE
EMBL → ENZYME

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
EMBL → ENZYME → PATHWAY
EMBL ← PIR ← PMD
EMBL → MEDLINE
EMBL → GenBank → MEDLINE
EMBL → SWISS-PROT → MEDLINE
EMBL → SWISS-PROT → OMIM
EMBL ← ACeDB
EMBL → ENZYME ← E.coli
EMBL → ENZYME ← H.influenzae
EMBL → ENZYME ← B.subtilis
EMBL → ENZYME ← M.genitalium
EMBL → ENZYME ← M.pneumoniae
EMBL → ENZYME ← M.jannaschii
EMBL → ENZYME ← Synechocystis
EMBL → ENZYME ← S.cerevisiae
EMBL → ENZYME ← H.sapiens
* Sequence Similarity Links
EMBL → nr-nt
* Biological Links
EMBL → ENZYME ← (PATHWAY) → ENZYME ← EMBL
EMBL → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
ENZYME ← GenBank
ENZYME ← PIR → GenBank
ENZYME ← EMBL
ENZYME ← PIR → EMBL
ENZYME ← SWISS-PROT
ENZYME ← PIR ← SWISS-PROT
ENZYME → PDB ← SWISS-PROT
ENZYME → OMIM ← SWISS-PROT
ENZYME ↔ PIR
ENZYME ← SWISS-PROT → PIR
ENZYME ← PRF
ENZYME ← PIR ← PRF
ENZYME → PDB ← PRF
ENZYME ↔ PDB
ENZYME ← SWISS-PROT → PDB
ENZYME ← PDBSTR
ENZYME → PDB ← PDBSTR
ENZYME ← SWISS-PROT → PDB ← PDBSTR
ENZYME → PROSITE
ENZYME ← SWISS-PROT → Prosite
ENZYME → PDB ← Prosite
ENZYME ← PIR ← SWISS-PROT → Prosite
ENZYME ↔ ENZYME
ENZYME ↔ COMPOUND
ENZYME → PATHWAY

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
ENZYME ← PMD
ENZYME ← PIR ← PMD
ENZYME → PDB ← PMD
ENZYME ← PIR → MEDLINE
ENZYME ← SWISS-PROT → MEDLINE
ENZYME → OMIM
ENZYME ← SWISS-PROT → OMIM
ENZYME ← PIR ← SWISS-PROT → OMIM
ENZYME → PDB ← SWISS-PROT → OMIM
ENZYME ← E.coli
ENZYME ← H.influenzae
ENZYME ← B.subtilis
ENZYME ← M.genitalium
ENZYME ← M.pneumoniae
ENZYME ← M.jannaschii
ENZYME ← Synechocystis
ENZYME ← S.cerevisiae
ENZYME ← H.sapiens
* Biological Links
ENZYME ← (PATHWAY) → ENZYME
* Factual Links
EPD ← EMBL → GenBank
EPD ↔ EMBL
EPD ← EMBL ← SWISS-PROT
EPD ← EMBL ← SWISS-PROT → PDB
EPD ← EMBL → TFSITE
EPD ← EMBL ← TFFACTOR
EPD ← EMBL ← SWISS-PROT → PROSITE ← TFCLASS
EPD ← EMBL ← TFFACTOR ← TFMATRIX
EPD ← EMBL ← SWISS-PROT → PROSITE
EPD ← EMBL → ENZYME
EPD ← EMBL → ENZYME → PATHWAY
EPD ← EMBL ← SWISS-PROT → OMIM
EPD ← EMBL → GenBank → MEDLINE
EPD ← EMBL ← SWISS-PROT → MEDLINE
EPD ← EMBL → ENZYME ← E.coli
EPD ← EMBL → ENZYME ← H.influenzae
EPD ← EMBL → ENZYME ← B.subtilis
EPD ← EMBL → ENZYME ← M.genitalium
EPD ← EMBL → ENZYME ← M.pneumoniae
EPD ← EMBL → ENZYME ← M.jannaschii
EPD ← EMBL → ENZYME ← Synechocystis
EPD ← EMBL → ENZYME ← S.cerevisiae
EPD ← EMBL → ENZYME ← H.sapiens
* Biological Links
EPD ← EMBL → ENZYME ← (PATHWAY) → ENZYME ← EMBL → EPD
EPD ← EMBL → ENZYME ← (PATHWAY) → ENZYME ← EMBL

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
* Factual Links
GenBank ↔ GenBank
GenBank ↔ GenBank ↔ GenBank
GenBank ↔ EMBL
GenBank → EMBL ↔ SWISS-PROT
GenBank ← PIR
GenBank → EMBL ↔ SWISS-PROT → PIR
GenBank → ENZYME ← PIR
GenBank → ENZYME ← PRF
GenBank → ENZYME ← PIR ← PRF
GenBank → EMBL ↔ SWISS-PROT → PIR ← PRF
GenBank ← PDB
GenBank → EMBL ↔ SWISS-PROT → PDB
GenBank → ENZYME → PDB
GenBank ← PDB ← PDBSTR
GenBank → EMBL ↔ SWISS-PROT → PDB ← PDBSTR
GenBank → ENZYME → PDB ← PDBSTR
GenBank → EMBL → EPD
GenBank → EMBL → TFSITE
GenBank → EMBL ← TFFACTOR
GenBank → EMBL ↔ SWISS-PROT → PROSITE
GenBank → ENZYME
GenBank → ENZYME → PATHWAY
GenBank → ENZYME ← PMD
GenBank → MEDLINE
GenBank → EMBL ↔ SWISS-PROT → OMIM
GenBank → ENZYME → OMIM
GenBank → ENZYME ← E.coli
GenBank → ENZYME ← H.influenzae
GenBank → ENZYME ← B.subtilis
GenBank → ENZYME ← M.genitalium
GenBank → ENZYME ← M.pneumoniae
GenBank → ENZYME ← M.jannaschii
GenBank → ENZYME ← Synechocystis
GenBank → ENZYME ← S.cerevisiae
GenBank → ENZYME ← H.sapiens
* Sequence Similarity Links
GenBank → nr-nt
* Biological Links
GenBank → ENZYME ← (PATHWAY) → ENZYME ← GenBank
GenBank → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
LITDB ← PMD → PIR → GenBank
LITDB ← PRF → PIR → GenBank
LITDB ← PMD → PIR → EMBL
LITDB ← PRF → PIR → EMBL
LITDB ← PMD → PIR ← SWISS-PROT

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
LITDB ← PRF → PIR ← SWISS-PROT
LITDB ← PMD → PIR
LITDB ← PRF → PIR
LITDB ← PRF
LITDB ← PMD → PDB
LITDB ← PMD → PIR → ENZYME
LITDB ← PRF → ENZYME
LITDB ← PMD → PIR → ENZYME → PATHWAY
LITDB ← PRF → ENZYME → PATHWAY
LITDB ← PMD
LITDB ← AAindex
MEDLINE ← EMBL
MEDLINE ← GenBank
MEDLINE ← PDB
MEDLINE ← PIR
MEDLINE ← PRF
MEDLINE ← SWISS-PROT
MEDLINE ← GenBank → EMBL
MEDLINE ← SWISS-PROT → EMBL
MEDLINE ← SWISS-PROT → PDB
MEDLINE ← PRF → PDB
MEDLINE ← PRF → PDB ← PDBSTR
MEDLINE ← SWISS-PROT → PDB ← PDBSTR
MEDLINE ← SWISS-PROT → PROSITE
MEDLINE ← SWISS-PROT → OMIM
MEDLINE ← PIR → ENZYME
MEDLINE ← PIR ← PMD
MEDLINE ← PRF ← PMD
* Factual Links
OMIM ← SWISS-PROT → PIR → GenBank
OMIM ← ENZYME ← GenBank
OMIM ← SWISS-PROT → EMBL
OMIM ← SWISS-PROT
OMIM ← SWISS-PROT → PIR
OMIM ← SWISS-PROT → PIR ← PRF
OMIM ← SWISS-PROT → PDB
OMIM ← ENZYME → PDB
OMIM ← SWISS-PROT → PDB ← PDBSTR
OMIM ← ENZYME → PDB ← PDBSTR
OMIM ← SWISS-PROT → PROSITE
OMIM ← ENZYME
OMIM ← SWISS-PROT → ENZYME
OMIM ← SWISS-PROT → PIR → ENZYME
OMIM ← ENZYME → PATHWAY
OMIM ← SWISS-PROT → PIR ← PMD
OMIM ← ENZYME ← PIR ← PMD
OMIM ← SWISS-PROT → PDB ← PMD

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
OMIM ← ENZYME → PDB ← PMD
OMIM ↔ OMIM
OMIM ← SWISS-PROT → MEDLINE
OMIM ← GDB
OMIM ← ENZYME ← E.coli
OMIM ← ENZYME ← H.influenzae
OMIM ← ENZYME ← B.subtilis
OMIM ← ENZYME ← M.genitalium
OMIM ← ENZYME ← M.pneumoniae
OMIM ← ENZYME ← M.jannaschii
OMIM ← ENZYME ← Synechocystis
OMIM ← ENZYME ← S.cerevisiae
OMIM ← H.sapiens
OMIM ← ENZYME ← H.sapiens
* Factual Links
TEMPLATE → ENZYME ← GenBank
TEMPLATE → SWISS-PROT → EMBL → GenBank
TEMPLATE → ENZYME ← EMBL
TEMPLATE → SWISS-PROT
TEMPLATE → ENZYME ← PIR
TEMPLATE → ENZYME ← PRF
TEMPLATE → ENZYME ← PDB
TEMPLATE → ENZYME ← PDBSTR
TEMPLATE → ENZYME
TEMPLATE → ENZYME → COMPOUND
TEMPLATE → ENZYME → PATHWAY
* Sequence Similarity Links
TEMPLATE → nr-aa
* Biological Links
TEMPLATE → ENZYME ← (PATHWAY) → ENZYME ← TEMPLATE
TEMPLATE → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
PATHWAY ← ENZYME ← GenBank
PATHWAY ← ENZYME ← EMBL
PATHWAY ← ENZYME ← SWISS-PROT
PATHWAY ← ENZYME ← PIR
PATHWAY ← ENZYME ← PDB
PATHWAY ← ENZYME ← PDBSTR
PATHWAY ← ENZYME → PROSITE
PATHWAY ← ENZYME
PAHTWAY ← ENZYME ← PMD
PATHWAY ← ENZYME → OMIM
PATHWAY → WIT-PATHWAY
PATHWAY → ENZYME ← E.coli
PATHWAY → ENZYME ← H.influenzae
PATHWAY → ENZYME ← B.subtilis
PATHWAY → ENZYME ← M.genitalium

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
PATHWAY → ENZYME ← M.pneumoniae
PATHWAY → ENZYME ← M.jannaschii
PATHWAY → ENZYME ← Synechocysitis
PATHWAY → ENZYME ← S.cerevisiae
PATHWAY → ENZYME ← H.sapiens
* Factual Links
PDB → GenBank
PDB ← SWISS-PROT → EMBL → GenBank
PDB → ENZYME ← GenBank
PDB → EMBL
PDB ← SWISS-PROT → EMBL
PDB ↔ SWISS-PROT
PDB ↔ PIR
PDB ← SWISS-PROT → PIR
PDB ← PRF
PDB ↔ PDB
PDB ← PDBSTR
PDB ← PROSITE
PDB ↔ ENZYME
PDB ← SWISS-PROT → ENZYME
PDB → ENZYME → PATHWAY
PDB ← PMD
PDB ← SWISS-PROT → OMIM
PDB → MEDLINE
PDB ← SWISS-PROT → MEDLINE
PDB → ENZYME ← E.coli
PDB → ENZYME ← H.influenzae
PDB → ENZYME ← B.subtilis
PDB → ENZYME ← M.genitalium
PDB → ENZYME ← M.pneumoniae
PDB → ENZYME ← M.jannaschii
PDB → ENZYME ← Synechocystis
PDB → ENZYME ← S.cerevisiae
PDB → ENZYME ← H.sapiens
* Biological Links
PDB → ENZYME ← (PATHWAY) → ENZYME ← PDB
PDB → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
PDBSTR → PDB ← SWISS-PROT → EMBL → GenBank
PDBSTR → PDB ← SWISS-PROT → EMBL
PDBSTR → PDB ← SWISS-PROT
PDBSTR → PDB ← SWISS-PROT → PIR
PDBSTR → PDB ← SWISS-PROT → PIR ← PRF
PDBSTR → PDB
PDBSTR → PDB ← PROSITE
PDBSTR → ENZYME
PDBSTR → PDB ← ENZYME

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
PDBSTR → PDB → ENZYME → PATHWAY
PDBSTR → PDB ← PMD
PDBSTR → PDB → SWISS-PROT → OMIM
PDBSTR → PDB ← ENZYME → OMIM
PDBSTR → PDB → SWISS-PROT → MEDLINE
PDBSTR → ENZYME ← E.coli
PDBSTR → ENZYME ← H.influenzae
PDBSTR → ENZYME ← B.subtilis
PDBSTR → ENZYME ← M.genitalium
PDBSTR → ENZYME ← M.pneumoniae
PDBSTR → ENZYME ← M.jannaschii
PDBSTR → ENZYME ← Synechocystis
PDBSTR → ENZYME ← S.cerevisiae
PDBSTR → ENZYME ← H.sapiens
* Sequence Similarity Links
PDBSTR → nr-aa
* Biological Links
PDBSTR → ENZYME ← (PATHWAY) → ENZYME ← PDBSTR
PDBSTR → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
PIR → GenBank
PIR ← SWISS-PROT → EMBL → GenBank
PIR → EMBL
PIR ← SWISS-PROT → EMBL
PIR ← SWISS-PROT
PIR ↔ PDB
PIR ← SWISS-PROT → PDB
PIR → ENZYME → PDB
PIR ← PMD → PDB
PIR ↔ PDB ← PDBSTR
PIR ← SWISS-PROT → PDB ← PDBSTR
PIR ← TFFACTOR
PIR ← SWISS-PROT → PROSITE
PIR ↔ ENZYME
PIR → ENZYME → PATHWAY
PIR ← PMD
PIR → MEDLINE
PIR ← SWISS-PROT → OMIM
PIR → ENZYME ← E.coli
PIR → ENZYME ← H.influenzae
PIR → ENZYME ← B.subtilis
PIR → ENZYME ← M.genitalium
PIR → ENZYME ← M.pneumoniae
PIR → ENZYME ← M.jannaschii
PIR → ENZYME ← Synechocystis
PIR → ENZYME ← S.cerevisiae
PIR → ENZYME ← H.sapiens

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
* Sequence Similarity Links
PIR → nr-aa
* Biological Links
PIR → ENZYME ← (PATHWAY) → ENZYME ← PIR
PIR → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
PMD → PIR → GenBank
PMD → PIR → EMBL
PMD → PIR ← SWISS-PROT
PMD → PDB ← SWISS-PROT
PMD → PIR
PMD → PRF
PMD → PDB
PMD → PDB ← PDBSTR
PMD → PDB ← PROSITE
PMD → PIR ← SWISS-PROT → PROSITE
PMD → ENZYME
PMD → PIR → ENZYME
PMD → PDB ← ENZYME
PMD → PIR → ENZYME → PATHWAY
PMD → PDB → ENZYME → PATHWAY
PMD → PIR ← SWISS-PROT → OMIM
PMD → PDB ← SWISS-PROT → OMIM
PMD → PIR → ENZYME → OMIM
PMD → PDB ← ENZYME → OMIM
PMD → LITDB
PMD → PRF → MEDLINE
PMD → PIR → MEDLINE
PMD → ENZYME ← E.coli
PMD → ENZYME ← H.influenzae
PMD → ENZYME ← B.subtilis
PMD → ENZYME ← M.genitalium
PMD → ENZYME ← M.pneumoniae
PMD → ENZYME ← M.jannaschii
PMD → ENZYME ← Synechocystis
PMD → ENZYME ← S.cerevisiae
PMD → ENZYME ← H.sapiens
* Biological Links
PMD → PIR → ENZYME → PATHWAY ← ENZYME ← PIR ← PMD
PMD → PDB → ENZYME → PATHWAY ← ENZYME ← PDB ← PMD
PMD → PIR → ENZYME ← (PATHWAY) → ENZYME
PMD → PDB → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
PRF → PIR → GenBank
PRF → MEDLINE ← GenBank
PRF → PIR → EMBL
PRF → MEDLINE ← EMBL

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
PRF → PIR ← SWISS-PROT
PRF → PDB ← SWISS-PROT
PRF → MEDLINE ← SWISS-PROT
PRF → PIR
PRF → PDB
PRF → PDB ← PDBSTR
PRF → PIR ← TFFACTOR
PRF → PDB ← PROSITE
PRF → PIR ← SWISS-PROT → PROSITE
PRF → ENZYME
PRF → PIR → ENZYME
PRF → PDB → ENZYME
PRF → ENZYME → PATHWAY
PRF → PIR → ENZYME → PATHWAY
PRF → PDB → ENZYME → PATHWAY
PRF ← PMD
PRF → LITDB
PRF → MEDLINE
PRF → PIR → MEDLINE
PRF → PIR ← SWISS-PROT → OMIM
PRF → PDB ← SWISS-PROT → OMIM
PRF → PIR → ENZYME → OMIM
PRF → PDB → ENZYME → OMIM
PRF → ENZYME ← E.coli
PRF → ENZYME ← H.influenzae
PRF → ENZYME ← B.subtilis
PRF → ENZYME ← M.genitalium
PRF → ENZYME ← M.pneumoniae
PRF → ENZYME ← M.jannaschii
PRF → ENZYME ← Synechocystis
PRF → ENZYME ← S.cerevisiae
PRF → ENZYME ← H.sapiens
* Sequence Similarity Links
PRF → nr-aa
* Biological Links
PRF → ENZYME ← (PATHWAY) → ENZYME ← PRF
PRF → PIR → ENZYME ← (PATHWAY) → ENZYME ← PIR ← PRF
PRF → PDB → ENZYME ← (PATHWAY) → ENZYME ← PDB ← PRF
PRF → PIR → ENZYME ← (PATHWAY) → ENZYME
PRF → PDB → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
PROSITE ↔ SWISS-PROT → EMBL → GenBank
PROSITE ↔ SWISS-PROT → EMBL
PROSITE ↔ SWISS-PROT
PROSITE ↔ SWISS-PROT → PIR
PROSITE → PDB
PROSITE ← TFCLASS

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
PROSITE ← ENZYME
PROSITE ← ENZYME → PAHTWAY
PROSITE ↔ SWISS-PROT → OMIM
PROSITE ↔ SWISS-PROT → MEDLINE
PROSITE ↔ SWISS-PROT → EMBL → GenBank → Medline
PROSITE ← ENZYME ← E.coli
PROSITE ← ENZYME ← H.influenzae
PROSITE ← ENZYME ← B.subtilis
PROSITE ← ENZYME ← M.genitalium
PROSITE ← ENZYME ← M.pneumoniae
PROSITE ← ENZYME ← M.jannaschii
PROSITE ← ENZYME ← Synechocystis
PROSITE ← ENZYME ← S.cerevisiae
PROSITE ← ENZYME ← H.sapiens
* Biological Links
PROSITE ← ENZYME ← (PATHWAY) → ENZYME → PROSITE
PROSITE ← ENZYME ← (PATHWAY) → ENZYME
* Factual Links
SWISS-PROT → EMBL → GenBank
SWISS-PROT → PIR → GenBank
SWISS-PROT ↔ EMBL
SWISS-PROT → PIR
SWISS-PROT → PIR ← PRF
SWISS-PROT ↔ PDB
SWISS-PROT ↔ PDB ← PDBSTR
SWISS-PROT ↔ TFFACTOR
SWISS-PROT ↔ PROSITE
SWISS-PROT → ENZYME
SWISS-PROT → ENZYME → PATHWAY
SWISS-PROT → PIR ← PMD
SWISS-PROT → MEDLINE
SWISS-PROT → PIR → GenBank → MEDLINE
SWISS-PROT → OMIM
SWISS-PROT ← TDB
SWISS-PROT ← SacchDB
SWISS-PROT ← ACeDB
SWISS-PROT ← MGD
SWISS-PROT → ENZYME ← E.coli
SWISS-PROT → ENZYME ← H.influenzae
SWISS-PROT → ENZYME ← B.subtilis
SWISS-PROT → ENZYME ← M.genitalium
SWISS-PROT → ENZYME ← M.pneumoniae
SWISS-PROT → ENZYME ← M.jannaschii
SWISS-PROT → ENZYME ← Synechocystis
SWISS-PROT → ENZYME ← S.cerevisiae
SWISS-PROT → ENZYME ← H.sapiens
* Sequence Similarity Links

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
SWISS-PROT → nr-aa
* Biological Links
SWISS-PROT → ENZYME ← (PATHWAY) → ENZYME ← SWISS-PROT
SWISS-PROT → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
SWISS-PROT → EMBL → GenBank
SWISS-PROT → PIR → GenBank
SWISS-PROT ↔ EMBL
SWISS-PROT → PIR
SWISS-PROT → PIR ← PRF
SWISS-PROT ↔ PDB
SWISS-PROT ↔ PDB ← PDBSTR
SWISS-PROT ↔ TFFACTOR
SWISS-PROT ↔ PROSITE
SWISS-PROT → ENZYME
SWISS-PROT → ENZYME → PATHWAY
SWISS-PROT → PIR ← PMD
SWISS-PROT → MEDLINE
SWISS-PROT → PIR → GenBank → MEDLINE
SWISS-PROT → OMIM
SWISS-PROT ← TDB
SWISS-PROT ← SacchDB
SWISS-PROT ← ACeDB
SWISS-PROT ← MGD
SWISS-PROT → ENZYME ← E.coli
SWISS-PROT → ENZYME ← H.influenzae
SWISS-PROT → ENZYME ← B.subtilis
SWISS-PROT → ENZYME ← M.genitalium
SWISS-PROT → ENZYME ← M.pneumoniae
SWISS-PROT → ENZYME ← M.jannaschii
SWISS-PROT → ENZYME ← Synechocystis
SWISS-PROT → ENZYME ← S.cerevisiae
SWISS-PROT → ENZYME ← H.sapiens
* Sequence Similarity Links
SWISS-PROT → nr-aa
* Biological Links
SWISS-PROT → ENZYME ← (PATHWAY) → ENZYME ← SWISS-PROT
SWISS-PROT → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
Synechocystis → ENZYME ← GenBank
Synechocystis → SWISS-PROT → EMBL → GenBank
Synechocystis → ENZYME ← EMBL
Synechocystis → SWISS-PROT
Synechocystis → ENZYME ← PIR
Synechocystis → ENZYME ← PRF
Synechocystis → ENZYME ← PDB
Synechocystis → ENZYME ← PDBSTR

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
Synechocystis → ENZYME
Synechocystis → ENZYME → COMPOUND
Synechocystis → ENZYME → PATHWAY
* Sequence Similarity Links
Synechocystis → nr-aa
* Biological Links
Synechocystis → ENZYME ← (PATHWAY) → ENZYME ← Synechocystis
Synechocystis → ENZYME ← (PATHWAY) → ENZYME
* Factual Links
TFCELL ← TFSITE → EMBL → GenBank
TFCELL ← TFSITE → EMBL
TFCELL ← TFSITE → EMBL → SWISS-PROT
TFCELL ← TFSITE → EMBL → SWISS-PROT → PDB
TFCELL ← TFSITE
TFCELL ← TFSITE → TFFACTOR
TFCELL ← TFSITE → TFFACTOR ← TFCLASS
TFCELL ← TFSITE → TFFACTOR ← TFMATRIX
TFCELL ← TFSITE → EMBL → SWISS-PROT → PROSITE
TFCELL ← TFSITE → TFFACTOR ← TFCLASS → PROSITE
TFCELL ← TFSITE → EMBL → SWISS-PROT → OMIM
TFCELL ← TFSITE → EMBL → SWISS-PROT → MEDLINE
TFCELL ← TFSITE → EMBL → GenBank → MEDLINE
* Factual Links
TFCLASS → TFFACTOR → EMBL → GenBank
TFCLASS → TFFACTOR → EMBL
TFCLASS → TFFACTOR → SWISS-PROT
TFCLASS → TFFACTOR → SWISS-PROT → PIR
TFCLASS → TFFACTOR
TFCLASS → PROSITE
TFCLASS → TFFACTOR → SWISS-PROT → OMIM
TFCLASS → TFFACTOR → SWISS-PROT → MEDLINE
TFCLASS → TFFACTOR → EMBL → GenBank → MEDLINE
* Factual Links
TFFACTOR → → EMBL → GenBank
TFFACTOR → EMBL
TFFACTOR ↔ SWISS-PROT
TFFACTOR → PIR
TFFACTOR → SWISS-PROT → PDB
TFFACTOR ↔ TFFACTOR
TFFACTOR ↔ TFSITE
TFFACTOR ← TFCLASS
TFFACTOR ↔ TFMATRIX
TFFACTOR → SWISS-PROT → PROSITE
TFFACTOR ← TFCLASS → PROSITE
TFFACTOR → SWISS-PROT → OMIM
TFFACTOR → SWISS-PROT → MEDLINE
TFFACTOR → EMBL → GenBank → MEDLINE

表 3.8: (continued)

LinkDB 検索によるデータベースの経路一覧
* Factual Links
TFMATRIX → TFFACTOR → EMBL → GenBank
TFMATRIX → TFFACTOR → EMBL
TFMATRIX → TFFACTOR → SWISS-PROT
TFMATRIX → TFFACTOR → SWISS-PROT → PIR
TFMATRIX ↔ TFFACTOR
TFMATRIX → TFFACTOR → SWISS-PROT → OMIM
TFMATRIX → TFFACTOR → SWISS-PROT → MEDLINE
TFMATRIX → TFFACTOR → EMBL → GenBank → Medline
* Factual Links
TFSITE → EMBL → GenBank
TFSITE ↔ EMBL
TFSITE → EMBL → SWISS-PROT
TFSITE → EMBL → SWISS-PROT → PDB
TFSITE ↔ TFFACTOR
TFSITE → TFFACTOR ← TFCLASS
TFSITE → TFFACTOR → TFMATRIX
TFSITE → TFFACTOR ← TFCLASS → PROSITE
TFSITE → EMBL → SWISS-PROT → OMIM
TFSITE → EMBL → SWISS-PROT → MEDLINE
TFSITE → EMBL → GenBank → MEDLINE

3.5.4 WWW 版統合化システム

WebDBGETserver では、これらに加えて他の Web 上のツールとの統合化を図っている。例えば、データベース配列に対し相同性検索や MOTIF 検索 [39] を行った後に、すぐさまそのエントリーを取得するには結果のエントリー名を DBGET へ *bget* による取得要求を行えば良い。さらに、この取得したエントリーの配列を元に新たな相同性検索を行うことも可能であり、見方を変えれば、相同性検索もリンクの一つとして見做すことができる。従って、WebDBGETserver では相同性検索によるリンクをエントリー検索後からでも行うことができるようになっている。

3.5.5 リンクの拡張的検索による推論

我々は必要に応じて、どのデータベースのどの種類のリンク（ファクト、相同性、生物学的）がどの順番で組み合わせれば、より良い情報が得られるかを経験的に知っていることがある。例えば、図 3.3 に示したように、自分が知りたいことが、自分の持っている分子の反応パートナーなどであれば、まず、近縁種で相同性リンクを辿り、次にその結果から生物学的リンクによってその近縁種での反応

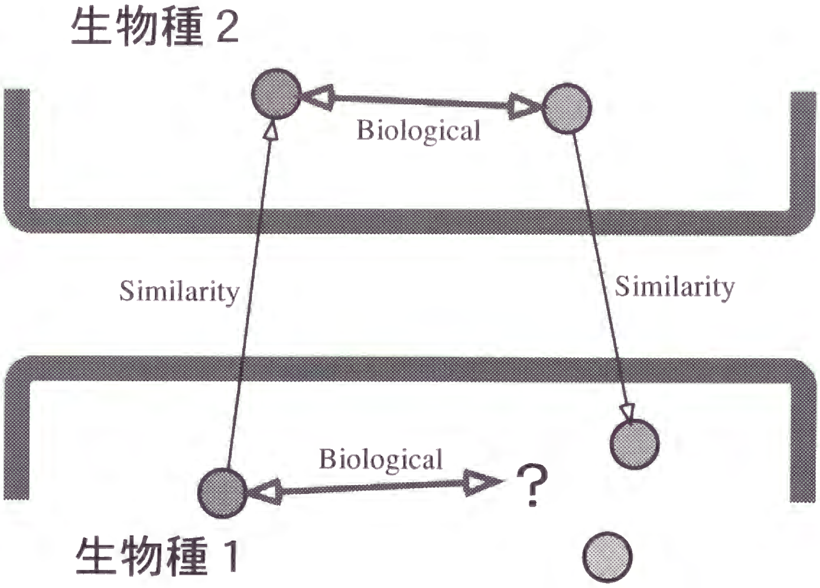


図 3.3: **リンクの組み合わせによる推論** 生物種1のある分子の反応分子がわからない場合に、生物種2の生物学リンクを使って推論を行う。

分子を見つけ、さらに手元のデータベースに対して相同性リンクを逆に辿るようにすれば、手元の分子の反応物の候補が得られるであろう。

LinkDB の統合検索では、この様な有効な経路をテーブルとして、相同性リンクも含めて、定義することが可能であり、逆にこの定義により、より情報の低い、無駄な経路を検索することを省略することが可能である。表3.9 に示したのは、*Eco* の遺伝子を出発点にし、まず、ゲノム位置に関する生物学リンクを辿る（上の行）

database	**route**
Eco	b(genome position)
Eco	s(*Hin*):b(genome position):s(*Eco*)

表 3.9: **経路テーブルによるリンク方法の指定** 一行目は *Eco* でのゲノム位置に対する生物学的リンク（b）を検索し、二行目は *Hin* に対する相同性リンク（s）を検索した結果を生物学リンクを検索してまた *Eco* に対して相同性リンクを検索しに戻ってくるものである。

ものと、*Hin* に対して相同性リンク検索を行い、そこからゲノム位置を辿り、見つかった隣の遺伝子をもとにして、今度は逆に *Eco* に対して相同性検索を行って

その対応する遺伝子を抽出する（下の行）を定義してある。

この経路テーブルを使用することで、リンクの手順がはじめから指定でき、この上と下の行の結果を比較して、一致するものがあれば、その遺伝子群はクラスターを形成していると見做すことができるものである。

3.6 考察

3.6.1 構成上の利点

著者は統合データベースシステムの開発を通じて、存在する種々様々なデータベース中を関連するエントリー間のリンクを辿る緩い統合方式により、既存の個々の生物学データを同じプラットフォーム上で検索できることを可能にした。このことは、新たなデータベースを追加する場合にも、データベースの構成を考えずに済むので、追加が簡単であるという利点がある。また、既に統合されているデータベースのデータ構成が変ってもそのデータベースに関する部分だけの最小限の修正で済むと考えられる。このことは、今後ますます増加する完全ゲノム配列を同じように簡単に追加できることを意味しており、配列決定プロジェクトに入っている生物種の量、種類の豊富さから考えても、わずかなデータ形式の違いが発生し、従来の関係データベース方式では破綻しそうなデータの追加がた易く行えるものと期待できる。

3.6.2 リソース上の利点

また、緩い統合化のため、指数的に増え続けるデータベースの量に対しても時間の問題を克服できる。GenBank(103.0) は現在のところ 5GB の膨大なデータ量を持つが、これが CPU 時間にしてわずか 8 時間足らずでインデックス化できることは、非常に大きな利点である。

さらに、時間的な面だけでなく、ディスク容量的な面でもこの統合化は優れている。GenBank(103.0) ではインデクスファイルが本体の大きさの約五分の一程度ですむことは全体を作り替えることでデータを保持する関係データベースの方式よりも有利である。しかもこれは、データベースが大きくなっても、本体との割合はそれほど変らないはずであり、将来的にも期待がもてる。

3.6.3 ネットワークとデータベース

これまでデータベースは一つの計算機上にあるサーバーにクライアントが見に行くようなイメージであったが、今後は分散サーバーへと次第に移り変わっていくことが考えられる。これは、一つにはもちろん単純にデータベースの量の増加の問題もあるが、同時に多様化するデータベースを同じ地域で管理できないことも考えられるからである。例えば、バクテリアに関するデータベースは、関西におき、植物に関するデータベースは関東におき、動物は九州におく、などといった分散型のデータベース形態をとる可能性がある。これが多種多様化した時に、全体を統合的に検索するのにこの DBGET/LinkDB があたかも一つのサーバーを利用しているかのようにユーザーには見えるので非常に有効である。言い換えるなら、データベース自身が多様化しているが、その所在も多様化しており、各研究者がネットワークで繋がったデータベースを解放し、リンクで繋げることが、本当の意味での生物学データの統合処理に繋がるのではないだろうか。

3.6.4 リンクと生物学との関連

これまでそうであったように、生物学は知識の集大成が必要となる学問である。人間の脳は幸いにもこれらの様々な知識についても同様に一度に考えることが可能であり、関連する事象を思い付くことがしばしばある。計算機でこれをするには思いきった単純化が必要であり、ここで全ての意味の関係をただ「リンク」という概念に置き換えたことは第一次的な概念の近似としては優れたものであると思われる。

しかしながら、実際に我々の脳が考えていることには、ただ単に「関連がある／ない」の二状態だけではなくて、「どの程度」関連があるか、や「どう言った観点から」関連があると言えるのか、と言ったような関連に対して、重みや評価の物差しを取り替えることが可能である。あまり難しいシステムにすると統合化が逆に困難になっていくが、少しずつこの様な「重み付け」などを取り入れたリンク検索にしていくことが、ノイズの情報からより有益な情報を選択するのに有効になると考えられる。しかし、もちろん情報の選択は情報を落とすことにもなりかねない問題は抱えている。

3.6.5 リンクの経路の学習について

現実問題として、我々が何かデータベースから情報を取り出そうとすると、どのような検索をすればよいか、を頭の中で計画し、それを実行する、と言うこと

を行っているが、この計画立てにはまさに適切なリンクを辿るなどのことを行っていると考えられる。この様に、我々が何かの情報を得たい時に、その考える経路を計算機に学習させて、そこから次の問題が来たときに推論させることが可能であると考えられる。これは、人工知能や、agentと言った分野と関連して、以後ますます発展していくに違いないと思われ、最終的には人間が考えるプロセスにダイレクトに迫る研究へとこの生物学データベースの検索は繋がっていくものと考えられる。今後の研究に最も期待が持てる一面であることには間違いないであろう。

第4章　結果２：遺伝子クラスターの抽出とオペロン予測

4.1　序論

機能的に関連している遺伝子を、ゲノム上に近接して配置しようとすることは、遺伝子発現調節の一つとして、広い範囲の生物で観察されていることである。その最も顕著な例は、バクテリアに見られるオペロンであり、うまく同調して遺伝子が機能するためには、転写単位を同じくすることが有利だったと考えられるものである。

ここ二、三年の間に、ゲノム構造に関する論文が数多く出されてきている。例えば、*Eco* と *Hin* のそれぞれのゲノム上で、機能的に近い遺伝子は、そうでない遺伝子に比べ、ゲノム上に隣接して並んでいる事が、確率的に有意に高い事を示す論文が報告されている [49]。また、五種のバクテリアゲノム中で、遺伝子クラスターの並びを比較したところ、古細菌を除く四種のバクテリアで、共通な１６クラスターの遺伝子の並びが保存されていることがみつかり、古細菌を入れた五種ではそのうち８クラスターが保存されていたということが報告されている [45]。他の論文では、*Eco* と *Hin* の比較からゲノム構造はダイナミックに変化しており、オペロン構造も壊れるケースがしばしば存在する、との報告がある [50, 52]。

しかし、これらの遺伝子クラスターが存在するという報告はあるものの、まだ多くの疑問が残されている。例えば、遺伝子クラスターはどのバクテリアにも同じように存在するのか、クラスターを形成する遺伝子に特徴はあるのか、どうやってクラスターはできてきたのかなどである。また、ゲノムの水平移動（horizontal transfer）に関しての論文もたくさんあり、*Bsu* の完全ゲノムの論文中 [34] でも水平移動によってやってきたと思われるような遺伝子群が解析されている。さらに、これらの遺伝子クラスターが単位になった機能単位で遺伝子群を獲得すれば、進化が加速され、種の分化にも繋がるのではないか、と言った論文まである [35, 36]。

一方、オペロンが同定できることは、実験者にとって、非常に重要であるが、現在、オペロン予測の話となると、良い方法があるわけではない。例えば、ターミネーター予測に基づく方法は、ρ 因子非依存型のものだけに限り [13, 9, 8]、しか

も大腸菌の場合で実験的な解析が進んでいるので、学習セットが大腸菌のものになってしまい、殆んど大腸菌に似た生物種でしか予測を行うことができない。

著者は、これらの背景を念頭におきながら、オペロン予測へ向けての予備的な研究として、DBGET/LinkDB 統合検索を用いて、１０生物種から総当たりで共通に存在する遺伝子クラスターを抽出し、その特徴を解析した。実際には、効率化を図るため、連続で DBGET/LinkDB を起動し、遺伝子クラスター検索ができるような perl 言語によるスクリプトを書いて解析を行っている。

4.2　相同性遺伝子の密度解析

始めに、相同性リンクによる閾値を FASTA の opt 値 80 以上と定めたが、このことによって、種間による相同性遺伝子の見つけられ方が、どのように異なっているのかを検討した。図 4.1(a) に示したように、*Mge* と *Hpy* から見つけられる相同性遺伝子をドットマトリックスで表現すると（左)、*Mge* と *Mpn* から見つけられるそれら（中央）とは、密度的に異なっていることが認識される。

4.2.1　種内でのパラログの傾向

Mge の自己ゲノム内で見つかる相同性遺伝子についても図中に示してある（右)。そこでは、同一遺伝子をプロットしている相同性に当たる対角線がくっきりと浮かび上がっている。この図では、対角線がところどころ切れたようになっているが、相同性検索は ORF 部分にだけかけているのに対し、ゲノム上の RNA をコードしている部分も同時に示しているためである。種内の相同性遺伝子ではどれもこの図と似た傾向を示した。

4.2.2　種間でのホモログの傾向

また、種間比較による相同性遺伝子の分布は、通常、*Mge-Hpy* のようになり、一カ所だけに長いクラスターが見つかることが殆んどである（マトリックスの右の部分)。エントリーを調べてみると、これは、リボソーム蛋白質（群）であると同定される。しかし、他のどのマトリックスとも違っていたことは、、この図（中）に示したように *Mge-Mpn* では、非常に長い領域に渡って相同性遺伝子のクラスターが並び、ゲノムが殆んど同じ構成であることがわかった。さらに良く見ると、大きくゲノムの部分同士の入れ替わり（転座）があったのが見られ、また *Mpn* の方がゲノムが長い分だけ部分部分に挿入があり、対角線が少しずつずれたように

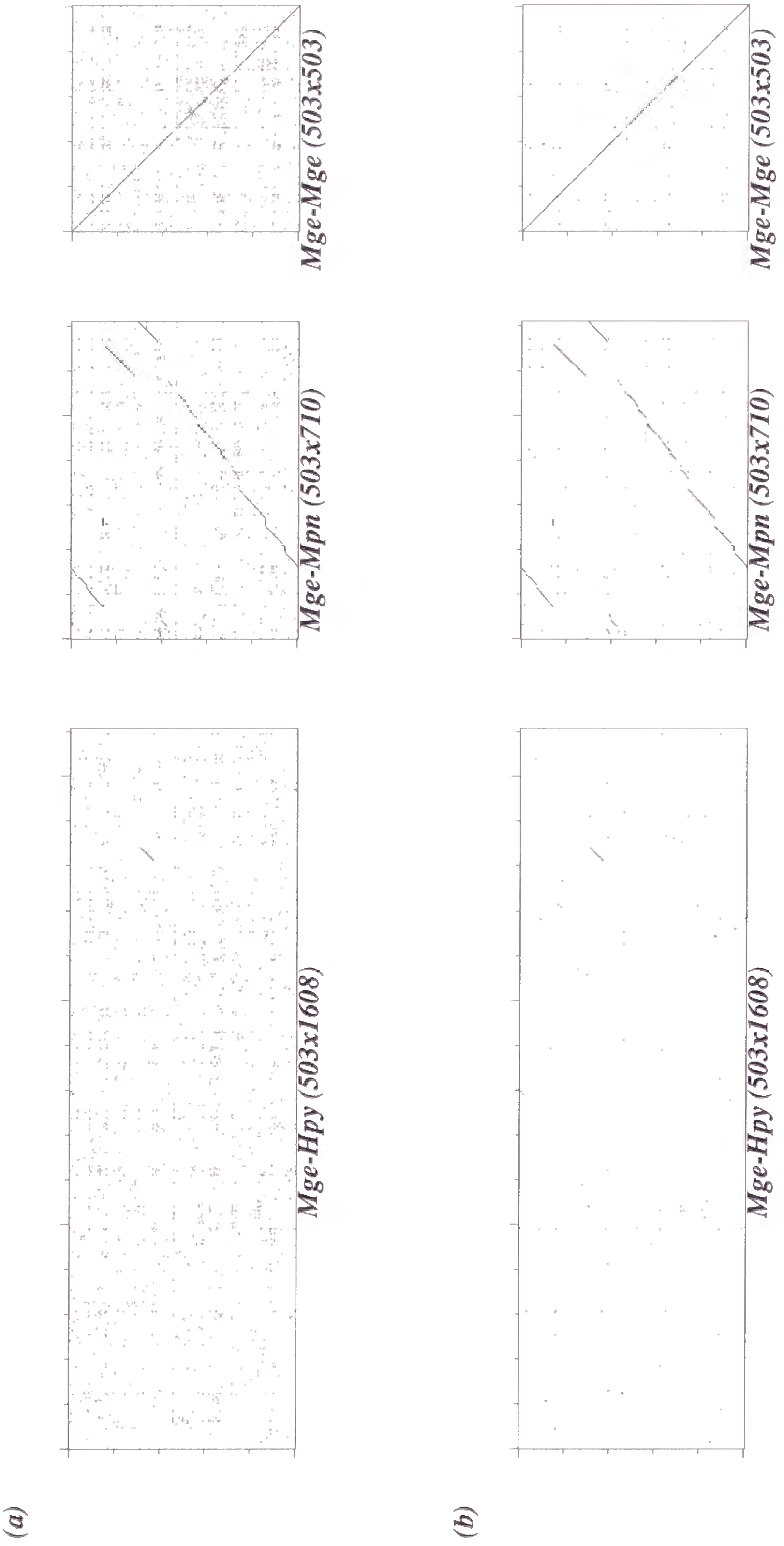


図 4.1: **相同性の密度解析および遺伝子クラスターのスクリーニングの様子** 軸はゲノム上の遺伝子の順番を表わし、ドットは相同性のあったORFを記した。遺伝子クラスターのスクリーニング前（a）と後で（b）は殆んどのドットが消えてしまう。

なっているのが見られた。

4.2.3 スクリーニングによる遺伝子クラスターの特徴

図4.1(b)では、この相同性検索の結果から斜め方向に連続で出現する相同性遺伝子の組をクラスターとして残して表示したものである。これによると、先ほどの点の大部分が単独で出現していたため消えてしまい、クラスターになっているところだけが残っているのが確認できる。

また、場合によってはクラスター間の相同性がとれたものが、一対一ではなく一対多になる場合もある。このような種間でクラスターのパラログにも注意して以後の解析を行った。

4.3 遺伝子クラスターの抽出

抽出されたクラスターを先ほど述べた一対多になっている場合の重複を除いて表にしたものが、表4.1である。例えば、*Eco*を軸にして相手の生物種と比較したときに抽出されるクラスターは、三行目を見ることになり、*Hin*との比較による抽出数は528だが、逆に*Hin*を*Eco*と比較して*Hin*から抽出したクラスター数は四行三列目の409になる。

Organisms (ORFs)	*Mja*	*Mth*	*Eco*	*Hin*	*Hpy*	*Bsu*	*Mge*	*Mpn*	*Syn*	*Sce*	All
Mja(1681)	401	186	91	64	100	138	55	38	61	140	723
Mth(1871)	198	267	140	76	55	142	25	28	98	56	629
Eco(4289)	136	190	835	528	208	602	108	132	388	169	1788
Hin(1717)	68	78	409	159	117	227	68	78	135	81	757
Hpy(1566)	106	59	129	107	227	175	66	75	84	200	650
Bsu(4100)	183	202	571	280	224	767	120	146	324	303	1574
Mge(467)	59	27	67	61	66	91	78	119	56	98	320
Mpn(678)	49	27	79	69	70	104	150	222	62	118	496
Syn(3166)	74	122	326	146	105	266	64	73	447	158	978
Sce(6064)	170	72	171	98	324	338	204	195	197	2431	2831

表 4.1: **冗長性を除いた抽出クラスターの数**

4.3.1 種内で保存されているクラスター

自己ゲノムと比較することにより、相同性遺伝子（パラログ）とそれらがクラスターになっている部分の数を調べ、次の式4.1によって遺伝子密度をとったものを、図4.2に示した。

$$\text{相同性密度} = \frac{\text{ホモログ遺伝子}}{\text{遺伝子数}^2} \tag{4.1}$$

これを見ると、明らかにもとから相同性遺伝子の密度が高い生物が確認できる。例えば、*Mge, Mpn, Mja, Sce* は自分の中に比較的パラログを見つけやすいゲノムであると言えるのではないだろうか。しかも、*Sce* だけは例外であるが、これはどうやらゲノムが小さくなると、パラログが見つけやすくなっている傾向がある。言い換えると、小さいゲノムになっても、必要なパラログで存在する遺伝子の絶対数は変らないことにより、密度が高くなって残ってくるとも言えるのではないだろうか。そう考えると、今度は *Mja* と *Hpy* ではゲノムサイズが殆んど変らないのに、*Hpy* の遺伝子密度はずっと低いことは特徴的である。

また、全く逆に *Sce* ゲノムのように大きくなるときにもパラログ密度が高まっている。

しかしながら、これがクラスターになりやすいかどうかを見てみると、*Mpn* だけがそれ以外の生物種に比べ、クラスター密度が高い。逆に、*Mja* や *Sce* では単独遺伝子の密度に比べて、クラスターの密度が低い傾向が見られている。

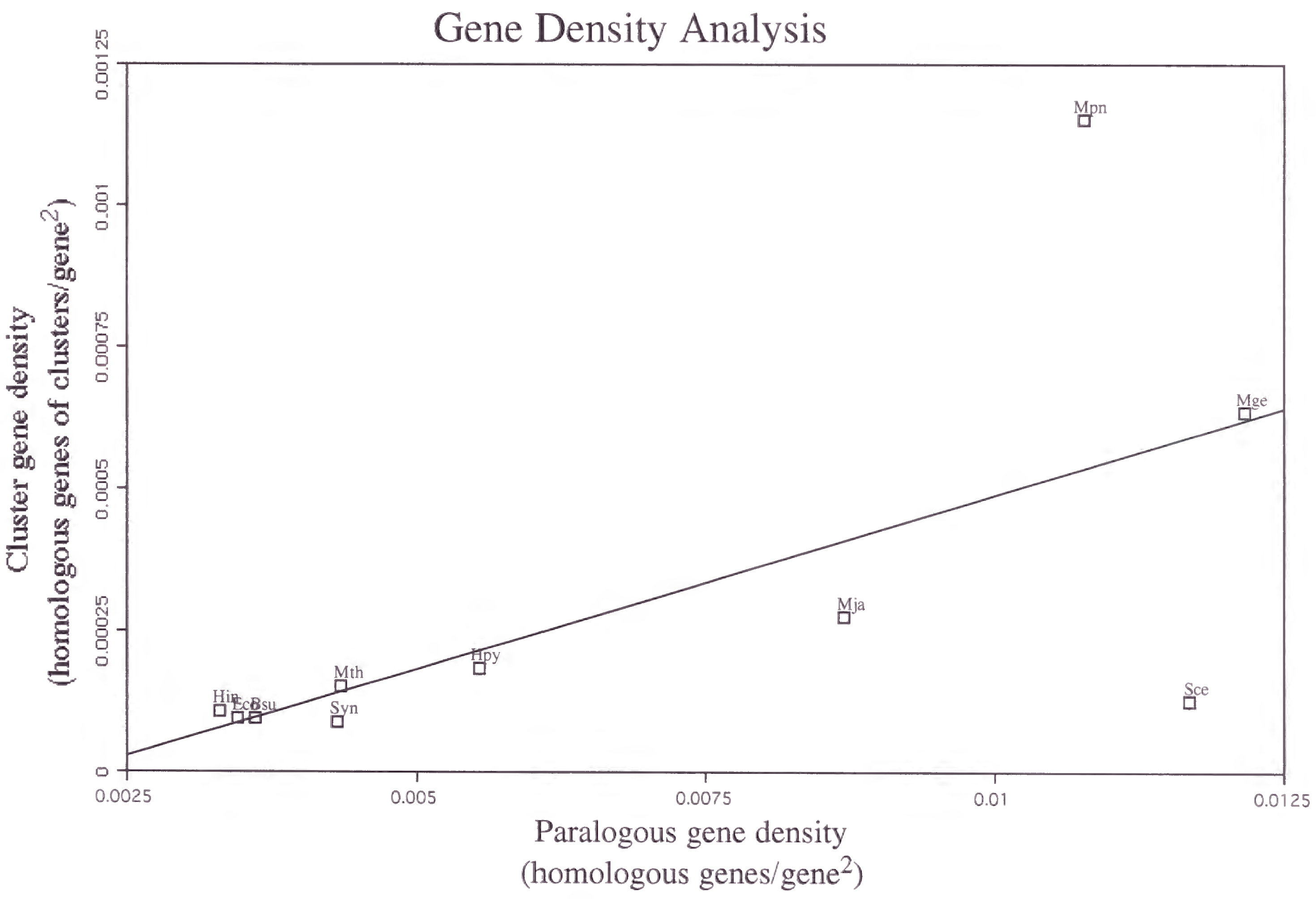


図 4.2: 遺伝子密度解析によるクラスターの抽出

4.3.2 種間で保存されているクラスター

種内でパラログの出現数を念頭におきながら、今度は種間でどの程度クラスターが抽出できるのかを解析した。ここでは、表4.1の場合と同じように、パラログのクラスター数の重複を除くため、同じクラスターは一度しか数えない方式で抽出してある。

抽出数の比較

生物の分類ごとに五つにまとめて図4.3には示した。それらは、(a)古細菌、(b)グラム陰性細菌、(c)グラム陽性細菌、(d)シアノバクテリア、(e)酵母、である。また、同時にゲノム上の遺伝子を切り混ぜて（シャフリングして）みることで、ランダムな配置をしたときに期待されるカウント数を同時にプロットして評価の基準とした。シャフリングは１０回行い、その平均値をプロットし、その時の標本標準偏差の3倍（3s）の幅を同時に図中に示してある。

古細菌　全体に共通な一般的な傾向としては、近縁種間で抽出したクラスター数はランダムに期待される数よりもかなり多いようである。*Mja* は同じ古細菌でも *Mth* と違い、自己ゲノム内でクラスターが少ない。これは、先ほどの密度解析の結果とも一致している。

グラム陰性菌　グラム陰性菌をみると、*Eco* と *Hin* は知られているように、かなりの近縁種であり、共通のクラスターをたくさん含んでいるが、*Hpy* はそれほどでもなく、*Bsu* などグラム陽性菌に対してもグラム陰性菌と同じ程度の共通クラスターを持つ。自己ゲノム内パラログは *Eco-Eco* が *Hin-Hin* よりもずっと多いことが観察される。これは恐らく、遺伝子密度解析で、相同遺伝子そのものの密度はさほど変らなかったことから、*Eco* のゲノムサイズが *Hin* のそれより二倍以上であることに起因していると考えられるであろう。また、*Hpy* においては、*Hin* とそれほどゲノムサイズで変りがないのに、全体的に抽出したクラスター数が少ない。また、*Mja* と *Mge* とのクラスターが特に少ないことが特徴として現れている。

グラム陽性菌　グラム陽性菌では、グラム陽性菌どうしの *Bsu* と *Mge* と *Mpn* の間でクラスターが多く抽出されているのが観察されていること以外には、どの他の生物種に対してもほぼ同じ程度の共通クラスターが抽出されたのみであった。変っていたことは、*Sce* との種間でのクラスター数が 3s より外側に大きくはずれた

のは、*Sce* を除く全9生物種の中で *Bsu* の時だけであった。自己クラスターでは *Mge-Mge* の時に特に抽出できたクラスターが少なかった。

シアノバクテリア　シアノバクテリアではどの生物種に対しても共通なクラスターがよく見られたが、ゲノムサイズが大きな割には、全体的にどの他のゲノムに対しても共通のクラスターは幾分少なめな傾向がある。これは、やはりシアノバクテリアは光合成を行うためにかなりゲノムの構成が違っているのではないかと考えられる。

酵母　酵母においては自己パラロググクラスターが非常に多く、ゲノムサイズが大きいにもかかわらず、他の生物種との間では比較的少ないクラスターしか拾えていない。

(a) Archaea

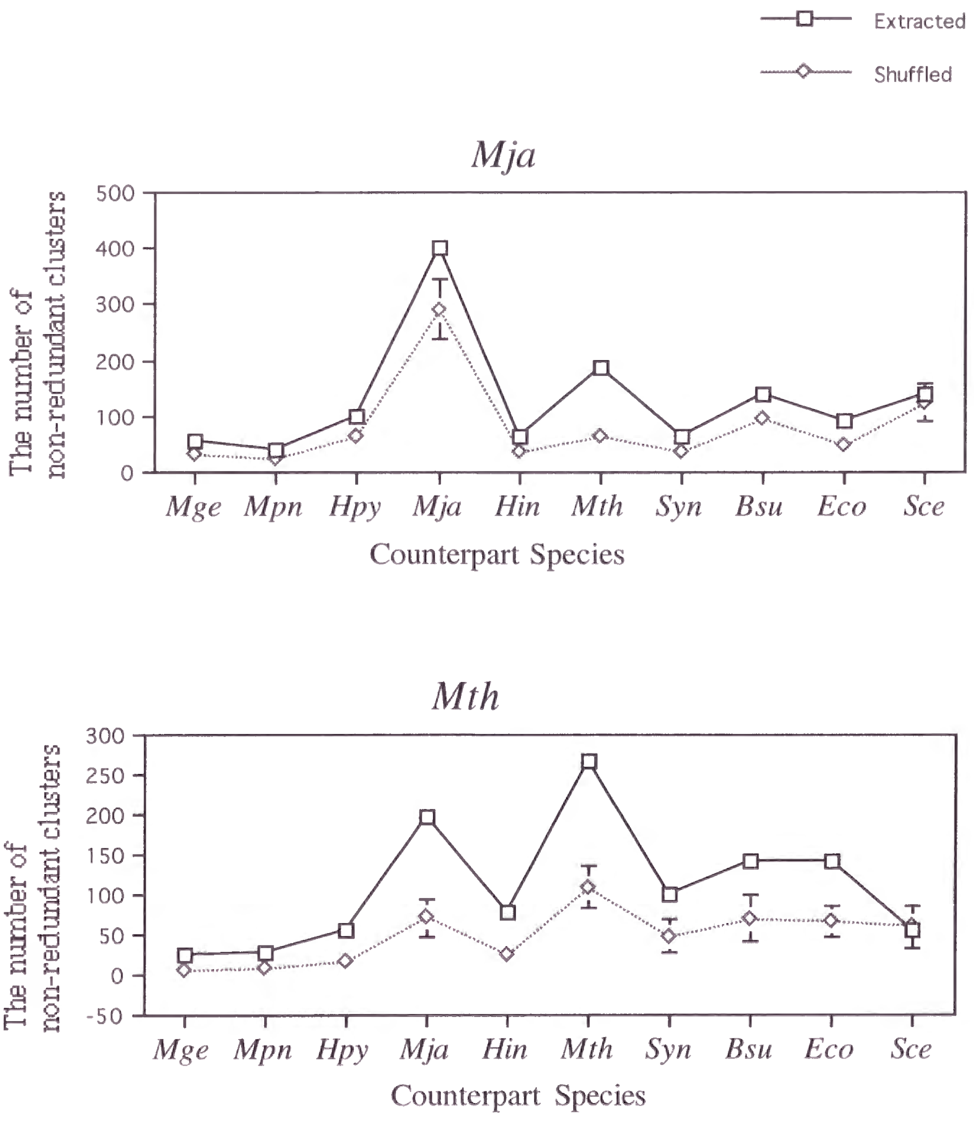
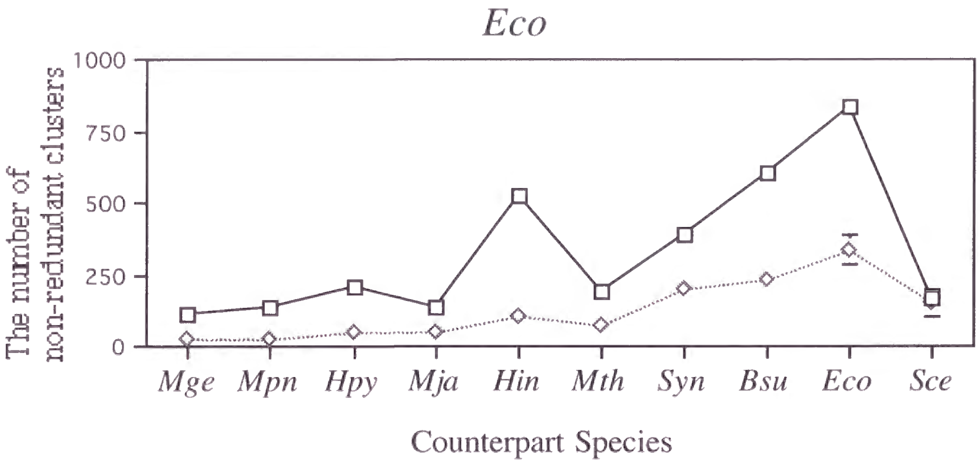
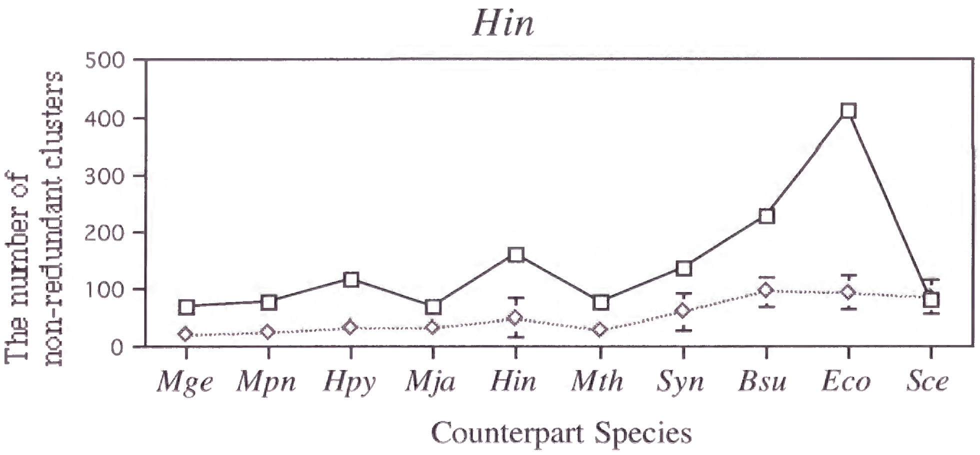
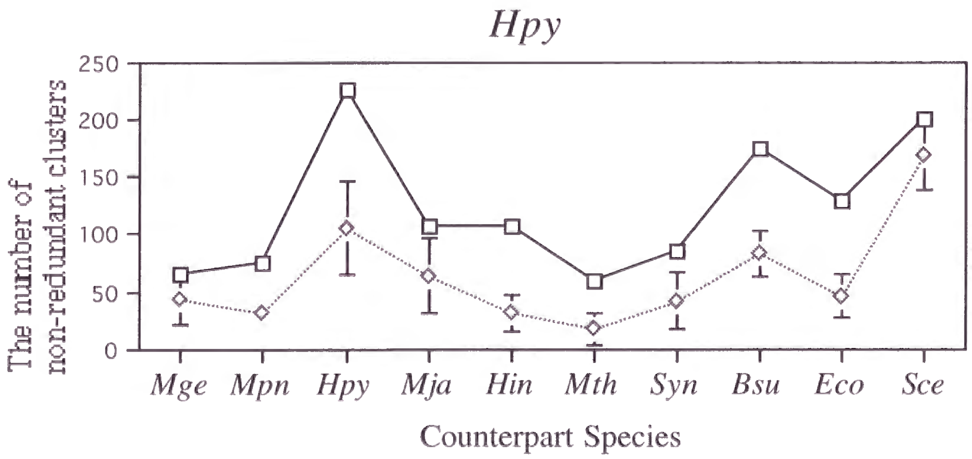


図 4.3: 遺伝子クラスターの抽出数の分布

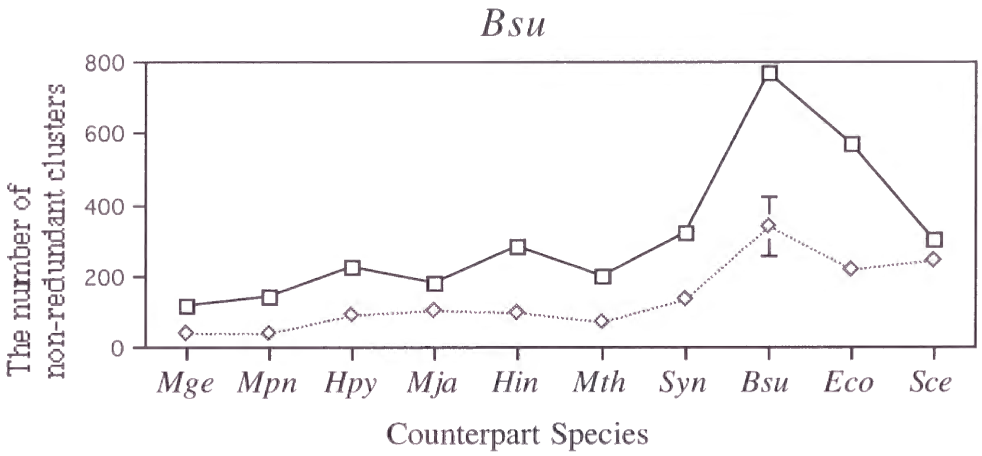
(b) Gram-negative Bacteria

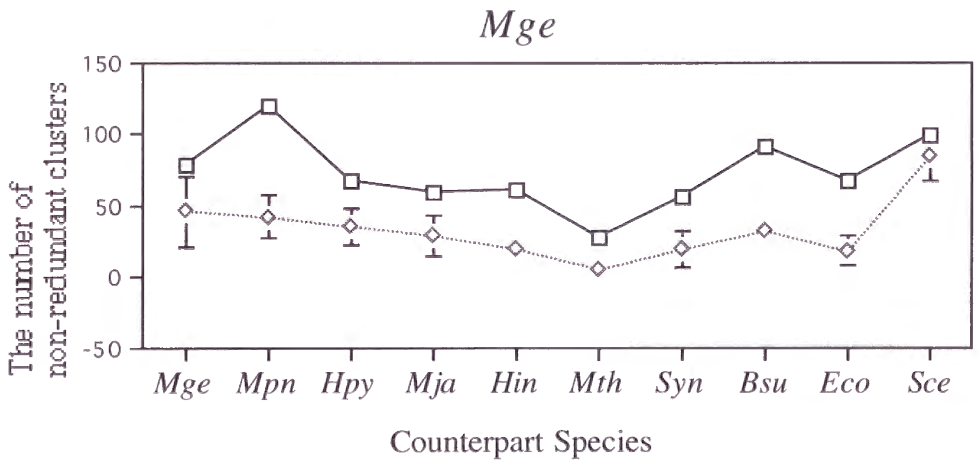

Eco

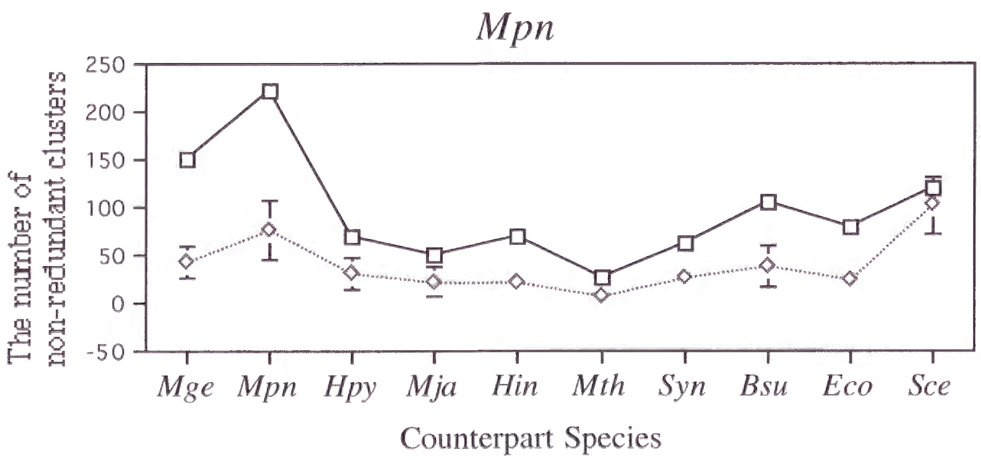

Hin


Hpy

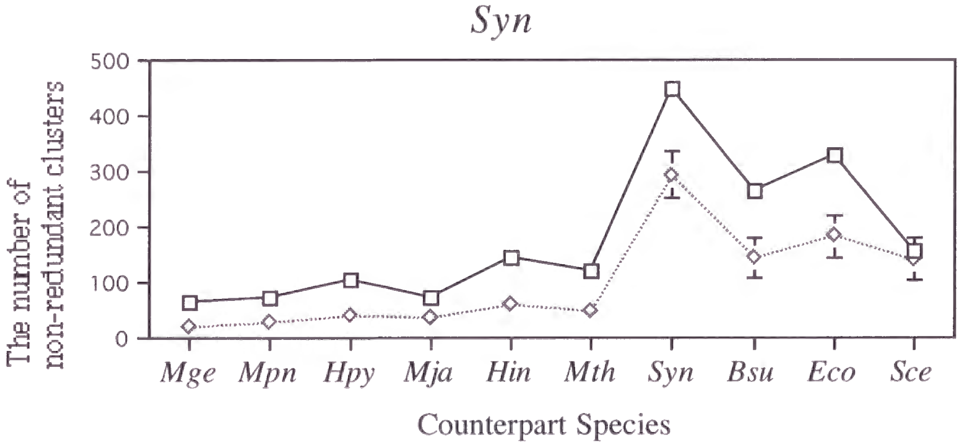
(c) Gram-positive Bacteria



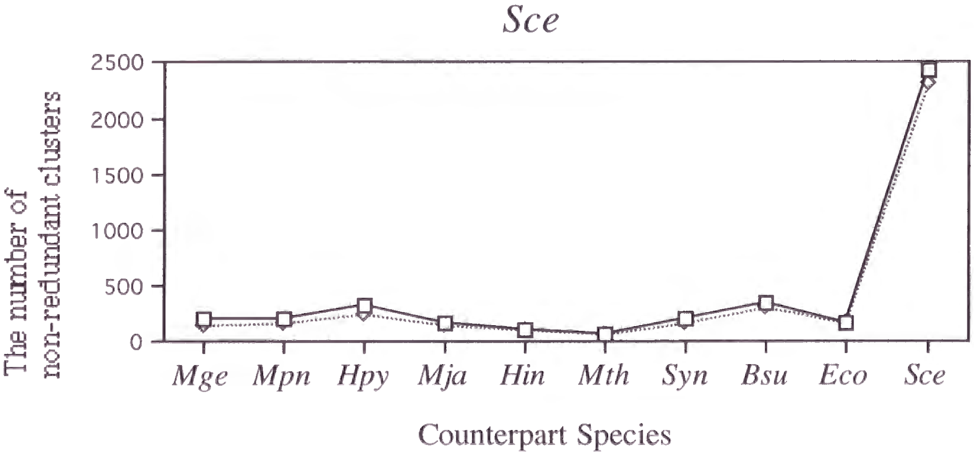




(d) Cyanobacteria



(e) Yeast



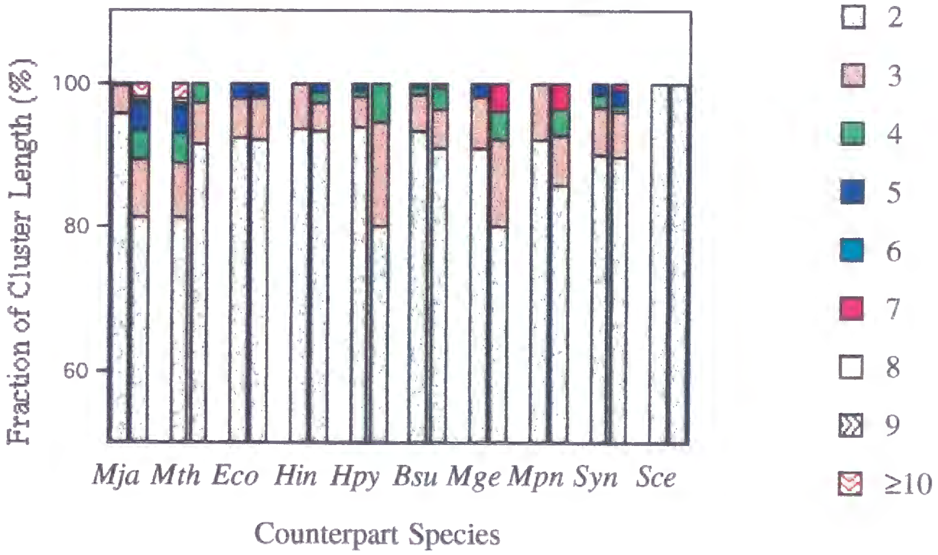
クラスター長の比較

重複を除いたクラスターの長さ、すなわち含まれる遺伝子数の数の分布は図4.4に示した。図中では生物種ごとに抽出数が違うので全抽出数にに対する割合で示している。

全体的には、ゲノムサイズが大きくなると短いクラスターの数が増える傾向にある。種内での自己クラスターに着目すると、*Mja, Sce* であまり長いクラスターが抽出できなかったが、それ以外の生物種では長いクラスターがシャフリングによって期待されるよりも、かなり多く抽出されてくる（シャフリングの場合のデータは未提示)。

種間での抽出クラスターを見てみると、*Mge-Mpn* においては様々な長さのクラスターが、平均的に抽出できているのが他の生物種と大きく違う点である。しかし、かなりの近縁種間の比較とは言え、*Hin-Eco* の場合は *Mge-Mpn* の場合と比べて、長いクラスターの割合が少ない。

(a) Archaea (*Mja* : *Mth*)



(b) Gram-Negative Bacteria (*Eco* : *Hin* : *Hpy*)

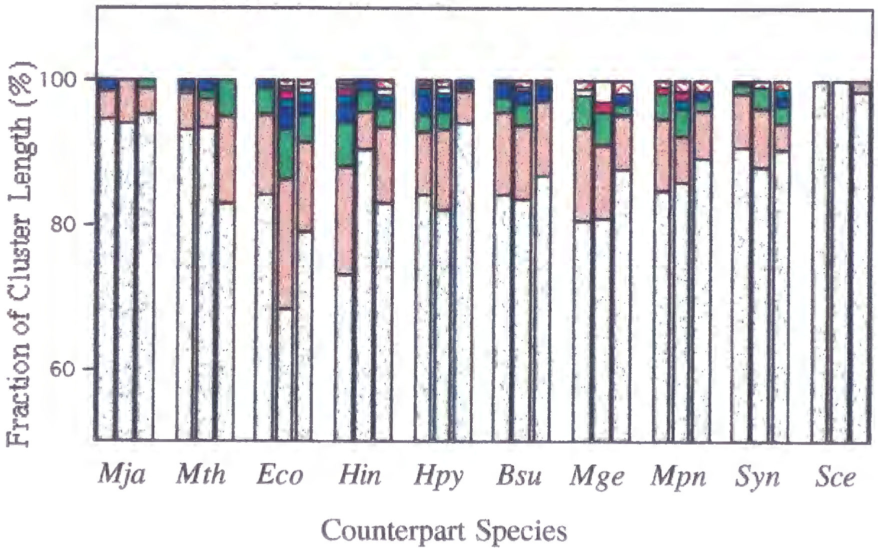
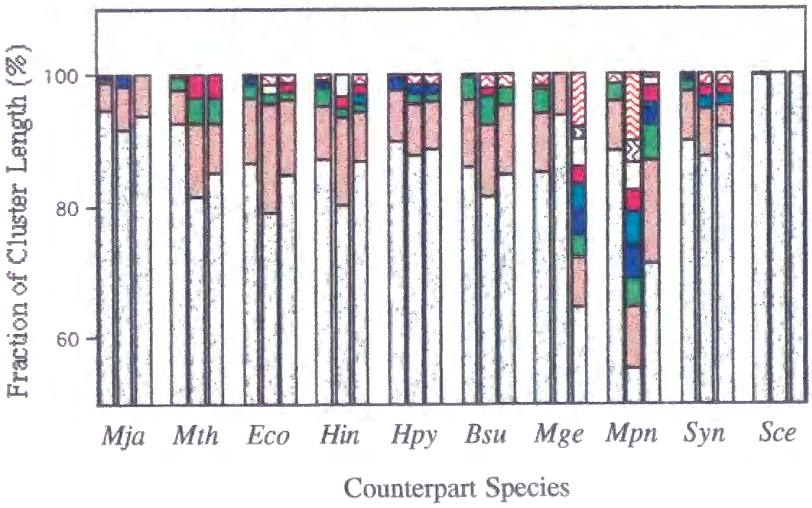
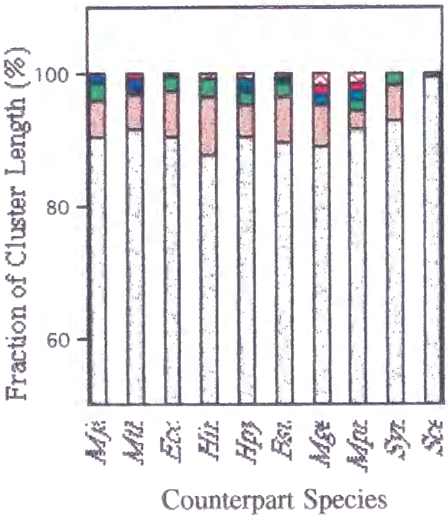


図 4.4: クラスター長の分布

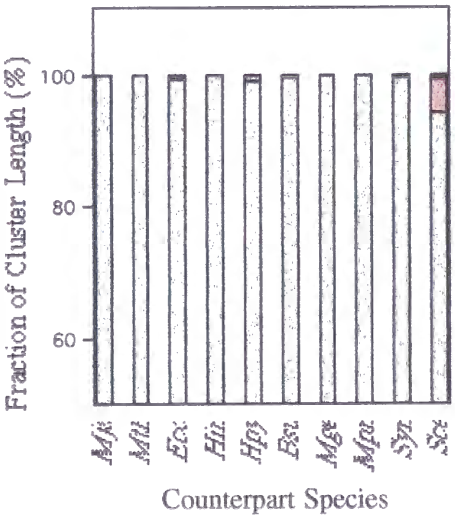
(c) Gram-Positive Bacteria (*Bsu* : *Mge* : *Mpn*)



(d) Cyanobacteria (*Syn*)



(e) Yeast (*Sce*)



4.4　大腸菌におけるオペロンとの比較

抽出できたクラスターはオペロンとどの程度対応がつくのかを調べるために、Blattner らの論文 [7] から読み取ったオペロン８５０個との対応をみた。ここでは、*Eco* が他の生物種との比較で抽出できた共通クラスターを生物種ごとに分けてオペロンとの比較を行った。図4.5 に抽出したクラスター数とそれに対する完全マッチを行った結果および部分的にオペロンに含まれていた結果を示した。

完全マッチ　完全マッチの場合には、わずか 20% 程度にしか抽出したクラスターが一致していない。すなわち、共通クラスターはあるがそれはオペロンとは食い違っている。このことは、*Eco* と全く同じオペロンを他の生物種が持つことの少なさを意味している。しかしながら、近縁種の *Hin* との間ではわずかながらオペロンと一致するクラスターが抽出できている可能性が高そうでもある。

部分マッチ　さらに、部分マッチによる比較を行ったところ、驚いたことにマッチ率が *Mja* の場合に最高で 80% にまで達した。理論的には Blattner らの論文 [7] によると、遺伝子数と転写産物数がそれぞれ 4397 と 2649 であり、したがって *Eco* の転写産物の平均長は 1.7 (4397/2649) 遺伝子以下である。これから、偶然にも長さ２のクラスターがオペロン内に落ちる可能性は、計算すると 41% (1 - 1/1.7) くらいにしかならないので、この数は有意にオペロンの中からクラスターを抽出していると思われる。

しかし、この部分マッチは *Mja* のような遠縁の種間だとよくオペロンと合っているが、*Hin* との共通クラスターでは幾分、その率が下がっているように見える (59%)。これは、種が近いためにオペロンのボーダーを越えてクラスターを抽出した、言い換えれば、関連するオペロンがさらに集合している部分を抽出しているのではないかと思われる。このことは、遺伝子が集まってオペロンを形成し、さらにオペロンが集まって大きなオペロン群を形成するような階層の存在を示唆している。

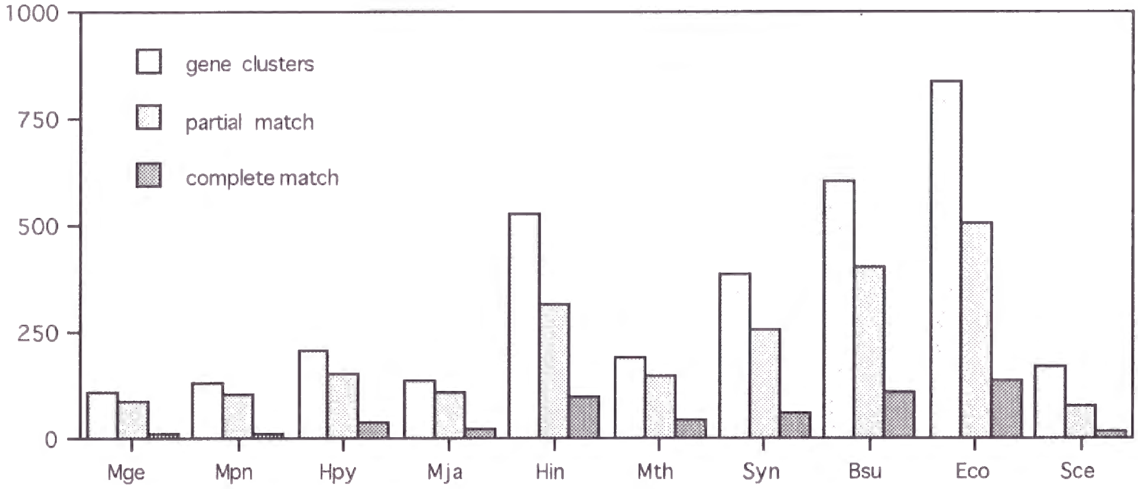


図 4.5: 遺伝子クラスターとオペロンとの対応度

4.4.1 部分マッチしたクラスターの例

オペロンとのマッチングを部分マッチを許して行った時に抽出できた遺伝子クラスターを付録に付した。そのうち、最も部分マッチ率の高かった *Eco-Mja* で抽出したクラスターの遺伝子の機能とその出現回数を、クラスター内での重複を許して数えた時に、多いものから列挙してみると、表4.2の様になる。

これを見ると、transport protein と energy metabolism 関連が非常に多い。しかし、cell process やアミノ酸合成、DNA 複製から脂肪酸代謝等に至るまで幅広い機能を持つクラスターが抽出できている。これは、やはり広い範囲の生物種にとって基本的なクラスターばかりと言えるのではないだろうか。

4.4.2 オペロン予測との関連について

これらの解析からオペロン予測について考えてみると、オペロンかまたはオペロンを構成することになる遺伝子のセットを抽出したい場合には、比較的遠縁の種間で抽出したクラスターを用いるとよいと思われる。この場合には、種が遠く離れたとしても保存されることが強く起こる遺伝子のペアやセットがよく抽出され、これらは「最小遺伝子クラスター」として定義ができると考えられる。

Function of genes in extracted clusters	*Number of genes*
Transport and binding proteins	71
Energy metabolism	36
Putative transport proteins	32
Translation, post-translational modification	25
Hypothetical, unclassified, unknown	20
Central intermediary metabolism	10
Putative enzymes	10
Cell processes (incl. adaptation, protection)	5
Transcription, RNA processing and degradation	5
Amino acid biosynthesis and metabolism	3
Putative regulatory proteins	3
DNA replication, recombination, modification and repair	2
Membrane proteins	2
Nucleotide biosynthesis and metabolism	2
Regulatory function	2
Carbon compound catabolism	1
Fatty acid and phospholipid metabolism	1

表 4.2: ***Eco-Mja*** **から抽出した遺伝子クラスターの機能** クラスター中に含まれていた遺伝子の機能を列挙し、それらの数をクラスター内の重複も許して数えた時の数を記した。

4.5 考察

4.5.1 クラスターの役割と進化的意義

Mge と *Mpn* ゲノムについて　*Mge* と *Mpn* のゲノム比較により、これら二種がゲノム全体において殆んどが相同性のある遺伝子の並びをもっていることから、これらは種分化してからそれほど、時を経ていないことが示唆される。恐らく、これ程までに全ゲノム上の遺伝子の並びまでが酷似していると言う事実は、全ゲノムが発表された時期から考えてもまだどの論文でも発表されていない、または現在どこかで解析中であると考えられるくらいのことであり、著者の発見である可能性が高い。しかも、面白いことには、ゲノム長の違いが、どこか数ヵ所に大きな挿入があるのではなく、ゲノムのあちこちが切れたように、細かな挿入が発生している（図 4.1）。この事は、種が分岐する時の様子を物語る一つの状況証拠であり、非常に興味深い。

図をよく見ると、ドットマトリックスの左上がゲノム位置で 0 番を表わすので、全体としては、お互いにちょうど番号の付け方が逆になっている。KEGG データベースのゲノムマップで確認すると（図 4.6）、ゲノム全体が、*Mpn* の方は時計回りに約 1／4 回転ほどずれ、しかも番号の付け方が丁度逆（鏡像）である。

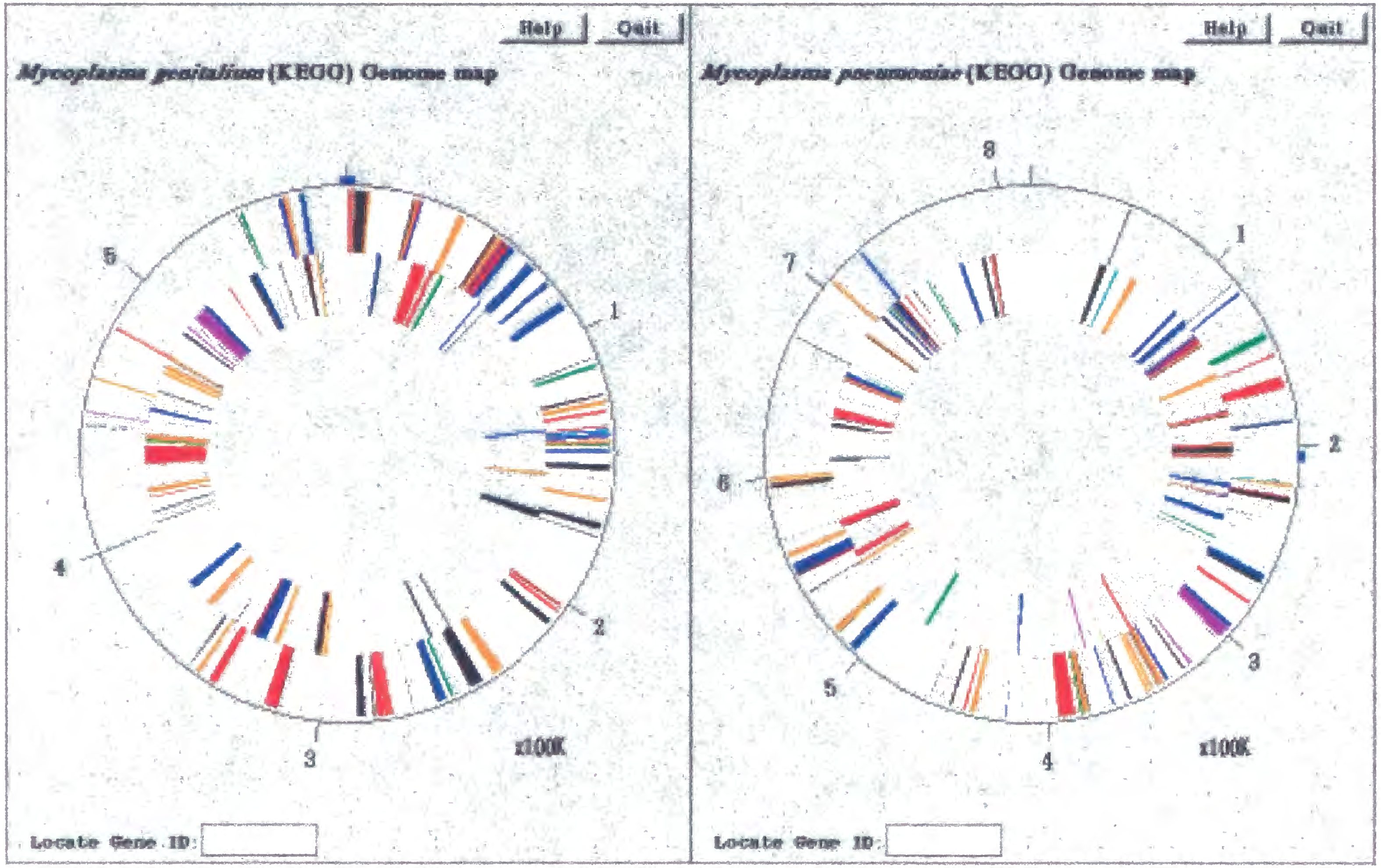


図 4.6: **KEGG によるゲノムマップ** 左が *Mge* 右が *Mpn* のゲノムマップ。*Mpn* の方は *Mge* に比べて 1／4 ほど時計回りに回転していて、しかも鏡像になっている。

先ほどの図4.1に戻ると、この細かなゲノム上の挿入は、すぐとなりの遺伝子のパラログの重複らしき場合（図中、階段状の横線）と、もう一つは完全に別の遺伝子（群）の挿入（図中、斜めの線が途切れた部分）が存在するらしき事がわかる。図4.7にドットマトリックスを拡大したものを示した。

これは、ゲノムの挿入とはまるで逆に考えると、長いゲノムがデリーションによって短くなったとの想定も可能である。しかし、その場合にはドットが切れる方には進行しても、すぐとなりの遺伝子が相同性を残したまま繋がることは、まず考えにくい。しかも目で見た限りにおいて、それらのパターンが出現する場所に違いがあるようにも思える。

試しに、この横方向に大きく重複のあったように見える三カ所（*Mpn* ゲノム上でそれぞれ110、200、250遺伝子付近）について、一致した *Mpn* 遺伝子を抜き出してみると、表4.3の様に全て hypothetical protein/lipoprotein であった。

Mpn ゲノム位置（遺伝子付近）	*Mge* 遺伝子名（出現回数）
110	MG032(5) hypothetical protein
200	MG439(9) hypothetical lipoprotein
	MG440(12) hypothetical lipoprotein
250	MG395(14) hypothetical lipoprotein

表 4.3: 横方向への挿入のあった付近の頻出遺伝子

また、図4.7で言うと、左の方は重複が多く、右の方は別からの挿入が多い。恐らく、これはゲノムの複製開始点との関連性が高いと思われる。すなわち、推定上の複製開始点付近（dnaA と dnaN の間、図4.6外周円上にある印）はすぐ隣への重複が起きやすく、複製開始点から遠いところでは、他からの挿入が起こる様にも見える。

遺伝子密度について　遺伝子密度とはすなわちパラログの出現しやすさである。パラログの多さが遺伝子クラスターを形成しているかと言う問題になると種によって異なっていた。*Mpn* は *Mge* に比べてクラスター存在率が高い。先ほどの事と一緒に考えると、これら二種のゲノムは殆んど同じであり、ゲノム長の違いを生じさせる挿入遺伝子が違うので、挿入部分がクラスターになっていることが多いと考えられる。すなわち、ゲノムを増やすのには遺伝子単位でなく遺伝子クラスター単位で増えることが多いのではないだろうか。

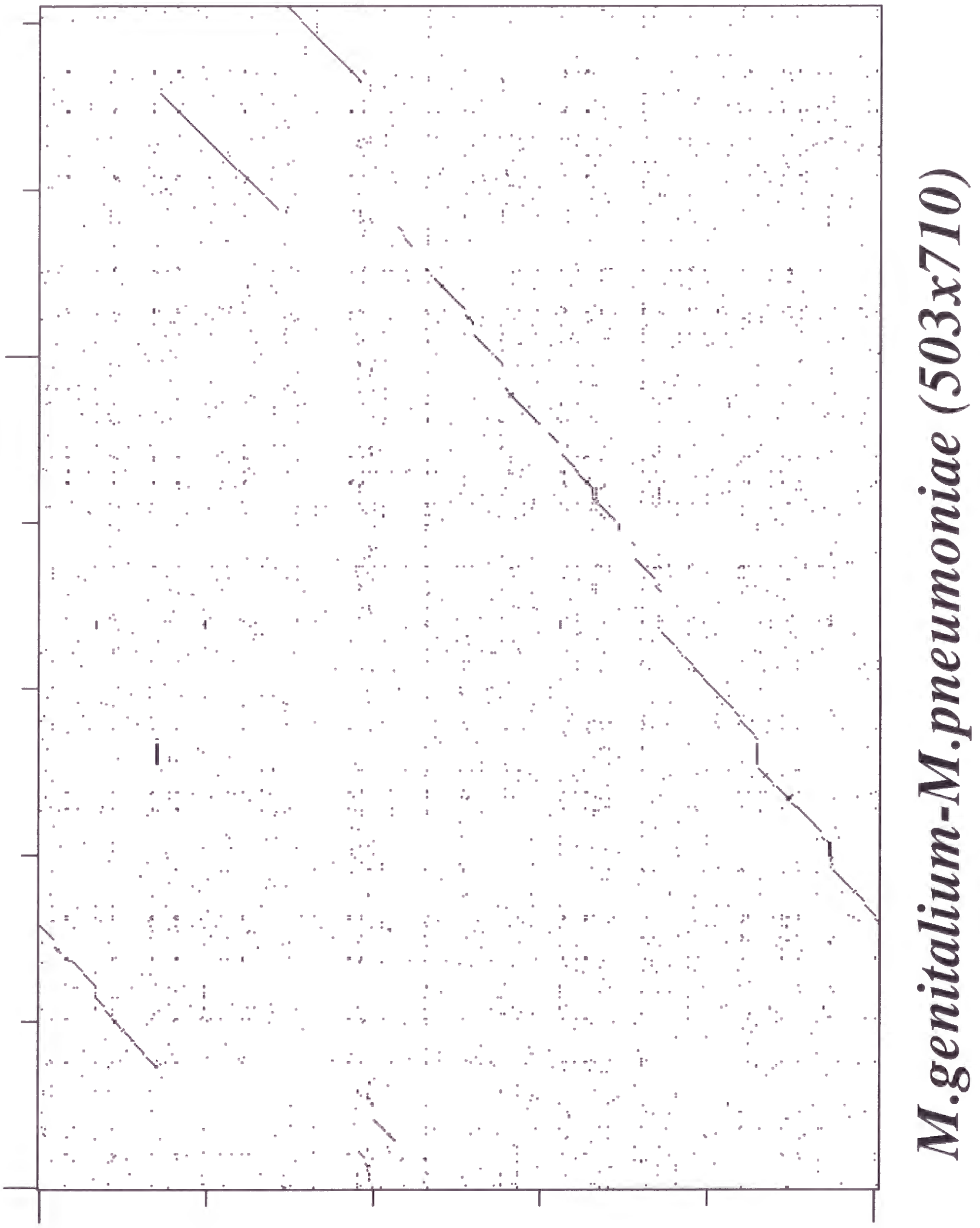


図 4.7: *Mge-Mpn* **のドットマトリックスでのゲノム変遷の様子** この二種の違いを分けるゲノムの長さの違いは、ところどころに存在するゲノムへの挿入部分であると考えられる。

種間比較から言えること ほとんど当然の事ながら、近縁種間ではクラスターを抽出しやすい。しかしながら、遠縁の種と言えども期待されるランダムな遺伝子の配置に比べ、遺伝子は共通クラスターになって存在している。また、長さの分布からは、同じ分類種に属していてもゲノムサイズが大きくなると、全体の割合中、短いクラスターが増加する傾向にあった。また、*Sce* と比べたときにどの生物種も長いクラスターが殆んど抽出できていない。しかも、抽出クラスターが少ない場合も多かった。やはり、これは全く違うゲノム構造を反映しているのではないだろうか。

4.5.2 オペロン予測について

オペロンとの比較について

遠縁の種から抽出できた遺伝子クラスターは驚くほど、Blattner らのオペロンの部分遺伝子群と一致していた。これは、基本的に遠い生物種にまで共通の遺伝子のクラスターの存在を示唆する。すなわち、生物種が遠くても生命にとって重要なクラスターほど保存されやすいと考えられるので、これらの大部分は恐らくどの生物種でもオペロンやクラスターとして出現しているのではないだろうか。実際に付録のリストで確かめてみると、*Mja* で出現していたクラスターは他の生物種でも出現している傾向がありそうである。逆に、近縁種間で抽出したクラスターは、オペロンのボーダーをまたいでいるものになりやすいと思われる。これは、ゲノムどうしが余りにも似ているために起こると考えられる。

階層的な遺伝子群

オペロンとの完全マッチ、および部分マッチの結果から、遺伝子群が階層性を持っているのではないかということに気付かされる。つまり、遠縁の種間でも保存されていた遺伝子クラスターを最小の機能単位として、そのクラスターにそれぞれ生物種に特有の遺伝子（例えば、転写制御因子など）を含めたり、また、それらのクラスターを組み合わせてさらに大きなクラスターを形成することがあると考えられる。図4.8にそのことを摸式化して示した。

また、遺伝子群が階層的に次第に大きな単位へと変っていくことは、ゲノム構成を考える上で、真核生物との比較において非常に面白い。真核生物の酵素の研究から、原核生物で Orthologous な蛋白質がばらばらの遺伝子に単独で存在し、時にはオペロンを形成するようなものが、真核生物では、遺伝子が融合し、マルチエンザイム蛋白質となっていることが、アミノ酸、葉酸、プリン、ピリミジン、脂肪酸代謝などの経路で見つかっている [14]。

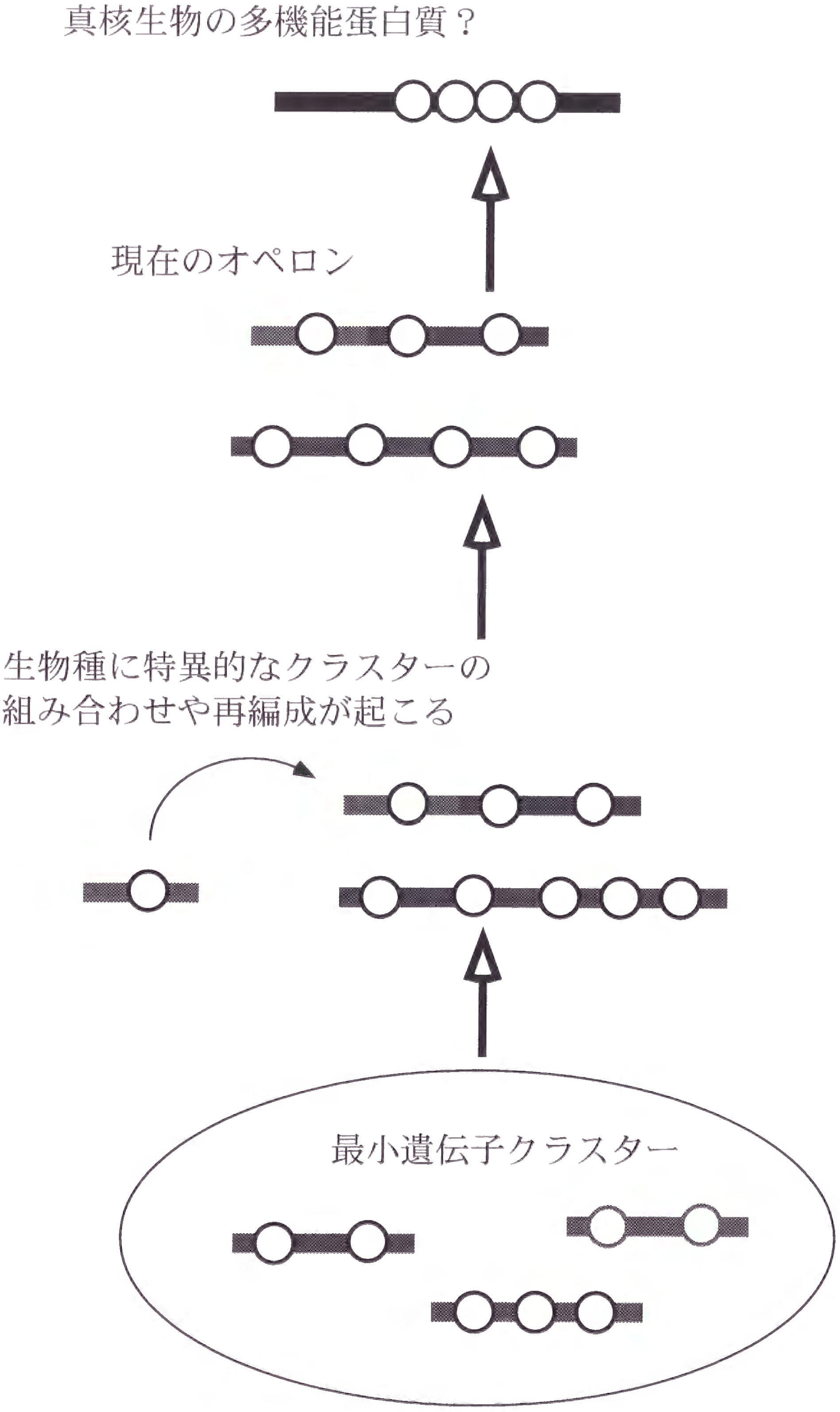


図 4.8: **遺伝子群の階層性** 機能的に最小単位を集めた遺伝子クラスターが生物種ごとに再編成されてオペロンができ、さらにそれらが融合して、真核生物のマルチ機能蛋白質になるのかも知れない。

オペロン予測の実用化について

ここで行った解析をもとに著者は、今後オペロン予測へと発展するため、次のようなステップで研究を行うことが可能である。

1. **最小機能遺伝子群（クラスター）の同定**
   遠縁の種から保存されているクラスターを抽出する。
2. **遺伝子群の再編成パターンの抽出および階層的定義**
   最小クラスターを単位として組み合わせた時に種間で共通に出現する最小クラスターから構成されるクラスターの抽出と、新たな遺伝子を取り入れたときに出現する再編成クラスターの同定をする。
3. **遺伝子クラスター階層辞書の編成**
   遺伝子クラスターに系統的に番号付けを行い、オーソロガスクラスターを定義する。
4. **遺伝子クラスター予測**
   辞書を鋳型にして、検索をかける。

大事な点は、近縁種間でゲノムを比較したときに、関係のないオペロンのボーダーをいかに拾わないようにすることができるかである。これができれば、種間で共通なクラスターはオペロンである可能性が高いと思われる。

最後に、基本的な問題としてそもそも最小機能単位となる遺伝子クラスターはどのようにしてできたのか、ゲノムがクラスターを作る原理が大きな問題として残されている。

4.6 幾つかの問題点

ここでは、これまで触れなかった手法上の幾つかの問題点について触れたいと思う。

4.6.1 クラスター内の遺伝子のシャフリング

遺伝子クラスターは種によって再編成を受けると考えられるが、このことにより、クラスター内の遺伝子の並びもまた再編成を受け、シャフリングによって遺伝子の連続性が変化する場合が考えれれる。今回の手法では完全に並びが保存されていると考えられる遺伝子クラスターのみを抽出しており、このシャフリングの問題は考慮されていない。統計的には少数にすぎないと考えられるが、考慮すべき問題点である。

4.6.2　酵母における遺伝子統合化

4.5.2節のところでも述べたが、遺伝子クラスターが融合し、一つの多機能蛋白質になった場合には、当然のことながら、クラスターの検出はできなくなる。*Sce*においては長い遺伝子クラスターを殆んど検出できなかったが、これは多機能蛋白質を調べていくことでクラスターの融合が確認できるかもしれない。もちろん、このことは*Sce*だけに限らず、どの生物種においても多かれ少なかれ起こりうることであり、この遺伝子の融合化を考慮してクラスター検出を行えば、より精密な予測が行えるものと期待される。

4.6.3　相同性検索上の問題点

クラスターを抽出する基本的な方法として相同性検索を用いているが、これもあくまで一つの評価基準であるという内的な問題を持っている。すなわち、相同性検索によっても検出できないくらい分化の激しいオーソロガス蛋白質や全く別の方向から進化し、最終的に同じような機能を持った蛋白質も存在しうるからである。逆に、また相同性があるからと言って同じ機能の蛋白質であるとは限らない。この点は僅かな統計的な誤差を生じていると考えられる。

第5章　結論

生物学はついにかつてない大量情報の時代へと突入した。情報をどう整理し扱うか、またどうやってこれらから有益な情報を生み出すかが焦点である。

著者は一つのアプローチとして、データベースの多様性を吸収できるような統合データベース検索システムを開発した。このシステムによって、現在１７種類のデータベースを統合的に同じ方法で検索でき、データベース間の関連性もまたリンクという同じ方法で取り出すことができるようになった。さらに、大量にまた各地へとデータベースのサーバーを広げていくことが可能なようにネットワーク分散型のシステムを作成した。

この統合データベースシステムを利用して、遺伝子クラスターの抽出および解析を行った。この解析により、まず種内で遺伝子を増加させるときにクラスターで増加するような顕著な例が *Mge* と *Mpn* の比較から観察された。また、種間で共通のクラスターは明らかに存在し、基本的な最小の遺伝子クラスターを抽出したい場合や、偶然に隣り合わせた遺伝子の抽出などノイズを避けるのには比較的遠縁の種間での共通クラスターを探す方が良いことが示唆された。このようにして *Eco* と *Mja* との比較により抽出されたクラスターは大腸菌のオペロン内のものであることが 80% と高かった。

今後は、オペロン予測を行うために、遺伝子クラスターの階層性を考慮し、さらに系統的な基本単位のクラスター抽出からスーパークラスターの定義、そして遺伝子融合による多機能蛋白質へと解析を進めていく予定である。

最後に、ここではオペロン予測へと向かう例を示したが、統合検索を用いれば、これ以外にも様々な解析が行うことができる可能性を我々の DBGET/LinkDB システムは秘めていることを記しておきたい。

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付 録A　大腸菌との比較による抽出遺伝子クラスター一覧

１０生物種を大腸菌と比較した場合に共通に存在した遺伝子クラスターを、Blattner らのオペロンとどの程度一致しているかを調べた結果の一覧表を記した。オペロンの数は８５０種あり、これらについて順にオペロン番号を割り振ってある。左端から、オペロン番号、遺伝子のb番号、遺伝子名、ORF の方向、アミノ酸長、機能、そして一致した生物種名を表記してある。Blattner の完全なオペロンは **B** と表わしてあり、完全に一致でなくともオペロン内の部分遺伝子群に対するマッチも記した。完全にマッチした場合には生物種名の先頭にこの **B** が記されている。

operon#	b#	gene	dir	length	function	species
o0001	b0001	thrL	>	21	Amino acid biosynthesis and metabolism	B
	b0002	thrA	>	820	Amino acid biosynthesis and metabolism	B
	b0003	thrB	>	310	Amino acid biosynthesis and metabolism	B
	b0004	thrC	>	428	Amino acid biosynthesis and metabolism	B
o0001	b0002	thrA	>	820	Amino acid biosynthesis and metabolism	Mth
	b0003	thrB	>	310	Amino acid biosynthesis and metabolism	Mth
o0001	b0002	thrA	>	820	Amino acid biosynthesis and metabolism	Hin
	b0003	thrB	>	310	Amino acid biosynthesis and metabolism	Hin
	b0004	thrC	>	428	Amino acid biosynthesis and metabolism	Hin
o0001	b0003	thrB	>	310	Amino acid biosynthesis and metabolism	Bsu Mth Syn
	b0004	thrC	>	428	Amino acid biosynthesis and metabolism	Bsu Mth Syn
o0002	b0014	dnaK	>	638	"Cell processes (incl. adaptation, protection)"	B Bsu Hin Mja Mth Sce Syn
	b0015	dnaJ	>	376	"Cell processes (incl. adaptation, protection)"	B Bsu Hin Mja Mth Sce Syn
o0003	b0021	insB_1	<	167	"phage, transposon, or plasmid"	B Eco Syn
	b0022	insA_1	<	91	"phage, transposon, or plasmid"	B Eco Syn
o0004	b0024	b0024	>	72	"Hypothetical, unclassified, unknown"	B
	b0025	yaaC	>	313	Putative regulatory proteins	B
o0005	b0026	ileS	>	938	"Translation, post-translational modification"	B
	b0027	lspA	>	164	Transport and binding proteins	B
	b0028	yaaD	>	149	"Hypothetical, unclassified, unknown"	B
o0006	b0032	carA	>	382	Nucleotide biosynthesis and metabolism	B Bsu Mth
	b0033	carB	>	1073	Nucleotide biosynthesis and metabolism	B Bsu Mth
o0007	b0035	caiE	<	203	"Cell processes (incl. adaptation, protection)"	B
	b0036	caiD	<	297	"Cell processes (incl. adaptation, protection)"	B
	b0037	caiC	<	522	"Cell processes (incl. adaptation, protection)"	B
	b0038	caiB	<	405	"Cell processes (incl. adaptation, protection)"	B
	b0039	caiA	<	380	"Cell processes (incl. adaptation, protection)"	B
	b0040	caiT	<	504	"Cell processes (incl. adaptation, protection)"	B
o0007	b0036	caiD	<	297	"Cell processes (incl. adaptation, protection)"	Bsu
	b0037	caiC	<	522	"Cell processes (incl. adaptation, protection)"	Bsu
o0007	b0039	caiA	<	380	"Cell processes (incl. adaptation, protection)"	Bsu
	b0040	caiT	<	504	"Cell processes (incl. adaptation, protection)"	Bsu
o0008	b0041	fixA	>	268	Energy metabolism	Bsu Eco
	b0042	fixB	>	313	Energy metabolism	Bsu Eco
o0008	b0041	fixA	>	268	Energy metabolism	B Eco
	b0042	fixB	>	313	Energy metabolism	B Eco
	b0043	fixC	>	428	"Hypothetical, unclassified, unknown"	B Eco
	b0044	fixX	>	95	Energy metabolism	B Eco
o0008	b0043	fixC	>	428	"Hypothetical, unclassified, unknown"	Eco
	b0044	fixX	>	95	Energy metabolism	Eco
o0009	b0046	yabF	>	176	Putative enzymes	B Eco
	b0047	kefC	>	620	Transport and binding proteins	B Eco
o0010	b0050	apaG	<	125	"Hypothetical, unclassified, unknown"	B
	b0051	ksgA	<	273	"Cell processes (incl. adaptation, protection)"	B
	b0052	pdxA	<	329	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0053	surA	<	428	Other known genes	B
o0010	b0052	pdxA	<	329	"Biosynthesis of cofactors, prosthetic groups and carriers"	Syn
	b0053	surA	<	428	Other known genes	Syn

o0011	b0056	yabP	>	216	"Hypothetical, unclassified, unknown"	B
	b0057	yabQ	>	52	"Hypothetical, unclassified, unknown"	B
o0012	b0058	yabO	<	219	"Hypothetical, unclassified, unknown"	B Hin
	b0059	hepA	<	968	"Transcription, RNA processing and degradation"	B Hin
o0013	b0061	araD	<	231	Carbon compound catabolism	Eco
	b0062	araA	<	500	Carbon compound catabolism	Eco
o0013	b0061	araD	<	231	Carbon compound catabolism	B
	b0062	araA	<	500	Carbon compound catabolism	B
	b0063	araB	<	566	Carbon compound catabolism	B
o0013	b0062	araA	<	500	Carbon compound catabolism	Bsu
	b0063	araB	<	566	Carbon compound catabolism	Bsu
o0014	b0066	yabJ	<	232	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
	b0067	yabK	<	536	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
o0014	b0066	yabJ	<	232	Putative transport proteins	B Hin Syn
	b0067	yabK	<	536	Putative transport proteins	B Hin Syn
	b0068	tbpA	<	327	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Hin Syn
o0014	b0067	yabK	<	536	Putative transport proteins	Bsu
	b0068	tbpA	<	327	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0015	b0071	leuD	<	201	Amino acid biosynthesis and metabolism	Mth
	b0072	leuC	<	466	Amino acid biosynthesis and metabolism	Mth
o0015	b0071	leuD	<	201	Amino acid biosynthesis and metabolism	Bsu Hin
	b0072	leuC	<	466	Amino acid biosynthesis and metabolism	Bsu Hin
	b0073	leuB	<	364	Amino acid biosynthesis and metabolism	Bsu Hin
	b0074	leuA	<	523	Amino acid biosynthesis and metabolism	Bsu Hin
o0015	b0071	leuD	<	201	Amino acid biosynthesis and metabolism	B
	b0072	leuC	<	466	Amino acid biosynthesis and metabolism	B
	b0073	leuB	<	364	Amino acid biosynthesis and metabolism	B
	b0074	leuA	<	523	Amino acid biosynthesis and metabolism	B
	b0075	leuL	<	28	Amino acid biosynthesis and metabolism	B
o0015	b0072	leuC	<	466	Amino acid biosynthesis and metabolism	Sce
	b0073	leuB	<	364	Amino acid biosynthesis and metabolism	Sce
o0015	b0073	leuB	<	364	Amino acid biosynthesis and metabolism	Eco
	b0074	leuA	<	523	Amino acid biosynthesis and metabolism	Eco
o0016	b0076	leuO	>	373	Amino acid biosynthesis and metabolism	Bsu Eco
	b0077	ilvI	>	604	Amino acid biosynthesis and metabolism	Bsu Eco
o0016	b0076	leuO	>	373	Amino acid biosynthesis and metabolism	B
	b0077	ilvI	>	604	Amino acid biosynthesis and metabolism	B
	b0078	ilvH	>	163	Amino acid biosynthesis and metabolism	B
o0016	b0077	ilvI	>	604	Amino acid biosynthesis and metabolism	Bsu Eco Hin Mth
	b0078	ilvH	>	163	Amino acid biosynthesis and metabolism	Bsu Eco Hin Mth
o0017	b0079	fruL	>	28	Energy metabolism	B
	b0080	fruR	>	334	Energy metabolism	B
o0018	b0081	yabB	>	152	"Hypothetical, unclassified, unknown"	Bsu Mge Mpn
	b0082	yabC	>	313	Structural proteins	Bsu Mge Mpn

o0018	b0081	yabB	>	152	"Hypothetical, unclassified, unknown"	B
	b0082	yabC	>	313	Structural proteins	B
	b0083	ftsL	>	121	"Cell processes (incl. adaptation, protection)"	B
	b0084	ftsI	>	588	"Cell processes (incl. adaptation, protection)"	B
	b0085	murE	>	495	Cell structure	B
	b0086	murF	>	452	Cell structure	B
	b0087	mraY	>	360	Cell structure	B
	b0088	murD	>	438	Cell structure	B
	b0089	ftsW	>	414	"Cell processes (incl. adaptation, protection)"	B
	b0090	murG	>	355	Cell structure	B
	b0091	murC	>	491	Cell structure	B
	b0092	ddlB	>	306	Cell structure	B
o0018	b0084	ftsI	>	588	"Cell processes (incl. adaptation, protection)"	Bsu
	b0085	murE	>	495	Cell structure	Bsu
o0018	b0085	murE	>	495	Cell structure	Hin
	b0086	murF	>	452	Cell structure	Hin
o0018	b0086	murF	>	452	Cell structure	Mth Syn
	b0087	mraY	>	360	Cell structure	Mth Syn
o0018	b0086	murF	>	452	Cell structure	Bsu Hin
	b0087	mraY	>	360	Cell structure	Bsu Hin
	b0088	murD	>	438	Cell structure	Bsu Hin
o0018	b0086	murF	>	452	Cell structure	Bsu
	b0087	mraY	>	360	Cell structure	Bsu
	b0088	murD	>	438	Cell structure	Bsu
	b0089	ftsW	>	414	"Cell processes (incl. adaptation, protection)"	Bsu
	b0090	murG	>	355	Cell structure	Bsu
o0018	b0087	mraY	>	360	Cell structure	Eco Hpy
	b0088	murD	>	438	Cell structure	Eco Hpy
o0018	b0090	murG	>	355	Cell structure	Bsu
	b0091	murC	>	491	Cell structure	Bsu
o0018	b0091	murC	>	491	Cell structure	Bsu
	b0092	ddlB	>	306	Cell structure	Bsu
o0019	b0093	ftsQ	>	276	"Cell processes (incl. adaptation, protection)"	B
	b0094	ftsA	>	420	"Cell processes (incl. adaptation, protection)"	B
	b0095	ftsZ	>	383	"Cell processes (incl. adaptation, protection)"	B
o0019	b0094	ftsA	>	420	"Cell processes (incl. adaptation, protection)"	Bsu Hpy Syn
	b0095	ftsZ	>	383	"Cell processes (incl. adaptation, protection)"	Bsu Hpy Syn
o0020	b0100	b0100	<	44	"Hypothetical, unclassified, unknown"	B
	b0101	yacG	<	65	"Hypothetical, unclassified, unknown"	B
	b0102	yacF	<	247	"Hypothetical, unclassified, unknown"	B
	b0103	yacE	<	206	"DNA replication, recombination, modification and repair"	B
o0021	b0105	b0105	<	35	"Hypothetical, unclassified, unknown"	B
	b0106	hofC	<	400	Cell structure	B
	b0107	hofB	<	461	Cell structure	B
	b0108	ppdD	<	146	Other known genes	B
o0021	b0106	hofC	<	400	Cell structure	Bsu Eco Mth Syn
	b0107	hofB	<	461	Cell structure	Bsu Eco Mth Syn
o0021	b0106	hofC	<	400	Cell structure	Hin
	b0107	hofB	<	461	Cell structure	Hin
	b0108	ppdD	<	146	Other known genes	Hin

o0021	b0107	hofB	<	461	Cell structure	Syn
	b0108	ppdD	<	146	Other known genes	Syn
o0022	b0110	ampD	>	183	"Cell processes (incl. adaptation, protection)"	B
	b0111	ampE	>	284	"Cell processes (incl. adaptation, protection)"	B
o0023	b0113	pdhR	>	254	Energy metabolism	Eco
	b0114	aceE	>	887	Energy metabolism	Eco
o0023	b0113	pdhR	>	254	Energy metabolism	B
	b0114	aceE	>	887	Energy metabolism	B
	b0115	aceF	>	630	Energy metabolism	B
	b0116	lpdA	>	474	Energy metabolism	B
o0023	b0114	aceE	>	887	Energy metabolism	Bsu Eco
	b0115	aceF	>	630	Energy metabolism	Bsu Eco
o0023	b0114	aceE	>	887	Energy metabolism	Hin
	b0115	aceF	>	630	Energy metabolism	Hin
	b0116	lpdA	>	474	Energy metabolism	Hin
o0023	b0115	aceF	>	630	Energy metabolism	Bsu Mge Mpn
	b0116	lpdA	>	474	Energy metabolism	Bsu Mge Mpn
o0024	b0120	speD	<	264	Central intermediary metabolism	B
	b0121	speE	<	288	Central intermediary metabolism	B
o0025	b0127	yadG	>	308	Putative transport proteins	B Bsu Eco Hin Mpn Mth Sce Syn
	b0128	yadH	>	256	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Mpn Mth Sce Syn
o0026	b0133	panC	<	283	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Bsu
	b0134	panB	<	264	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Bsu
o0027	b0135	yadC	<	412	"Cell processes (incl. adaptation, protection)"	B
	b0136	yadK	<	198	"Cell processes (incl. adaptation, protection)"	B
	b0137	yadL	<	201	"Cell processes (incl. adaptation, protection)"	B
	b0138	yadM	<	203	"Cell processes (incl. adaptation, protection)"	B
o0027	b0136	yadK	<	198	"Cell processes (incl. adaptation, protection)"	Eco
	b0137	yadL	<	201	"Cell processes (incl. adaptation, protection)"	Eco
o0028	b0139	htrE	<	865	Cell structure	B Eco Sce
	b0140	ecpD	<	246	Cell structure	B Eco Sce
o0029	b0142	folK	<	159	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Hin
	b0143	pcnB	<	454	"Transcription, RNA processing and degradation"	B Hin
o0030	b0145	dksA	<	151	"DNA replication, recombination, modification and repair"	B Hin
	b0146	sfsA	<	234	Carbon compound catabolism	B Hin
o0031	b0150	fhuA	>	747	Cell structure	Bsu Eco Syn
	b0151	fhuC	>	265	Transport and binding proteins	Bsu Eco Syn
o0031	b0150	fhuA	>	747	Cell structure	B
	b0151	fhuC	>	265	Transport and binding proteins	B
	b0152	fhuD	>	296	Transport and binding proteins	B
	b0153	fhuB	>	660	Transport and binding proteins	B
o0031	b0151	fhuC	>	265	Transport and binding proteins	Bsu Hin Syn
	b0152	fhuD	>	296	Transport and binding proteins	Bsu Hin Syn
o0031	b0152	fhuD	>	296	Transport and binding proteins	Bsu Eco
	b0153	fhuB	>	660	Transport and binding proteins	Bsu Eco
o0032	b0157	yadS	<	207	"Hypothetical, unclassified, unknown"	B
	b0158	yadT	<	266	"Hypothetical, unclassified, unknown"	B
	b0159	pfs	<	232	"Hypothetical, unclassified, unknown"	B

o0033	b0164	yaeI	<	247	"Hypothetical, unclassified, unknown"	B
	b0165	b0165	<	43	"Hypothetical, unclassified, unknown"	B
	b0166	dapD	<	274	Amino acid biosynthesis and metabolism	B
	b0167	glnD	<	890	Amino acid biosynthesis and metabolism	B
o0034	b0169	rpsB	>	241	"Translation, post-translational modification"	B Hin Hpy Syn
	b0170	tsf	>	283	"Translation, post-translational modification"	B Hin Hpy Syn
o0035	b0175	cdsA	>	249	Fatty acid and phospholipid metabolism	B
	b0176	yaeL	>	450	"Hypothetical, unclassified, unknown"	B
	b0177	b0177	>	810	"Hypothetical, unclassified, unknown"	B
o0036	b0178	hlpA	>	161	Cell structure	B
	b0179	lpxD	>	341	Cell structure	B
o0037	b0181	lpxA	>	262	Cell structure	Sce
	b0182	lpxB	>	382	Cell structure	Sce
o0037	b0181	lpxA	>	262	Cell structure	B
	b0182	lpxB	>	382	Cell structure	B
	b0183	rnhB	>	198	"DNA replication, recombination, modification and repair"	B
	b0184	dnaE	>	1160	"DNA replication, recombination, modification and repair"	B
o0038	b0186	ldcC	>	713	Energy metabolism	B
	b0187	b0187	>	138	"Hypothetical, unclassified, unknown"	B
o0039	b0190	yaeQ	>	181	"Hypothetical, unclassified, unknown"	B
	b0191	yaeJ	>	140	"Hypothetical, unclassified, unknown"	B
	b0192	cutF	>	236	"Cell processes (incl. adaptation, protection)"	B
o0040	b0193	yaeF	<	292	"Hypothetical, unclassified, unknown"	B
	b0194	proS	<	572	"Translation, post-translational modification"	B
o0041	b0195	yaeB	<	235	"Hypothetical, unclassified, unknown"	B
	b0196	rcsF	<	134	Cell structure	B
o0042	b0197	yaeC	<	271	Cell structure	B Bsu Hin
	b0198	yaeE	<	217	Membrane proteins	B Bsu Hin
	b0199	abc	<	343	Transport and binding proteins	B Bsu Hin
o0042	b0198	yaeE	<	217	Membrane proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
	b0199	abc	<	343	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
o0043	b0201	rrsH	>		rRNA	B
	b0202	ileV	>		tRNA	B
	b0203	alaV	>		tRNA	B
	b0204	rrlH	>		rRNA	B
	b0205	rrfH	>		rRNA	B
	b0206	aspU	>		tRNA	B
o0044	b0209	yafD	>	266	"Hypothetical, unclassified, unknown"	B
	b0210	yafE	>	207	Putative enzymes	B
o0045	b0225	yafQ	<	92	"Hypothetical, unclassified, unknown"	B Hin
	b0226	dinJ	<	86	Other known genes	B Hin
o0046	b0232	yafN	>	97	"Hypothetical, unclassified, unknown"	B
	b0233	yafO	>	132	"Hypothetical, unclassified, unknown"	B
	b0234	yafP	>	150	"Hypothetical, unclassified, unknown"	B
o0047	b0235	b0235	>	88	"Hypothetical, unclassified, unknown"	B
	b0236	prfH	>	166	"Translation, post-translational modification"	B
o0048	b0242	proB	>	367	Amino acid biosynthesis and metabolism	B Bsu
	b0243	proA	>	417	Amino acid biosynthesis and metabolism	B Bsu
o0049	b0245	b0245	<	113	"Hypothetical, unclassified, unknown"	B Eco
	b0246	yafW	<	105	"Hypothetical, unclassified, unknown"	B Eco

o0050	b0247	b0247	<	158	"DNA replication, recombination, modification and repair"	B
	b0248	yafX	<	152	"Hypothetical, unclassified, unknown"	B
o0051	b0250	ykfB	<	155	"Hypothetical, unclassified, unknown"	B Eco
	b0251	yafY	<	285	"Hypothetical, unclassified, unknown"	B Eco
o0052	b0255	b0255	>	134	"Hypothetical, unclassified, unknown"	B Eco
	b0256	tra8_1	>	383	"phage, transposon, or plasmid"	B Eco
o0053	b0260	ykfD	>	475	Central intermediary metabolism	B Bsu Sce
	b0261	yagD	>	310	Cell structure	B Bsu Sce
o0054	b0262	yagC	<	352	Central intermediary metabolism	Bsu Eco Hin Hpy Mja Mpn Mth Syn
	b0263	b0263	<	120	Putative transport proteins	Bsu Eco Hin Hpy Mja Mpn Mth Syn
o0054	b0262	yagC	<	352	Central intermediary metabolism	B
	b0263	b0263	<	120	Putative transport proteins	B
	b0264	insB_2	<	167	"phage, transposon, or plasmid"	B
	b0265	insA_2	<	91	"phage, transposon, or plasmid"	B
o0054	b0264	insB_2	<	167	"phage, transposon, or plasmid"	Eco Syn
	b0265	insA_2	<	91	"phage, transposon, or plasmid"	Eco Syn
o0055	b0268	yagE	>	309	Central intermediary metabolism	B Eco
	b0269	yagF	>	655	Amino acid biosynthesis and metabolism	B Eco
o0056	b0270	yagG	>	460	Carbon compound catabolism	B Bsu
	b0271	b0271	>	536	Carbon compound catabolism	B Bsu
o0057	b0274	insB_3	<	167	"phage, transposon, or plasmid"	B Eco Syn
	b0275	insA_3	<	91	"phage, transposon, or plasmid"	B Eco Syn

operon#	b#	gene	dir	length	function	species
o0058	b0278	yagL	<	232	Putative regulatory proteins	B
	b0279	b0279	<	284	"Hypothetical, unclassified, unknown"	B
o0059	b0282	yagP	<	136	"Hypothetical, unclassified, unknown"	B
	b0283	yagQ	<	318	"Hypothetical, unclassified, unknown"	B
	b0284	yagR	<	732	"Hypothetical, unclassified, unknown"	B
	b0285	yagS	<	318	"Hypothetical, unclassified, unknown"	B
	b0286	yagT	<	229	Central intermediary metabolism	B
o0059	b0284	yagR	<	732	"Hypothetical, unclassified, unknown"	Bsu
	b0285	yagS	<	318	"Hypothetical, unclassified, unknown"	Bsu
o0059	b0284	yagR	<	732	"Hypothetical, unclassified, unknown"	Eco
	b0285	yagS	<	318	"Hypothetical, unclassified, unknown"	Eco
	b0286	yagT	<	229	Central intermediary metabolism	Eco
o0060	b0289	yagV	<	251	"Hypothetical, unclassified, unknown"	B
	b0290	yagW	<	547	Putative regulatory proteins	B
	b0291	yagX	<	841	"Hypothetical, unclassified, unknown"	B
	b0292	yagY	<	222	"Hypothetical, unclassified, unknown"	B
o0061	b0297	eaeH	>	295	Structural proteins	B
	b0298	b0298	>	102	"Hypothetical, unclassified, unknown"	B
	b0299	b0299	>	288	"phage, transposon, or plasmid"	B
o0061	b0298	b0298	>	102	"Hypothetical, unclassified, unknown"	Eco
	b0299	b0299	>	288	"phage, transposon, or plasmid"	Eco
o0062	b0306	ykgE	>	239	"Hypothetical, unclassified, unknown"	Mja Mth
	b0307	ykgF	>	475	"Hypothetical, unclassified, unknown"	Mja Mth
o0062	b0306	ykgE	>	239	"Hypothetical, unclassified, unknown"	B Bsu Hpy
	b0307	ykgF	>	475	"Hypothetical, unclassified, unknown"	B Bsu Hpy
	b0308	ykgG	>	282	Putative transport proteins	B Bsu Hpy

o0062	b0307	ykgF	>	475	"Hypothetical, unclassified, unknown"	Bsu
	b0308	ykgG	>	282	Putative transport proteins	Bsu
o0063	b0311	betA	<	556	"Cell processes (incl. adaptation, protection)"	Bsu
	b0312	betB	<	490	"Cell processes (incl. adaptation, protection)"	Bsu
o0063	b0311	betA	<	556	"Cell processes (incl. adaptation, protection)"	B
	b0312	betB	<	490	"Cell processes (incl. adaptation, protection)"	B
	b0313	betI	<	195	"Cell processes (incl. adaptation, protection)"	B
o0063	b0312	betB	<	490	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hin
	b0313	betI	<	195	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hin
o0064	b0318	b0318	>	201	Putative regulatory proteins	B
	b0319	b0319	>	287	"Hypothetical, unclassified, unknown"	B
	b0320	b0320	>	515	"Hypothetical, unclassified, unknown"	B
	b0321	b0321	>	472	"Hypothetical, unclassified, unknown"	B
	b0322	b0322	>	106	"Hypothetical, unclassified, unknown"	B
o0064	b0320	b0320	>	515	"Hypothetical, unclassified, unknown"	Eco
	b0321	b0321	>	472	"Hypothetical, unclassified, unknown"	Eco
o0065	b0323	b0323	>	316	Putative enzymes	B
	b0324	b0324	>	460	Putative enzymes	B
o0066	b0333	b0333	>	389	Central intermediary metabolism	Bsu Sce
	b0334	b0334	>	483	"Hypothetical, unclassified, unknown"	Bsu Sce
o0066	b0333	b0333	>	389	Central intermediary metabolism	B
	b0334	b0334	>	483	"Hypothetical, unclassified, unknown"	B
	b0335	b0335	>	628	"Hypothetical, unclassified, unknown"	B
o0067	b0336	codB	>	419	Transport and binding proteins	B Eco
	b0337	codA	>	427	Nucleotide biosynthesis and metabolism	B Eco
o0068	b0339	cynT	>	219	Central intermediary metabolism	B
	b0340	cynS	>	156	Central intermediary metabolism	B
	b0341	cynX	>	384	Transport and binding proteins	B
o0069	b0342	lacA	<	203	Carbon compound catabolism	Bsu
	b0343	lacY	<	417	Transport and binding proteins	Bsu
o0069	b0342	lacA	<	203	Carbon compound catabolism	B
	b0343	lacY	<	417	Transport and binding proteins	B
	b0344	lacZ	<	1024	Carbon compound catabolism	B
o0070	b0347	b0347	>	554	"Hypothetical, unclassified, unknown"	B
	b0348	mhpB	>	314	Carbon compound catabolism	B
	b0349	b0349	>	309	Carbon compound catabolism	B
	b0350	b0350	>	271	Putative enzymes	B
	b0351	mhpE	>	316	Carbon compound catabolism	B
	b0352	b0352	>	337	Carbon compound catabolism	B
o0070	b0348	mhpB	>	314	Carbon compound catabolism	Sce
	b0349	b0349	>	309	Carbon compound catabolism	Sce
o0071	b0353	b0353	>	418	Putative transport proteins	B
	b0354	b0354	>	218	"DNA replication, recombination, modification and repair"	B
o0072	b0356	adhC	<	369	Energy metabolism	B
	b0357	b0357	<	98	Structural proteins	B
o0073	b0358	b0358	<	257	"Hypothetical, unclassified, unknown"	B
	b0359	b0359	<	147	"Hypothetical, unclassified, unknown"	B
o0074	b0360	yi21_1	>	136	"Hypothetical, unclassified, unknown"	B Eco
	b0361	yi22_1	>	301	"Transcription, RNA processing and degradation"	B Eco
o0075	b0362	b0362	<	128	"Hypothetical, unclassified, unknown"	B
	b0363	b0363	<	398	Cell structure	B

o0076	b0365	b0365	>	339	Putative transport proteins	Bsu Syn
	b0366	b0366	>	255	Central intermediary metabolism	Bsu Syn
o0076	b0365	b0365	>	339	Putative transport proteins	B
	b0366	b0366	>	255	Central intermediary metabolism	B
	b0367	b0367	>	275	Putative transport proteins	B
	b0368	b0368	>	283	"Hypothetical, unclassified, unknown"	B
o0076	b0366	b0366	>	255	Central intermediary metabolism	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
	b0367	b0367	>	275	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
o0077	b0372	tra5_1	<	288	"phage, transposon, or plasmid"	B Eco
	b0373	b0373	<	102	"Hypothetical, unclassified, unknown"	B Eco
o0078	b0374	b0374	>	467	Putative enzymes	B
	b0375	b0375	>	222	"Hypothetical, unclassified, unknown"	B
o0079	b0377	sbmA	>	406	"Cell processes (incl. adaptation, protection)"	B
	b0378	b0378	>	364	"Hypothetical, unclassified, unknown"	B
o0080	b0388	aroL	>	174	Amino acid biosynthesis and metabolism	B
	b0389	yaiA	>	63	"Hypothetical, unclassified, unknown"	B
	b0390	aroM	>	225	Amino acid biosynthesis and metabolism	B
o0081	b0394	yajF	>	348	"Hypothetical, unclassified, unknown"	B
	b0395	b0395	>	80	"Hypothetical, unclassified, unknown"	B
o0082	b0397	sbcC	<	1048	"Transcription, RNA processing and degradation"	B Bsu Mja Mth
	b0398	sbcD	<	400	"Transcription, RNA processing and degradation"	B Bsu Mja Mth
o0083	b0399	phoB	>	229	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
	b0400	phoR	>	431	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
o0084	b0405	queA	>	356	"Translation, post-translational modification"	Hin
	b0406	tgt	>	375	"Translation, post-translational modification"	Hin
o0084	b0405	queA	>	356	"Translation, post-translational modification"	Bsu
	b0406	tgt	>	375	"Translation, post-translational modification"	Bsu
	b0407	yajC	>	110	"Hypothetical, unclassified, unknown"	Bsu
o0084	b0405	queA	>	356	"Translation, post-translational modification"	B
	b0406	tgt	>	375	"Translation, post-translational modification"	B
	b0407	yajC	>	110	"Hypothetical, unclassified, unknown"	B
	b0408	secD	>	615	Transport and binding proteins	B
	b0409	secF	>	323	Transport and binding proteins	B
o0084	b0406	tgt	>	375	"Translation, post-translational modification"	Eco
	b0407	yajC	>	110	"Hypothetical, unclassified, unknown"	Eco
o0084	b0407	yajC	>	110	"Hypothetical, unclassified, unknown"	Hin Hpy
	b0408	secD	>	615	Transport and binding proteins	Hin Hpy
	b0409	secF	>	323	Transport and binding proteins	Hin Hpy
o0084	b0408	secD	>	615	Transport and binding proteins	Bsu Eco Hin Hpy Syn
	b0409	secF	>	323	Transport and binding proteins	Bsu Eco Hin Hpy Syn
o0085	b0413	ybaD	>	149	"Hypothetical, unclassified, unknown"	Eco Hin
	b0414	ribD	>	367	"Biosynthesis of cofactors, prosthetic groups and carriers"	Eco Hin
o0085	b0413	ybaD	>	149	"Hypothetical, unclassified, unknown"	B
	b0414	ribD	>	367	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0415	ribH	>	156	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0416	nusB	>	139	"Transcription, RNA processing and degradation"	B
o0085	b0415	ribH	>	156	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hpy
	b0416	nusB	>	139	"Transcription, RNA processing and degradation"	Hpy
o0086	b0417	b0417	>	325	Putative regulatory proteins	B Bsu Mja
	b0418	b0418	>	172	"Hypothetical, unclassified, unknown"	B Bsu Mja

o0087	b0421	ispA	<	299	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0422	xseB	<	80	"Transcription, RNA processing and degradation"	B
o0088	b0424	thiJ	<	198	"Hypothetical, unclassified, unknown"	B
	b0425	apbA	<	303	"Hypothetical, unclassified, unknown"	B
o0089	b0428	cyoE	<	296	Energy metabolism	B
	b0429	cyoD	<	109	Energy metabolism	B
	b0430	cyoC	<	204	Energy metabolism	B
	b0431	cyoB	<	663	Energy metabolism	B
	b0432	cyoA	<	315	Energy metabolism	B
o0089	b0429	cyoD	<	109	Energy metabolism	Bsu
	b0430	cyoC	<	204	Energy metabolism	Bsu
	b0431	cyoB	<	663	Energy metabolism	Bsu
	b0432	cyoA	<	315	Energy metabolism	Bsu
o0089	b0430	cyoC	<	204	Energy metabolism	Syn
	b0431	cyoB	<	663	Energy metabolism	Syn
o0089	b0430	cyoC	<	204	Energy metabolism	Syn
	b0431	cyoB	<	663	Energy metabolism	Syn
	b0432	cyoA	<	315	Energy metabolism	Syn
o0090	b0433	ampG	<	491	"Cell processes (incl. adaptation, protection)"	B Eco
	b0434	yajG	<	226	Putative enzymes	B Eco
o0091	b0437	clpP	>	207	"Translation, post-translational modification"	B Mja Mth
	b0438	clpX	>	424	"Translation, post-translational modification"	B Mja Mth
o0092	b0447	b0447	>	181	Putative regulatory proteins	Hin Syn
	b0448	mdlA	>	590	Transport and binding proteins	Hin Syn
o0092	b0447	b0447	>	181	Putative regulatory proteins	B
	b0448	mdlA	>	590	Transport and binding proteins	B
	b0449	mdlB	>	593	Transport and binding proteins	B
o0092	b0448	mdlA	>	590	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b0449	mdlB	>	593	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0093	b0450	glnK	>	112	Central intermediary metabolism	B Bsu Mja Mth
	b0451	amtB	>	428	Central intermediary metabolism	B Bsu Mja Mth
o0094	b0460	hha	<	72	"Translation, post-translational modification"	B
	b0461	ybaJ	<	124	"Hypothetical, unclassified, unknown"	B
o0095	b0462	acrB	<	1049	"Cell processes (incl. adaptation, protection)"	B Bsu Eco Hpy Mth Syn
	b0463	acrA	<	397	Cell structure	B Bsu Eco Hpy Mth Syn
o0096	b0466	ybaM	<	53	"Hypothetical, unclassified, unknown"	B
	b0467	priC	<	175	"DNA replication, recombination, modification and repair"	B
o0097	b0470	dnaX	>	643	"DNA replication, recombination, modification and repair"	B Bsu
	b0471	ybaB	>	109	"Hypothetical, unclassified, unknown"	B Bsu
	b0472	recR	>	201	"DNA replication, recombination, modification and repair"	B Bsu
o0097	b0471	ybaB	>	109	"Hypothetical, unclassified, unknown"	Hin
	b0472	recR	>	201	"DNA replication, recombination, modification and repair"	Hin
o0098	b0485	b0485	>	310	Putative enzymes	B Bsu
	b0486	b0486	>	430	Putative transport proteins	B Bsu
o0099	b0488	b0488	<	151	"Hypothetical, unclassified, unknown"	B Mja Mth Syn
	b0489	b0489	<	305	Membrane proteins	B Mja Mth Syn
o0100	b0490	b0490	>	225	Putative transport proteins	B Bsu Eco Hpy Mth Syn
	b0491	b0491	>	268	Putative transport proteins	B Bsu Eco Hpy Mth Syn
o0101	b0492	b0492	<	296	Energy metabolism	B
	b0493	b0493	<	269	Putative enzymes	B
	b0494	tesA	<	208	Fatty acid and phospholipid metabolism	B

o0102	b0495	ybbA	>	228	Transport and binding proteins	B
	b0496	b0496	>	804	Putative enzymes	B
o0103	b0497	rhsD	>	1426	"Hypothetical, unclassified, unknown"	Eco
	b0498	ybbC	>	122	"Hypothetical, unclassified, unknown"	Eco
o0103	b0497	rhsD	>	1426	"Hypothetical, unclassified, unknown"	B
	b0498	ybbC	>	122	"Hypothetical, unclassified, unknown"	B
	b0499	b0499	>	236	"Hypothetical, unclassified, unknown"	B
	b0500	ybbD	>	86	"Hypothetical, unclassified, unknown"	B
	b0501	b0501	>	63	"Hypothetical, unclassified, unknown"	B
o0103	b0498	ybbC	>	122	"Hypothetical, unclassified, unknown"	Eco
	b0499	b0499	>	236	"Hypothetical, unclassified, unknown"	Eco
o0104	b0507	gcl	>	593	Central intermediary metabolism	B
	b0508	gip	>	258	Central intermediary metabolism	B
o0105	b0509	b0509	>	292	Putative enzymes	B
	b0510	b0510	>	92	"Hypothetical, unclassified, unknown"	B
	b0511	b0511	>	437	Putative transport proteins	B
o0106	b0513	b0513	>	435	Putative transport proteins	B Bsu Hin Sce
	b0514	b0514	>	381	"Hypothetical, unclassified, unknown"	B Bsu Hin Sce
o0107	b0515	b0515	<	261	"Hypothetical, unclassified, unknown"	B
	b0516	b0516	<	411	Putative enzymes	B
	b0517	b0517	<	349	Central intermediary metabolism	B
o0108	b0519	b0519	>	333	"Hypothetical, unclassified, unknown"	B
	b0520	b0520	>	271	Putative enzymes	B
	b0521	ybcF	>	297	Central intermediary metabolism	B
o0108	b0520	b0520	>	271	Putative enzymes	Sce
	b0521	ybcF	>	297	Central intermediary metabolism	Sce
o0109	b0522	purK	<	355	Nucleotide biosynthesis and metabolism	B Bsu Hin
	b0523	purE	<	169	Nucleotide biosynthesis and metabolism	B Bsu Hin
o0110	b0524	ybbF	<	240	"Hypothetical, unclassified, unknown"	B
	b0525	ppiB	<	164	"Translation, post-translational modification"	B
o0111	b0528	ybcJ	<	77	"Hypothetical, unclassified, unknown"	B
	b0529	folD	<	288	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0112	b0531	b0531	>	230	Putative chaperones	Eco
	b0532	b0532	>	867	Cell structure	Eco
o0112	b0531	b0531	>	230	Putative chaperones	B
	b0532	b0532	>	867	Cell structure	B
	b0533	b0533	>	325	"Cell processes (incl. adaptation, protection)"	B
	b0534	ybcG	>	171	"Cell processes (incl. adaptation, protection)"	B
o0113	b0540	b0540	>	102	"Hypothetical, unclassified, unknown"	B Eco
	b0541	tra5_2	>	288	"phage, transposon, or plasmid"	B Eco
o0114	b0545	b0545	>	183	"Hypothetical, unclassified, unknown"	B
	b0546	b0546	>	265	"Translation, post-translational modification"	B
o0115	b0547	b0547	>	151	"Hypothetical, unclassified, unknown"	B
	b0548	b0548	>	56	"Hypothetical, unclassified, unknown"	B
	b0549	b0549	>	96	"Hypothetical, unclassified, unknown"	B
	b0550	b0550	>	120	"Hypothetical, unclassified, unknown"	B
o0116	b0552	yi52_2	<	338	"phage, transposon, or plasmid"	B
	b0553	nmpC	<	375	"phage, transposon, or plasmid"	B
o0117	b0554	b0554	>	71	"Hypothetical, unclassified, unknown"	B
	b0555	b0555	>	165	"Hypothetical, unclassified, unknown"	B
	b0556	b0556	>	153	"Hypothetical, unclassified, unknown"	B

o0118	b0560	nohB	>	181	"phage, transposon, or plasmid"	B
	b0561	b0561	>	247	"Hypothetical, unclassified, unknown"	B
o0119	b0565	ompT	<	317	Cell structure	B Eco
	b0566	envY	<	253	Cell structure	B Eco
o0120	b0568	nfrA	<	990	"phage, transposon, or plasmid"	B Eco
	b0569	nfrB	<	745	"phage, transposon, or plasmid"	B Eco
o0121	b0570	b0570	<	480	Putative regulatory proteins	B Bsu Eco Hin Mth Syn
	b0571	b0571	<	227	Putative regulatory proteins	B Bsu Eco Hin Mth Syn
o0122	b0573	b0573	>	110	"Hypothetical, unclassified, unknown"	B
	b0574	b0574	>	407	Putative transport proteins	B
	b0575	ybdE	>	1047	Putative transport proteins	B
o0122	b0574	b0574	>	407	Putative transport proteins	Eco Hin Hpy Syn
	b0575	ybdE	>	1047	Putative transport proteins	Eco Hin Hpy Syn
o0123	b0583	entD	<	209	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0584	fepA	<	746	Transport and binding proteins	B
o0124	b0585	fes	>	374	Transport and binding proteins	B
	b0586	entF	>	1293	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0587	fepE	>	377	Transport and binding proteins	B
o0125	b0588	fepC	<	271	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Mth Syn
	b0589	fepG	<	330	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Mth Syn
o0125	b0588	fepC	<	271	Transport and binding proteins	B Bsu Eco Syn
	b0589	fepG	<	330	Transport and binding proteins	B Bsu Eco Syn
	b0590	fepD	<	334	Transport and binding proteins	B Bsu Eco Syn

operon#	b#	gene	dir	length	function	species
o0125	b0589	fepG	<	330	Transport and binding proteins	Bsu Eco Mja Syn
	b0590	fepD	<	334	Transport and binding proteins	Bsu Eco Mja Syn
o0126	b0593	entC	>	391	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b0594	entE	>	536	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0126	b0593	entC	>	391	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b0594	entE	>	536	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b0595	entB	>	285	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0126	b0593	entC	>	391	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0594	entE	>	536	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0595	entB	>	285	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0596	entA	>	248	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0126	b0594	entE	>	536	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b0595	entB	>	285	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0127	b0601	b0601	<	209	"Hypothetical, unclassified, unknown"	B
	b0602	b0602	<	406	"Hypothetical, unclassified, unknown"	B
o0128	b0605	ahpC	>	187	"Cell processes (incl. adaptation, protection)"	B Bsu Syn
	b0606	ahpF	>	531	"Cell processes (incl. adaptation, protection)"	B Bsu Syn
o0129	b0613	b0613	<	292	"Hypothetical, unclassified, unknown"	B
	b0614	b0614	<	183	"Hypothetical, unclassified, unknown"	B
	b0615	b0615	<	510	Putative enzymes	B
	b0616	b0616	<	307	Putative enzymes	B
	b0617	b0617	<	98	Energy metabolism	B
	b0618	b0618	<	381	Putative enzymes	B

o0129	b0614	b0614	<	183	"Hypothetical, unclassified, unknown"	Hin
	b0615	b0615	<	510	Putative enzymes	Hin
	b0616	b0616	<	307	Putative enzymes	Hin
	b0617	b0617	<	98	Energy metabolism	Hin
	b0618	b0618	<	381	Putative enzymes	Hin
o0130	b0619	b0619	>	552	Putative regulatory proteins	B Bsu Eco Hin Mth Syn
	b0620	criR	>	226	Putative regulatory proteins	B Bsu Eco Hin Mth Syn
o0131	b0625	ybeH	>	75	"Hypothetical, unclassified, unknown"	B
	b0626	b0626	>	187	Putative enzymes	B
o0132	b0628	lipA	<	321	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin
	b0629	ybeF	<	266	"Hypothetical, unclassified, unknown"	Hin
o0132	b0628	lipA	<	321	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0629	ybeF	<	266	"Hypothetical, unclassified, unknown"	B
	b0630	lipB	<	191	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0132	b0629	ybeF	<	266	"Hypothetical, unclassified, unknown"	Bsu
	b0630	lipB	<	191	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0133	b0633	rlpA	<	362	Membrane proteins	B
	b0634	mrdB	<	370	Cell structure	B
	b0635	mrdA	<	633	Cell structure	B
	b0636	ybeA	<	155	"Hypothetical, unclassified, unknown"	B
	b0637	ybeB	<	69	"Hypothetical, unclassified, unknown"	B
o0134	b0638	phpB	<	203	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0639	b0639	<	213	"Hypothetical, unclassified, unknown"	B
	b0640	holA	<	343	"DNA replication, recombination, modification and repair"	B
	b0641	rlpB	<	193	Cell structure	B
	b0642	leuS	<	860	"Translation, post-translational modification"	B
o0134	b0640	holA	<	343	"DNA replication, recombination, modification and repair"	Syn
	b0641	rlpB	<	193	Cell structure	Syn
o0134	b0640	holA	<	343	"DNA replication, recombination, modification and repair"	Hin
	b0641	rlpB	<	193	Cell structure	Hin
	b0642	leuS	<	860	"Translation, post-translational modification"	Hin
o0135	b0645	b0645	>	235	"Hypothetical, unclassified, unknown"	B
	b0646	b0646	>	475	Putative enzymes	B
o0136	b0648	b0648	>	235	"Translation, post-translational modification"	B
	b0649	b0649	>	483	"Hypothetical, unclassified, unknown"	B
o0137	b0652	gltL	<	241	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja
	b0653	gltK	<	224	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja
o0137	b0652	gltL	<	241	Transport and binding proteins	B Bsu Hpy Syn
	b0653	gltK	<	224	Transport and binding proteins	B Bsu Hpy Syn
	b0654	gltJ	<	246	Transport and binding proteins	B Bsu Hpy Syn
o0137	b0653	gltK	<	224	Transport and binding proteins	Bsu Eco Hin Hpy
	b0654	gltJ	<	246	Transport and binding proteins	Bsu Eco Hin Hpy
o0138	b0657	lnt	<	512	Transport and binding proteins	B Hin Hpy
	b0658	b0658	<	292	Putative enzymes	B Hin Hpy
o0139	b0659	b0659	<	155	"Hypothetical, unclassified, unknown"	B
	b0660	b0660	<	359	Putative transport proteins	B
o0140	b0663	b0663	>	111	"Hypothetical, unclassified, unknown"	B
	b0667	b0667	>	45	"Hypothetical, unclassified, unknown"	B
	b0669	b0669	>	39	"Hypothetical, unclassified, unknown"	B
	b0671	b0671	>	50	"Hypothetical, unclassified, unknown"	B

o0141	b0664	glnX	<		tRNA	B
	b0665	glnV	<		tRNA	B
	b0666	metU	<		tRNA	B
	b0668	glnW	<		tRNA	B
	b0670	glnU	<		tRNA	B
	b0672	leuW	<		tRNA	B
	b0673	metT	<		tRNA	B
o0142	b0675	nagD	<	250	Central intermediary metabolism	Bsu
	b0676	nagC	<	406	Central intermediary metabolism	Bsu
o0142	b0675	nagD	<	250	Central intermediary metabolism	B
	b0676	nagC	<	406	Central intermediary metabolism	B
	b0677	nagA	<	382	Central intermediary metabolism	B
	b0678	nagB	<	266	Central intermediary metabolism	B
o0142	b0677	nagA	<	382	Central intermediary metabolism	Bsu Hin
	b0678	nagB	<	266	Central intermediary metabolism	Bsu Hin
o0143	b0681	b0681	>	468	"Hypothetical, unclassified, unknown"	B
	b0682	b0682	>	108	"Hypothetical, unclassified, unknown"	B
o0144	b0687	seqA	>	181	"DNA replication, recombination, modification and repair"	B
	b0688	pgm	>	546	Carbon compound catabolism	B
o0145	b0694	kdpE	<	225	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
	b0695	kdpD	<	894	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
o0146	b0696	kdpC	<	190	Transport and binding proteins	B
	b0697	kdpB	<	682	Transport and binding proteins	B
	b0698	kdpA	<	557	Transport and binding proteins	B
o0146	b0697	kdpB	<	682	Transport and binding proteins	Syn
	b0698	kdpA	<	557	Transport and binding proteins	Syn
o0147	b0700	rhsC	>	1397	"Hypothetical, unclassified, unknown"	B
	b0701	b0701	>	73	"Hypothetical, unclassified, unknown"	B
o0148	b0703	b0703	>	477	"Hypothetical, unclassified, unknown"	B
	b0704	ybfC	>	189	"Hypothetical, unclassified, unknown"	B
o0149	b0707	ybgA	>	169	"Hypothetical, unclassified, unknown"	B Mth
	b0708	phrB	>	472	"DNA replication, recombination, modification and repair"	B Mth
o0150	b0710	b0710	>	247	"Hypothetical, unclassified, unknown"	B
	b0711	b0711	>	218	Central intermediary metabolism	B
	b0712	b0712	>	310	Central intermediary metabolism	B
	b0713	b0713	>	244	Carbon compound catabolism	B
	b0714	nei	>	263	"DNA replication, recombination, modification and repair"	B
o0150	b0711	b0711	>	218	Central intermediary metabolism	Hin
	b0712	b0712	>	310	Central intermediary metabolism	Hin
	b0713	b0713	>	244	Carbon compound catabolism	Hin
o0151	b0716	b0716	<	362	"Hypothetical, unclassified, unknown"	B Eco
	b0717	b0717	<	242	Putative chaperones	B Eco
	b0718	b0718	<	818	Central intermediary metabolism	B Eco
o0151	b0717	b0717	<	242	Putative chaperones	Eco
	b0718	b0718	<	818	Central intermediary metabolism	Eco
o0152	b0721	sdhC	>	129	Energy metabolism	B
	b0722	sdhD	>	115	Energy metabolism	B
	b0723	sdhA	>	588	Energy metabolism	B
	b0724	sdhB	>	238	Energy metabolism	B
o0152	b0723	sdhA	>	588	Energy metabolism	Bsu Eco Hin Hpy
	b0724	sdhB	>	238	Energy metabolism	Bsu Eco Hin Hpy

o0153	b0726	sucA	>	933	Energy metabolism	Bsu Hin Mge Mpn
	b0727	sucB	>	405	Energy metabolism	Bsu Hin Mge Mpn
o0153	b0726	sucA	>	933	Energy metabolism	B
	b0727	sucB	>	405	Energy metabolism	B
	b0728	sucC	>	388	Energy metabolism	B
	b0729	sucD	>	289	Energy metabolism	B
o0153	b0728	sucC	>	388	Energy metabolism	Bsu Hin
	b0729	sucD	>	289	Energy metabolism	Bsu Hin
o0154	b0731	hrsA	>	658	"Translation, post-translational modification"	B
	b0732	ybgB	>	877	Carbon compound catabolism	B
o0155	b0733	cydA	>	523	Energy metabolism	Bsu Eco Hin Syn
	b0734	cydB	>	379	Energy metabolism	Bsu Eco Hin Syn
o0155	b0733	cydA	>	523	Energy metabolism	B
	b0734	cydB	>	379	Energy metabolism	B
	b0735	ybgE	>	97	"Hypothetical, unclassified, unknown"	B
o0156	b0737	tolQ	>	230	"phage, transposon, or plasmid"	Eco Hin Hpy Mth Syn
	b0738	tolR	>	142	"phage, transposon, or plasmid"	Eco Hin Hpy Mth Syn
o0156	b0737	tolQ	>	230	"phage, transposon, or plasmid"	Hpy
	b0738	tolR	>	142	"phage, transposon, or plasmid"	Hpy
	b0739	tolA	>	421	"phage, transposon, or plasmid"	Hpy
o0156	b0737	tolQ	>	230	"phage, transposon, or plasmid"	B
	b0738	tolR	>	142	"phage, transposon, or plasmid"	B
	b0739	tolA	>	421	"phage, transposon, or plasmid"	B
	b0740	tolB	>	430	"phage, transposon, or plasmid"	B
o0156	b0739	tolA	>	421	"phage, transposon, or plasmid"	Eco Syn
	b0740	tolB	>	430	"phage, transposon, or plasmid"	Eco Syn
o0157	b0741	pal	>	173	Cell structure	B
	b0742	ybgF	>	263	"Hypothetical, unclassified, unknown"	B
o0158	b0756	galM	<	346	Central intermediary metabolism	Sce
	b0757	galK	<	382	Carbon compound catabolism	Sce
o0158	b0756	galM	<	346	Central intermediary metabolism	Hin
	b0757	galK	<	382	Carbon compound catabolism	Hin
	b0758	galT	<	348	Carbon compound catabolism	Hin
o0158	b0756	galM	<	346	Central intermediary metabolism	B
	b0757	galK	<	382	Carbon compound catabolism	B
	b0758	galT	<	348	Carbon compound catabolism	B
	b0759	galE	<	338	Carbon compound catabolism	B
o0158	b0758	galT	<	348	Carbon compound catabolism	Bsu Sce
	b0759	galE	<	338	Carbon compound catabolism	Bsu Sce
o0159	b0763	modA	>	257	Transport and binding proteins	Bsu Mth Syn
	b0764	modB	>	229	Transport and binding proteins	Bsu Mth Syn
o0159	b0763	modA	>	257	Transport and binding proteins	B Hin Hpy
	b0764	modB	>	229	Transport and binding proteins	B Hin Hpy
	b0765	modC	>	352	Transport and binding proteins	B Hin Hpy
o0159	b0764	modB	>	229	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Sce Syn
	b0765	modC	>	352	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Sce Syn
o0160	b0775	bioB	>	346	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0776	bioF	>	384	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0777	bioC	>	251	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0778	bioD	>	225	"Biosynthesis of cofactors, prosthetic groups and carriers"	B

o0160	b0776	bioF	>	384	"Biosynthesis of cofactors, prosthetic groups and carriers"	Eco
	b0777	bioC	>	251	"Biosynthesis of cofactors, prosthetic groups and carriers"	Eco
o0160	b0777	bioC	>	251	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin
	b0778	bioD	>	225	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin
o0161	b0781	moaA	>	329	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0782	moaB	>	170	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0783	moaC	>	161	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0784	moaD	>	81	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b0785	moaE	>	150	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0161	b0782	moaB	>	170	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hpy
	b0783	moaC	>	161	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hpy
o0161	b0783	moaC	>	161	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin Syn
	b0784	moaD	>	81	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin Syn
	b0785	moaE	>	150	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin Syn
o0161	b0784	moaD	>	81	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu Hpy
	b0785	moaE	>	150	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu Hpy
o0162	b0788	b0788	<	318	"Hypothetical, unclassified, unknown"	B
	b0789	b0789	<	413	Central intermediary metabolism	B
	b0790	b0790	<	253	"Hypothetical, unclassified, unknown"	B
o0163	b0792	b0792	<	368	"Hypothetical, unclassified, unknown"	Eco Hpy
	b0793	b0793	<	377	"Hypothetical, unclassified, unknown"	Eco Hpy
o0163	b0792	b0792	<	368	"Hypothetical, unclassified, unknown"	Mth
	b0793	b0793	<	377	"Hypothetical, unclassified, unknown"	Mth
	b0794	b0794	<	583	Putative transport proteins	Mth
o0163	b0792	b0792	<	368	"Hypothetical, unclassified, unknown"	B
	b0793	b0793	<	377	"Hypothetical, unclassified, unknown"	B
	b0794	b0794	<	583	Putative transport proteins	B
	b0795	b0795	<	332	Cell structure	B
	b0796	ybiH	<	227	"Hypothetical, unclassified, unknown"	B
o0163	b0793	b0793	<	377	"Hypothetical, unclassified, unknown"	Bsu Hin Hpy Mge Mja Mpn Mth Sce
	b0794	b0794	<	583	Putative transport proteins	Bsu Hin Hpy Mge Mja Mpn Mth Sce
o0163	b0793	b0793	<	377	"Hypothetical, unclassified, unknown"	Eco
	b0794	b0794	<	583	Putative transport proteins	Eco
	b0795	b0795	<	332	Cell structure	Eco
o0163	b0794	b0794	<	583	Putative transport proteins	Bsu Eco Sce Syn
	b0795	b0795	<	332	Cell structure	Bsu Eco Sce Syn
o0163	b0795	b0795	<	332	Cell structure	Bsu Eco
	b0796	ybiH	<	227	"Hypothetical, unclassified, unknown"	Bsu Eco
o0164	b0799	dinG	>	716	"DNA replication, recombination, modification and repair"	B Mja
	b0800	ybiB	>	320	Putative enzymes	B Mja
o0165	b0804	b0804	<	237	Putative enzymes	B
	b0805	b0805	<	760	Putative regulatory proteins	B
o0166	b0809	glnQ	<	240	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
	b0810	glnP	<	219	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
o0166	b0809	glnQ	<	240	Transport and binding proteins	B Bsu Hin
	b0810	glnP	<	219	Transport and binding proteins	B Bsu Hin
	b0811	glnH	<	248	Transport and binding proteins	B Bsu Hin
o0166	b0810	glnP	<	219	Transport and binding proteins	Bsu Eco Hin Hpy
	b0811	glnH	<	248	Transport and binding proteins	Bsu Eco Hin Hpy
o0167	b0817	b0817	>	155	"Hypothetical, unclassified, unknown"	B
	b0818	b0818	>	372	"Hypothetical, unclassified, unknown"	B

o0168	b0823	b0823	<	810	Putative enzymes	B Eco Hin Mja Mth
	b0824	b0824	<	308	Putative enzymes	B Eco Hin Mja Mth
o0169	b0826	moeB	<	249	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Bsu Hin
	b0827	moeA	<	411	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Bsu Hin
o0170	b0828	ybiK	>	321	Amino acid biosynthesis and metabolism	B
	b0829	b0829	>	612	Transport and binding proteins	B
	b0830	b0830	>	512	Transport and binding proteins	B
	b0831	b0831	>	306	Transport and binding proteins	B
	b0832	b0832	>	303	Transport and binding proteins	B
o0170	b0829	b0829	>	612	Transport and binding proteins	Bsu
	b0830	b0830	>	512	Transport and binding proteins	Bsu
o0170	b0829	b0829	>	612	Transport and binding proteins	Bsu
	b0830	b0830	>	512	Transport and binding proteins	Bsu
	b0831	b0831	>	306	Transport and binding proteins	Bsu
	b0832	b0832	>	303	Transport and binding proteins	Bsu
o0170	b0830	b0830	>	512	Transport and binding proteins	Hpy
	b0831	b0831	>	306	Transport and binding proteins	Hpy
o0170	b0830	b0830	>	512	Transport and binding proteins	Bsu Eco Hin Hpy
	b0831	b0831	>	306	Transport and binding proteins	Bsu Eco Hin Hpy
	b0832	b0832	>	303	Transport and binding proteins	Bsu Eco Hin Hpy
o0170	b0831	b0831	>	306	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mpn Syn
	b0832	b0832	>	303	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mpn Syn
o0171	b0833	b0833	>	782	"Hypothetical, unclassified, unknown"	B Eco
	b0834	b0834	>	442	"Hypothetical, unclassified, unknown"	B Eco
o0172	b0844	b0844	<	262	"Hypothetical, unclassified, unknown"	B Bsu
	b0845	b0845	<	402	"Hypothetical, unclassified, unknown"	B Bsu
o0173	b0854	potF	>	370	Transport and binding proteins	Eco Sce
	b0855	potG	>	404	Transport and binding proteins	Eco Sce
o0173	b0854	potF	>	370	Transport and binding proteins	B Eco
	b0855	potG	>	404	Transport and binding proteins	B Eco
	b0856	potH	>	317	Transport and binding proteins	B Eco
	b0857	potI	>	281	Transport and binding proteins	B Eco
o0173	b0855	potG	>	404	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth
	b0856	potH	>	317	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth
o0173	b0855	potG	>	404	Transport and binding proteins	Eco Hin Mge Mja Mpn Syn
	b0856	potH	>	317	Transport and binding proteins	Eco Hin Mge Mja Mpn Syn
	b0857	potI	>	281	Transport and binding proteins	Eco Hin Mge Mja Mpn Syn
o0173	b0856	potH	>	317	Transport and binding proteins	Bsu Eco Hin Mge Mja Mpn Mth Syn
	b0857	potI	>	281	Transport and binding proteins	Bsu Eco Hin Mge Mja Mpn Mth Syn
o0174	b0858	b0858	>	162	"Hypothetical, unclassified, unknown"	B
	b0859	b0859	>	375	Putative enzymes	B
o0175	b0860	artJ	<	243	Transport and binding proteins	Bsu Eco Hin Hpy
	b0861	artM	<	222	Transport and binding proteins	Bsu Eco Hin Hpy

operon#	b#	gene	dir	length	function	species
o0175	b0860	artJ	<	243	Transport and binding proteins	Bsu Eco Hin
	b0861	artM	<	222	Transport and binding proteins	Bsu Eco Hin
	b0862	artQ	<	238	Transport and binding proteins	Bsu Eco Hin

o0175	b0860	artJ	<	243	Transport and binding proteins	Eco
	b0861	artM	<	222	Transport and binding proteins	Eco
	b0862	artQ	<	238	Transport and binding proteins	Eco
	b0863	artI	<	243	Transport and binding proteins	Eco
o0175	b0860	artJ	<	243	Transport and binding proteins	B
	b0861	artM	<	222	Transport and binding proteins	B
	b0862	artQ	<	238	Transport and binding proteins	B
	b0863	artI	<	243	Transport and binding proteins	B
	b0864	artP	<	242	Transport and binding proteins	B
o0175	b0861	artM	<	222	Transport and binding proteins	Eco Hpy
	b0862	artQ	<	238	Transport and binding proteins	Eco Hpy
o0175	b0861	artM	<	222	Transport and binding proteins	Bsu Eco
	b0862	artQ	<	238	Transport and binding proteins	Bsu Eco
	b0863	artI	<	243	Transport and binding proteins	Bsu Eco
o0175	b0861	artM	<	222	Transport and binding proteins	Bsu Hin
	b0862	artQ	<	238	Transport and binding proteins	Bsu Hin
	b0863	artI	<	243	Transport and binding proteins	Bsu Hin
	b0864	artP	<	242	Transport and binding proteins	Bsu Hin
o0175	b0862	artQ	<	238	Transport and binding proteins	Bsu Eco Hin Hpy
	b0863	artI	<	243	Transport and binding proteins	Bsu Eco Hin Hpy
o0175	b0863	artI	<	243	Transport and binding proteins	Hpy
	b0864	artP	<	242	Transport and binding proteins	Hpy
o0176	b0866	b0866	>	107	"Hypothetical, unclassified, unknown"	B
	b0867	b0867	>	276	"Cell processes (incl. adaptation, protection)"	B
o0177	b0869	b0869	<	486	Cell structure	Sce
	b0870	b0870	<	333	Putative enzymes	Sce
o0177	b0869	b0869	<	486	Cell structure	B
	b0870	b0870	<	333	Putative enzymes	B
	b0871	poxB	<	572	Carbon compound catabolism	B
o0178	b0872	b0872	<	322	Energy metabolism	B
	b0873	b0873	<	552	"Hypothetical, unclassified, unknown"	B
o0179	b0878	b0878	>	380	Structural proteins	B Bsu Eco Hpy Syn
	b0879	b0879	>	648	Putative transport proteins	B Bsu Eco Hpy Syn
o0180	b0881	b0881	>	106	"Hypothetical, unclassified, unknown"	B Hpy
	b0882	clpA	>	758	"Translation, post-translational modification"	B Hpy
o0181	b0886	cydC	<	573	Transport and binding proteins	B Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b0887	cydD	<	588	Transport and binding proteins	B Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0182	b0891	lolA	>	204	Transport and binding proteins	B
	b0892	ycaJ	>	447	"DNA replication, recombination, modification and repair"	B
o0183	b0894	dmsA	>	785	Energy metabolism	Bsu Eco Mja Mth
	b0895	dmsB	>	205	Energy metabolism	Bsu Eco Mja Mth
o0183	b0894	dmsA	>	785	Energy metabolism	B Eco Hin
	b0895	dmsB	>	205	Energy metabolism	B Eco Hin
	b0896	dmsC	>	287	Energy metabolism	B Eco Hin
o0183	b0895	dmsB	>	205	Energy metabolism	Bsu Eco Mth Syn
	b0896	dmsC	>	287	Energy metabolism	Bsu Eco Mth Syn
o0184	b0898	ycaD	>	382	Putative transport proteins	B
	b0899	b0899	>	540	Putative transport proteins	B
o0185	b0902	pflA	<	246	Energy metabolism	B Eco Mth
	b0903	pflB	<	760	Energy metabolism	B Eco Mth

o0186	b0907	serC	>	362	Amino acid biosynthesis and metabolism	B
	b0908	aroA	>	427	Amino acid biosynthesis and metabolism	B
o0187	b0913	ycaI	>	780	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Syn
	b0914	msbA	>	582	Transport and binding proteins	Bsu Eco Hin Syn
o0187	b0913	ycaI	>	780	"Hypothetical, unclassified, unknown"	Hin
	b0914	msbA	>	582	Transport and binding proteins	Hin
	b0915	ycaH	>	328	Putative enzymes	Hin
o0187	b0913	ycaI	>	780	"Hypothetical, unclassified, unknown"	B
	b0914	msbA	>	582	Transport and binding proteins	B
	b0915	ycaH	>	328	Putative enzymes	B
	b0916	b0916	>	410	"Hypothetical, unclassified, unknown"	B
o0187	b0914	msbA	>	582	Transport and binding proteins	Bsu Eco Syn
	b0915	ycaH	>	328	Putative enzymes	Bsu Eco Syn
o0188	b0917	b0917	>	60	"Hypothetical, unclassified, unknown"	B
	b0918	kdsB	>	248	Cell structure	B
o0189	b0921	smtA	>	261	"Hypothetical, unclassified, unknown"	B
	b0922	mukF	>	440	"Translation, post-translational modification"	B
	b0923	mukE	>	225	"Hypothetical, unclassified, unknown"	B
	b0924	mukB	>	1486	"Cell processes (incl. adaptation, protection)"	B
o0189	b0922	mukF	>	440	"Translation, post-translational modification"	Eco
	b0923	mukE	>	225	"Hypothetical, unclassified, unknown"	Eco
o0189	b0922	mukF	>	440	"Translation, post-translational modification"	Hin
	b0923	mukE	>	225	"Hypothetical, unclassified, unknown"	Hin
	b0924	mukB	>	1486	"Cell processes (incl. adaptation, protection)"	Hin
o0189	b0923	mukE	>	225	"Hypothetical, unclassified, unknown"	Eco
	b0924	mukB	>	1486	"Cell processes (incl. adaptation, protection)"	Eco
o0190	b0926	b0926	>	182	"Hypothetical, unclassified, unknown"	B
	b0927	b0927	>	215	"Hypothetical, unclassified, unknown"	B
o0191	b0933	ycbE	<	255	Putative regulatory proteins	Bsu Eco Hin Hpy Mja Syn
	b0934	b0934	<	278	Putative transport proteins	Bsu Eco Hin Hpy Mja Syn
o0191	b0933	ycbE	<	255	Putative regulatory proteins	B
	b0934	b0934	<	278	Putative transport proteins	B
	b0935	b0935	<	381	"Hypothetical, unclassified, unknown"	B
	b0936	b0936	<	333	"Hypothetical, unclassified, unknown"	B
	b0937	b0937	<	191	"Hypothetical, unclassified, unknown"	B
o0191	b0934	b0934	<	278	Putative transport proteins	Bsu Mge
	b0935	b0935	<	381	"Hypothetical, unclassified, unknown"	Bsu Mge
o0191	b0935	b0935	<	381	"Hypothetical, unclassified, unknown"	Bsu
	b0936	b0936	<	333	"Hypothetical, unclassified, unknown"	Bsu
o0192	b0939	b0939	>	233	Putative chaperones	Eco Hin
	b0940	b0940	>	866	Cell structure	Eco Hin
o0192	b0939	b0939	>	233	Putative chaperones	B
	b0940	b0940	>	866	Cell structure	B
	b0941	b0941	>	356	Cell structure	B
	b0942	b0942	>	180	Cell structure	B
	b0943	b0943	>	187	Cell structure	B
	b0944	ycbF	>	245	Putative chaperones	B
o0192	b0942	b0942	>	180	Cell structure	Eco
	b0943	b0943	>	187	Cell structure	Eco

o0192	b0942	b0942	>	180	Cell structure	Eco
	b0943	b0943	>	187	Cell structure	Eco
	b0944	ycbF	>	245	Putative chaperones	Eco
o0192	b0943	b0943	>	187	Cell structure	Eco
	b0944	ycbF	>	245	Putative chaperones	Eco
o0193	b0948	b0948	>	702	"Hypothetical, unclassified, unknown"	B Sce
	b0949	b0949	>	635	Putative transport proteins	B Sce
o0194	b0950	pqiA	>	417	Other known genes	Eco Hin Sce
	b0951	pqiB	>	546	Other known genes	Eco Hin Sce
o0194	b0950	pqiA	>	417	Other known genes	B
	b0951	pqiB	>	546	Other known genes	B
	b0952	b0952	>	182	"Hypothetical, unclassified, unknown"	B
o0195	b0960	b0960	<	720	"Hypothetical, unclassified, unknown"	B
	b0961	yccF	<	148	"Hypothetical, unclassified, unknown"	B
o0196	b0966	b0966	<	122	"Hypothetical, unclassified, unknown"	B
	b0967	b0967	<	367	"Hypothetical, unclassified, unknown"	B
o0197	b0969	yccK	<	128	Central intermediary metabolism	B
	b0970	yccA	<	219	Putative transport proteins	B
o0198	b0972	hyaA	>	372	Energy metabolism	Eco Mja Mth
	b0973	hyaB	>	597	Energy metabolism	Eco Mja Mth
o0198	b0972	hyaA	>	372	Energy metabolism	Hpy
	b0973	hyaB	>	597	Energy metabolism	Hpy
	b0974	hyaC	>	235	Energy metabolism	Hpy
	b0975	hyaD	>	195	Energy metabolism	Hpy
o0198	b0972	hyaA	>	372	Energy metabolism	B
	b0973	hyaB	>	597	Energy metabolism	B
	b0974	hyaC	>	235	Energy metabolism	B
	b0975	hyaD	>	195	Energy metabolism	B
	b0976	hyaE	>	132	Energy metabolism	B
	b0977	hyaF	>	285	Energy metabolism	B
o0199	b0978	appC	>	514	Energy metabolism	Bsu Eco Hin Syn
	b0979	appB	>	378	Energy metabolism	Bsu Eco Hin Syn
o0199	b0978	appC	>	514	Energy metabolism	B
	b0979	appB	>	378	Energy metabolism	B
	b0980	appA	>	432	Central intermediary metabolism	B
o0199	b0979	appB	>	378	Energy metabolism	Syn
	b0980	appA	>	432	Central intermediary metabolism	Syn
o0200	b0981	yccC	<	726	"Hypothetical, unclassified, unknown"	Eco
	b0982	b0982	<	152	Putative enzymes	Eco
	b0983	b0983	<	379	Cell structure	Eco
o0200	b0981	yccC	<	726	"Hypothetical, unclassified, unknown"	B
	b0982	b0982	<	152	Putative enzymes	B
	b0983	b0983	<	379	Cell structure	B
	b0984	b0984	<	698	"Hypothetical, unclassified, unknown"	B
	b0985	b0985	<	248	"Hypothetical, unclassified, unknown"	B
	b0986	b0986	<	214	Putative regulatory proteins	B
o0201	b0996	torC	>	390	Energy metabolism	Eco Hin
	b0997	torA	>	848	Energy metabolism	Eco Hin
o0201	b0996	torC	>	390	Energy metabolism	B
	b0997	torA	>	848	Energy metabolism	B
	b0998	torD	>	199	Energy metabolism	B

o0202	b0999	yccD	<	101	"Hypothetical, unclassified, unknown"	B
	b1000	cbpA	<	306	"Cell processes (incl. adaptation, protection)"	B
o0203	b1003	yccJ	<	75	"Hypothetical, unclassified, unknown"	B
	b1004	wrbA	<	198	Amino acid biosynthesis and metabolism	B
o0204	b1006	b1006	<	464	Putative enzymes	B
	b1007	b1007	<	152	"Hypothetical, unclassified, unknown"	B
	b1008	b1008	<	196	"Hypothetical, unclassified, unknown"	B
	b1009	b1009	<	266	Central intermediary metabolism	B
	b1010	b1010	<	128	"Hypothetical, unclassified, unknown"	B
	b1011	b1011	<	244	Putative enzymes	B
	b1012	b1012	<	382	"Hypothetical, unclassified, unknown"	B
o0205	b1016	b1016	>	39	"Hypothetical, unclassified, unknown"	B
	b1017	b1017	>	243	Energy metabolism	B
o0206	b1018	b1018	>	375	"Hypothetical, unclassified, unknown"	B
	b1019	ycdB	>	423	"Hypothetical, unclassified, unknown"	B
o0207	b1021	b1021	<	137	"Hypothetical, unclassified, unknown"	B
	b1022	b1022	<	441	"Hypothetical, unclassified, unknown"	B
	b1023	b1023	<	672	"Hypothetical, unclassified, unknown"	B
	b1024	b1024	<	807	"Hypothetical, unclassified, unknown"	B
o0207	b1023	b1023	<	672	"Hypothetical, unclassified, unknown"	Eco
	b1024	b1024	<	807	"Hypothetical, unclassified, unknown"	Eco
o0208	b1026	tra5_3	<	288	"phage, transposon, or plasmid"	B Eco
	b1027	b1027	<	102	"Hypothetical, unclassified, unknown"	B Eco
o0209	b1028	b1028	>	107	"Hypothetical, unclassified, unknown"	B Bsu
	b1029	b1029	>	328	"Hypothetical, unclassified, unknown"	B Bsu
o0210	b1030	b1030	>	83	"Hypothetical, unclassified, unknown"	B Eco
	b1031	b1031	>	137	"Translation, post-translational modification"	B Eco
o0211	b1034	b1034	>	245	"Hypothetical, unclassified, unknown"	B
	b1035	b1035	>	184	"Hypothetical, unclassified, unknown"	B
o0212	b1037	csgG	<	277	Cell structure	B
	b1038	csgF	<	138	Cell structure	B
	b1039	csgE	<	129	Cell structure	B
	b1040	csgD	<	216	Cell structure	B
o0213	b1041	csgB	>	151	Cell structure	B Eco
	b1042	csgA	>	151	Cell structure	B Eco
o0214	b1045	b1045	>	177	"Hypothetical, unclassified, unknown"	B
	b1046	b1046	>	493	"Hypothetical, unclassified, unknown"	B
o0215	b1048	mdoG	>	511	"Cell processes (incl. adaptation, protection)"	B
	b1049	mdoH	>	847	"Cell processes (incl. adaptation, protection)"	B
o0216	b1051	msyB	<	125	Transport and binding proteins	B
	b1052	b1052	<	32	"Hypothetical, unclassified, unknown"	B
	b1053	yceE	<	408	"Hypothetical, unclassified, unknown"	B
o0217	b1056	yceI	<	191	"Hypothetical, unclassified, unknown"	B
	b1057	b1057	<	188	"Hypothetical, unclassified, unknown"	B
o0218	b1058	b1058	<	46	"Hypothetical, unclassified, unknown"	B
	b1059	b1059	<	372	Putative enzymes	B
o0219	b1066	rimJ	>	194	"Translation, post-translational modification"	B
	b1067	yceH	>	215	"Hypothetical, unclassified, unknown"	B
	b1068	mviM	>	307	"Cell processes (incl. adaptation, protection)"	B

o0220	b1070	flgN	<	138	"Cell processes (incl. adaptation, protection)"	B
	b1071	flgM	<	97	"Cell processes (incl. adaptation, protection)"	B
	b1072	flgA	<	219	"Cell processes (incl. adaptation, protection)"	B
o0221	b1073	flgB	>	138	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hpy
	b1074	flgC	>	134	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hpy
o0221	b1073	flgB	>	138	"Cell processes (incl. adaptation, protection)"	B
	b1074	flgC	>	134	"Cell processes (incl. adaptation, protection)"	B
	b1075	flgD	>	231	"Cell processes (incl. adaptation, protection)"	B
	b1076	flgE	>	402	"Cell processes (incl. adaptation, protection)"	B
	b1077	flgF	>	251	"Cell processes (incl. adaptation, protection)"	B
	b1078	flgG	>	260	"Cell processes (incl. adaptation, protection)"	B
	b1079	flgH	>	232	"Cell processes (incl. adaptation, protection)"	B
	b1080	flgI	>	365	"Cell processes (incl. adaptation, protection)"	B
	b1081	flgJ	>	313	"Cell processes (incl. adaptation, protection)"	B
	b1082	flgK	>	547	"Cell processes (incl. adaptation, protection)"	B
o0221	b1075	flgD	>	231	"Cell processes (incl. adaptation, protection)"	Bsu Hpy Sce
	b1076	flgE	>	402	"Cell processes (incl. adaptation, protection)"	Bsu Hpy Sce
o0221	b1075	flgD	>	231	"Cell processes (incl. adaptation, protection)"	Eco
	b1076	flgE	>	402	"Cell processes (incl. adaptation, protection)"	Eco
	b1077	flgF	>	251	"Cell processes (incl. adaptation, protection)"	Eco
o0221	b1076	flgE	>	402	"Cell processes (incl. adaptation, protection)"	Bsu Eco Syn
	b1077	flgF	>	251	"Cell processes (incl. adaptation, protection)"	Bsu Eco Syn
o0221	b1077	flgF	>	251	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hpy
	b1078	flgG	>	260	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hpy
o0221	b1081	flgJ	>	313	"Cell processes (incl. adaptation, protection)"	Sce
	b1082	flgK	>	547	"Cell processes (incl. adaptation, protection)"	Sce
o0222	b1091	fabH	>	317	Fatty acid and phospholipid metabolism	B
	b1092	fabD	>	309	Fatty acid and phospholipid metabolism	B
	b1093	fabG	>	244	Fatty acid and phospholipid metabolism	B
o0223	b1094	acpP	>	78	Fatty acid and phospholipid metabolism	B Bsu Hpy Syn
	b1095	fabF	>	413	Fatty acid and phospholipid metabolism	B Bsu Hpy Syn
o0224	b1096	pabC	>	269	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1097	yceG	>	340	Putative enzymes	B
	b1098	tmk	>	213	Nucleotide biosynthesis and metabolism	B
	b1099	holB	>	334	"DNA replication, recombination, modification and repair"	B
	b1100	ycfH	>	265	"Hypothetical, unclassified, unknown"	B
o0224	b1097	yceG	>	340	Putative enzymes	Eco
	b1098	tmk	>	213	Nucleotide biosynthesis and metabolism	Eco
o0224	b1097	yceG	>	340	Putative enzymes	Hin
	b1098	tmk	>	213	Nucleotide biosynthesis and metabolism	Hin
	b1099	holB	>	334	"DNA replication, recombination, modification and repair"	Hin
	b1100	ycfH	>	265	"Hypothetical, unclassified, unknown"	Hin
o0224	b1098	tmk	>	213	Nucleotide biosynthesis and metabolism	Eco Mge Mpn
	b1099	holB	>	334	"DNA replication, recombination, modification and repair"	Eco Mge Mpn
o0225	b1103	ycfF	>	119	"Hypothetical, unclassified, unknown"	Hin
	b1104	b1104	>	125	"Hypothetical, unclassified, unknown"	Hin

o0225	b1103	ycfF	>	119	"Hypothetical, unclassified, unknown"	B
	b1104	b1104	>	125	"Hypothetical, unclassified, unknown"	B
	b1105	b1105	>	213	"Hypothetical, unclassified, unknown"	B
	b1106	b1106	>	274	Carbon compound catabolism	B
	b1107	b1107	>	341	"Hypothetical, unclassified, unknown"	B
	b1108	b1108	>	199	"Hypothetical, unclassified, unknown"	B
o0226	b1116	b1116	>	399	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Mge Mja Mpn Mth Syn
	b1117	b1117	>	228	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Mge Mja Mpn Mth Syn
o0226	b1116	b1116	>	399	"Hypothetical, unclassified, unknown"	B
	b1117	b1117	>	228	"Hypothetical, unclassified, unknown"	B
	b1118	b1118	>	414	Putative enzymes	B
	b1119	b1119	>	303	Putative regulatory proteins	B
	b1120	b1120	>	279	"Hypothetical, unclassified, unknown"	B
o0226	b1117	b1117	>	228	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Mge Mja Mpn Syn
	b1118	b1118	>	414	Putative enzymes	Bsu Eco Hin Mge Mja Mpn Syn
o0227	b1121	b1121	<	262	"Hypothetical, unclassified, unknown"	B
	b1122	b1122	<	156	"Hypothetical, unclassified, unknown"	B
o0228	b1123	potD	<	348	Transport and binding proteins	Eco Mge Syn
	b1124	potC	<	264	Transport and binding proteins	Eco Mge Syn
o0228	b1123	potD	<	348	Transport and binding proteins	Bsu
	b1124	potC	<	264	Transport and binding proteins	Bsu
	b1125	potB	<	275	Transport and binding proteins	Bsu
o0228	b1123	potD	<	348	Transport and binding proteins	B
	b1124	potC	<	264	Transport and binding proteins	B
	b1125	potB	<	275	Transport and binding proteins	B
	b1126	potA	<	378	Transport and binding proteins	B
o0228	b1124	potC	<	264	Transport and binding proteins	Bsu Eco Hin Mge Mpn Mth Syn
	b1125	potB	<	275	Transport and binding proteins	Bsu Eco Hin Mge Mpn Mth Syn

operon#	b#	gene	dir	length	function	species
o0228	b1124	potC	<	264	Transport and binding proteins	Bsu Eco Mge Mpn Mth Syn
	b1125	potB	<	275	Transport and binding proteins	Bsu Eco Mge Mpn Mth Syn
	b1126	potA	<	378	Transport and binding proteins	Bsu Eco Mge Mpn Mth Syn
o0228	b1125	potB	<	275	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Mth Syn
	b1126	potA	<	378	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Mth Syn
o0229	b1129	phoQ	<	486	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
	b1130	phoP	<	223	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
o0230	b1132	ycfC	<	213	"Hypothetical, unclassified, unknown"	B
	b1133	ycfB	<	383	"Hypothetical, unclassified, unknown"	B
	b1134	b1134	<	153	Putative enzymes	B
	b1135	b1135	<	207	"Hypothetical, unclassified, unknown"	B
o0231	b1137	b1137	<	221	"Hypothetical, unclassified, unknown"	B
	b1138	b1138	<	234	"Hypothetical, unclassified, unknown"	B
o0232	b1140	b1140	<	375	"phage, transposon, or plasmid"	B
	b1141	b1141	<	81	"Hypothetical, unclassified, unknown"	B
	b1142	b1142	<	103	"Hypothetical, unclassified, unknown"	B

o0233	b1146	b1146	>	167	"Hypothetical, unclassified, unknown"	B
	b1147	b1147	>	189	"Hypothetical, unclassified, unknown"	B
	b1148	b1148	>	112	"Hypothetical, unclassified, unknown"	B
	b1149	b1149	>	455	"Hypothetical, unclassified, unknown"	B
	b1150	b1150	>	60	"Hypothetical, unclassified, unknown"	B
	b1151	b1151	>	157	"Hypothetical, unclassified, unknown"	B
	b1152	b1152	>	263	"Hypothetical, unclassified, unknown"	B
	b1153	b1153	>	194	"Hypothetical, unclassified, unknown"	B
	b1154	ycfK	>	209	"Hypothetical, unclassified, unknown"	B
	b1155	b1155	>	137	"Hypothetical, unclassified, unknown"	B
o0233	b1152	b1152	>	263	"Hypothetical, unclassified, unknown"	Hin
	b1153	b1153	>	194	"Hypothetical, unclassified, unknown"	Hin
	b1154	ycfK	>	209	"Hypothetical, unclassified, unknown"	Hin
o0234	b1156	ycfA	<	200	"Hypothetical, unclassified, unknown"	B Eco
	b1157	b1157	<	179	"phage, transposon, or plasmid"	B Eco
o0235	b1164	b1164	>	78	"Hypothetical, unclassified, unknown"	B
	b1165	b1165	>	90	"Hypothetical, unclassified, unknown"	B
	b1166	b1166	>	88	"Hypothetical, unclassified, unknown"	B
o0236	b1171	b1171	<	111	"Hypothetical, unclassified, unknown"	B
	b1172	b1172	<	94	"Hypothetical, unclassified, unknown"	B
o0237	b1174	minE	<	88	"Cell processes (incl. adaptation, protection)"	Hpy
	b1175	minD	<	270	"Cell processes (incl. adaptation, protection)"	Hpy
o0237	b1174	minE	<	88	"Cell processes (incl. adaptation, protection)"	B Syn
	b1175	minD	<	270	"Cell processes (incl. adaptation, protection)"	B Syn
	b1176	minC	<	231	"Cell processes (incl. adaptation, protection)"	B Syn
o0237	b1175	minD	<	270	"Cell processes (incl. adaptation, protection)"	Bsu
	b1176	minC	<	231	"Cell processes (incl. adaptation, protection)"	Bsu
o0238	b1183	umuD	>	139	"DNA replication, recombination, modification and repair"	B
	b1184	umuC	>	422	"DNA replication, recombination, modification and repair"	B
o0239	b1189	dadA	>	432	Amino acid biosynthesis and metabolism	B
	b1190	dadX	>	356	Amino acid biosynthesis and metabolism	B
o0240	b1198	ycgC	<	473	Putative enzymes	Syn
	b1199	b1199	<	210	Putative enzymes	Syn
o0240	b1198	ycgC	<	473	Putative enzymes	B
	b1199	b1199	<	210	Putative enzymes	B
	b1200	b1200	<	366	Putative enzymes	B
o0241	b1208	ychB	<	283	"Hypothetical, unclassified, unknown"	B
	b1209	hemM	<	207	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0242	b1210	hemA	>	418	"Biosynthesis of cofactors, prosthetic groups and carriers"	Syn
	b1211	prfA	>	360	"Translation, post-translational modification"	Syn
o0242	b1210	hemA	>	418	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1211	prfA	>	360	"Translation, post-translational modification"	B
	b1212	hemK	>	277	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1213	b1213	>	130	"Hypothetical, unclassified, unknown"	B
	b1214	ychA	>	269	"Hypothetical, unclassified, unknown"	B
	b1215	kdsA	>	284	Cell structure	B
o0242	b1211	prfA	>	360	"Translation, post-translational modification"	Bsu Hin Mge Mpn
	b1212	hemK	>	277	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu Hin Mge Mpn
o0242	b1214	ychA	>	269	"Hypothetical, unclassified, unknown"	Hin
	b1215	kdsA	>	284	Cell structure	Hin

o0243	b1217	chaB	>	76	Transport and binding proteins	B
	b1218	chaC	>	238	Transport and binding proteins	B
o0244	b1221	narL	<	216	Energy metabolism	B Bsu Eco Mth Syn
	b1222	narX	<	598	Energy metabolism	B Bsu Eco Mth Syn
o0245	b1224	narG	>	1247	Energy metabolism	Eco Hin Mja
	b1225	narH	>	512	Energy metabolism	Eco Hin Mja
o0245	b1224	narG	>	1247	Energy metabolism	B Bsu
	b1225	narH	>	512	Energy metabolism	B Bsu
	b1226	narJ	>	236	Energy metabolism	B Bsu
	b1227	narI	>	225	Energy metabolism	B Bsu
o0246	b1232	purU	<	280	Nucleotide biosynthesis and metabolism	B
	b1233	ychJ	<	152	"Hypothetical, unclassified, unknown"	B
o0247	b1239	ychG	<	196	"Hypothetical, unclassified, unknown"	B
	b1240	b1240	<	76	"Hypothetical, unclassified, unknown"	B
o0248	b1243	oppA	>	543	Transport and binding proteins	Bsu
	b1244	oppB	>	306	Transport and binding proteins	Bsu
o0248	b1243	oppA	>	543	Transport and binding proteins	Bsu Eco
	b1244	oppB	>	306	Transport and binding proteins	Bsu Eco
	b1245	oppC	>	302	Transport and binding proteins	Bsu Eco
o0248	b1243	oppA	>	543	Transport and binding proteins	B Eco
	b1244	oppB	>	306	Transport and binding proteins	B Eco
	b1245	oppC	>	302	Transport and binding proteins	B Eco
	b1246	oppD	>	337	Transport and binding proteins	B Eco
o0248	b1244	oppB	>	306	Transport and binding proteins	Eco Hin
	b1245	oppC	>	302	Transport and binding proteins	Eco Hin
o0248	b1244	oppB	>	306	Transport and binding proteins	Bsu Hin Mge
	b1245	oppC	>	302	Transport and binding proteins	Bsu Hin Mge
	b1246	oppD	>	337	Transport and binding proteins	Bsu Hin Mge
o0248	b1245	oppC	>	302	Transport and binding proteins	Bsu Eco Hpy Mja Mpn Syn
	b1246	oppD	>	337	Transport and binding proteins	Bsu Eco Hpy Mja Mpn Syn
o0249	b1248	b1248	<	135	"Hypothetical, unclassified, unknown"	B
	b1249	cls	<	486	Fatty acid and phospholipid metabolism	B
o0250	b1254	yciB	<	179	"Hypothetical, unclassified, unknown"	B Bsu
	b1255	yciC	<	247	"Hypothetical, unclassified, unknown"	B Bsu
o0251	b1257	yciE	<	168	"Hypothetical, unclassified, unknown"	B Eco
	b1258	yciF	<	166	Structural proteins	B Eco
o0252	b1260	trpA	<	268	Amino acid biosynthesis and metabolism	Hin Mja
	b1261	trpB	<	397	Amino acid biosynthesis and metabolism	Hin Mja
o0252	b1260	trpA	<	268	Amino acid biosynthesis and metabolism	Bsu Mth
	b1261	trpB	<	397	Amino acid biosynthesis and metabolism	Bsu Mth
	b1262	trpC	<	453	Amino acid biosynthesis and metabolism	Bsu Mth
o0252	b1260	trpA	<	268	Amino acid biosynthesis and metabolism	Hpy
	b1261	trpB	<	397	Amino acid biosynthesis and metabolism	Hpy
	b1262	trpC	<	453	Amino acid biosynthesis and metabolism	Hpy
	b1263	trpD	<	531	Amino acid biosynthesis and metabolism	Hpy
	b1264	trpE	<	520	Amino acid biosynthesis and metabolism	Hpy

o0252	b1260	trpA	<	268	Amino acid biosynthesis and metabolism	B
	b1261	trpB	<	397	Amino acid biosynthesis and metabolism	B
	b1262	trpC	<	453	Amino acid biosynthesis and metabolism	B
	b1263	trpD	<	531	Amino acid biosynthesis and metabolism	B
	b1264	trpE	<	520	Amino acid biosynthesis and metabolism	B
	b1265	trpL	<	14	Amino acid biosynthesis and metabolism	B
o0252	b1262	trpC	<	453	Amino acid biosynthesis and metabolism	Hin Mth
	b1263	trpD	<	531	Amino acid biosynthesis and metabolism	Hin Mth
o0252	b1262	trpC	<	453	Amino acid biosynthesis and metabolism	Bsu Mth
	b1263	trpD	<	531	Amino acid biosynthesis and metabolism	Bsu Mth
	b1264	trpE	<	520	Amino acid biosynthesis and metabolism	Bsu Mth
o0252	b1263	trpD	<	531	Amino acid biosynthesis and metabolism	Bsu Hin
	b1264	trpE	<	520	Amino acid biosynthesis and metabolism	Bsu Hin
o0253	b1266	b1266	>	293	Putative enzymes	B
	b1267	yciO	>	218	"Hypothetical, unclassified, unknown"	B
	b1268	yciQ	>	631	"Hypothetical, unclassified, unknown"	B
o0254	b1270	btuR	<	196	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1271	yciK	<	252	Putative enzymes	B
o0255	b1279	b1279	>	102	"Hypothetical, unclassified, unknown"	B
	b1280	yciM	>	389	"Hypothetical, unclassified, unknown"	B
o0256	b1281	pyrF	>	245	Nucleotide biosynthesis and metabolism	B
	b1282	yciH	>	109	"Hypothetical, unclassified, unknown"	B
o0257	b1290	sapF	<	268	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b1291	sapD	<	330	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0257	b1290	sapF	<	268	Transport and binding proteins	Syn
	b1291	sapD	<	330	Transport and binding proteins	Syn
	b1292	sapC	<	296	Transport and binding proteins	Syn
o0257	b1290	sapF	<	268	Transport and binding proteins	Hin Mge Mpn
	b1291	sapD	<	330	Transport and binding proteins	Hin Mge Mpn
	b1292	sapC	<	296	Transport and binding proteins	Hin Mge Mpn
	b1293	sapB	<	321	Transport and binding proteins	Hin Mge Mpn
o0257	b1290	sapF	<	268	Transport and binding proteins	B Bsu Eco Hin Hpy
	b1291	sapD	<	330	Transport and binding proteins	B Bsu Eco Hin Hpy
	b1292	sapC	<	296	Transport and binding proteins	B Bsu Eco Hin Hpy
	b1293	sapB	<	321	Transport and binding proteins	B Bsu Eco Hin Hpy
	b1294	sapA	<	547	Transport and binding proteins	B Bsu Eco Hin Hpy
o0257	b1291	sapD	<	330	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Syn
	b1292	sapC	<	296	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Syn
o0257	b1291	sapD	<	330	Transport and binding proteins	Bsu Hin
	b1292	sapC	<	296	Transport and binding proteins	Bsu Hin
	b1293	sapB	<	321	Transport and binding proteins	Bsu Hin
o0257	b1291	sapD	<	330	Transport and binding proteins	Eco
	b1292	sapC	<	296	Transport and binding proteins	Eco
	b1293	sapB	<	321	Transport and binding proteins	Eco
	b1294	sapA	<	547	Transport and binding proteins	Eco
o0257	b1292	sapC	<	296	Transport and binding proteins	Bsu Eco Mpn
	b1293	sapB	<	321	Transport and binding proteins	Bsu Eco Mpn
o0257	b1292	sapC	<	296	Transport and binding proteins	Bsu Eco
	b1293	sapB	<	321	Transport and binding proteins	Bsu Eco
	b1294	sapA	<	547	Transport and binding proteins	Bsu Eco

o0257	b1293	sapB	<	321	Transport and binding proteins	Hpy
	b1294	sapA	<	547	Transport and binding proteins	Hpy
o0258	b1298	b1298	>	258	Putative enzymes	B
	b1299	ycjC	>	185	"Hypothetical, unclassified, unknown"	B
o0259	b1300	aldH	>	495	Energy metabolism	B
	b1301	ordL	>	426	Putative enzymes	B
	b1302	goaG	>	421	Central intermediary metabolism	B
o0259	b1301	ordL	>	426	Putative enzymes	Bsu Hin Mth
	b1302	goaG	>	421	Central intermediary metabolism	Bsu Hin Mth
o0260	b1304	pspA	>	222	"phage, transposon, or plasmid"	B
	b1305	pspB	>	74	"phage, transposon, or plasmid"	B
	b1306	pspC	>	119	"phage, transposon, or plasmid"	B
	b1307	pspD	>	73	"phage, transposon, or plasmid"	B
	b1308	pspE	>	104	"phage, transposon, or plasmid"	B
o0261	b1309	b1309	>	568	Putative enzymes	Eco
	b1310	b1310	>	430	"Hypothetical, unclassified, unknown"	Eco
o0261	b1309	b1309	>	568	Putative enzymes	B
	b1310	b1310	>	430	"Hypothetical, unclassified, unknown"	B
	b1311	b1311	>	293	Putative transport proteins	B
	b1312	b1312	>	280	Putative transport proteins	B
	b1313	b1313	>	350	Putative enzymes	B
	b1314	b1314	>	265	Putative regulatory proteins	B
	b1315	b1315	>	351	Putative enzymes	B
	b1316	b1316	>	755	"Hypothetical, unclassified, unknown"	B
	b1317	b1317	>	219	"Hypothetical, unclassified, unknown"	B
	b1318	b1318	>	322	Putative transport proteins	B
o0261	b1310	b1310	>	430	"Hypothetical, unclassified, unknown"	Bsu
	b1311	b1311	>	293	Putative transport proteins	Bsu
o0261	b1310	b1310	>	430	"Hypothetical, unclassified, unknown"	Bsu Eco
	b1311	b1311	>	293	Putative transport proteins	Bsu Eco
	b1312	b1312	>	280	Putative transport proteins	Bsu Eco
o0261	b1311	b1311	>	293	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Syn
	b1312	b1312	>	280	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Syn
o0261	b1312	b1312	>	280	Putative transport proteins	Bsu Sce Syn
	b1313	b1313	>	350	Putative enzymes	Bsu Sce Syn
o0261	b1317	b1317	>	219	"Hypothetical, unclassified, unknown"	Hpy
	b1318	b1318	>	322	Putative transport proteins	Hpy
o0262	b1321	b1321	>	465	Putative enzymes	B
	b1322	ycjF	>	353	"Hypothetical, unclassified, unknown"	B
o0263	b1335	ogt	<	171	"DNA replication, recombination, modification and repair"	B
	b1336	ydaH	<	510	Putative transport proteins	B
	b1337	b1337	<	481	"Hypothetical, unclassified, unknown"	B
	b1338	b1338	<	441	Putative enzymes	B
o0263	b1336	ydaH	<	510	Putative transport proteins	Bsu Mja Syn
	b1337	b1337	<	481	"Hypothetical, unclassified, unknown"	Bsu Mja Syn
o0263	b1337	b1337	<	481	"Hypothetical, unclassified, unknown"	Eco
	b1338	b1338	<	441	Putative enzymes	Eco
o0264	b1345	b1345	<	411	"phage, transposon, or plasmid"	B
	b1346	b1346	<	79	"Hypothetical, unclassified, unknown"	B
	b1347	ydaC	<	69	"Hypothetical, unclassified, unknown"	B

o0265	b1348	lar	<	64	"DNA replication, recombination, modification and repair"	B
	b1349	recT	<	269	"DNA replication, recombination, modification and repair"	B
	b1350	recE	<	866	"Transcription, RNA processing and degradation"	B
o0265	b1349	recT	<	269	"DNA replication, recombination, modification and repair"	Mja
	b1350	recE	<	866	"Transcription, RNA processing and degradation"	Mja
o0266	b1351	racC	<	91	"phage, transposon, or plasmid"	B
	b1352	ydaD	<	77	"Hypothetical, unclassified, unknown"	B
o0267	b1353	sieB	>	203	"phage, transposon, or plasmid"	B
	b1354	b1354	>	58	"Hypothetical, unclassified, unknown"	B
o0268	b1357	b1357	>	98	"Hypothetical, unclassified, unknown"	B
	b1358	b1358	>	140	"Hypothetical, unclassified, unknown"	B
	b1359	b1359	>	285	"Hypothetical, unclassified, unknown"	B
	b1360	b1360	>	248	"DNA replication, recombination, modification and repair"	B
	b1361	b1361	>	203	"Hypothetical, unclassified, unknown"	B
	b1362	b1362	>	101	"phage, transposon, or plasmid"	B
o0268	b1359	b1359	>	285	"Hypothetical, unclassified, unknown"	Eco
	b1360	b1360	>	248	"DNA replication, recombination, modification and repair"	Eco
o0269	b1363	trkG	>	485	Transport and binding proteins	B
	b1364	b1364	>	93	"Hypothetical, unclassified, unknown"	B
	b1365	b1365	>	87	"Hypothetical, unclassified, unknown"	B
	b1366	b1366	>	119	"Hypothetical, unclassified, unknown"	B
o0270	b1368	b1368	>	342	Structural proteins	B
	b1369	b1369	>	51	"Hypothetical, unclassified, unknown"	B
o0271	b1372	b1372	>	1122	"phage, transposon, or plasmid"	B Eco Sce
	b1373	b1373	>	191	"Hypothetical, unclassified, unknown"	B Eco Sce
o0272	b1381	b1381	>	879	"Hypothetical, unclassified, unknown"	B
	b1382	b1382	>	61	"Hypothetical, unclassified, unknown"	B
	b1383	b1383	>	110	"Hypothetical, unclassified, unknown"	B
o0273	b1388	b1388	>	309	"Hypothetical, unclassified, unknown"	B
	b1389	b1389	>	95	"Hypothetical, unclassified, unknown"	B
	b1390	b1390	>	248	"Hypothetical, unclassified, unknown"	B
	b1391	b1391	>	167	"Hypothetical, unclassified, unknown"	B
	b1392	b1392	>	356	Energy metabolism	B
	b1393	b1393	>	255	Putative enzymes	B
	b1394	b1394	>	262	Putative enzymes	B
	b1395	b1395	>	475	Fatty acid and phospholipid metabolism	B
	b1396	b1396	>	140	"Hypothetical, unclassified, unknown"	B
	b1397	b1397	>	401	Fatty acid and phospholipid metabolism	B
	b1398	b1398	>	437	"Hypothetical, unclassified, unknown"	B
o0273	b1393	b1393	>	255	Putative enzymes	Bsu Eco
	b1394	b1394	>	262	Putative enzymes	Bsu Eco
o0273	b1397	b1397	>	401	Fatty acid and phospholipid metabolism	Bsu Eco
	b1398	b1398	>	437	"Hypothetical, unclassified, unknown"	Bsu Eco
o0274	b1399	b1399	>	316	"Hypothetical, unclassified, unknown"	B
	b1400	b1400	>	196	"Hypothetical, unclassified, unknown"	B
o0275	b1402	yi22_2	<	301	"Hypothetical, unclassified, unknown"	B Eco
	b1403	yi21_2	<	136	"Hypothetical, unclassified, unknown"	B Eco
o0276	b1408	b1408	>	203	Putative enzymes	Bsu Sce
	b1409	b1409	>	298	Fatty acid and phospholipid metabolism	Bsu Sce

o0276	b1408	b1408	>	203	Putative enzymes	B
	b1409	b1409	>	298	Fatty acid and phospholipid metabolism	B
	b1410	b1410	>	585	"Hypothetical, unclassified, unknown"	B
	b1411	b1411	>	430	Putative enzymes	B
o0276	b1409	b1409	>	298	Fatty acid and phospholipid metabolism	Bsu Eco Syn
	b1410	b1410	>	585	"Hypothetical, unclassified, unknown"	Bsu Eco Syn
o0277	b1416	gapC_2	<	83	Energy metabolism	B
	b1417	gapC_1	<	134	Energy metabolism	B
o0278	b1429	tehA	>	330	"Cell processes (incl. adaptation, protection)"	B Bsu
	b1430	tehB	>	197	"Cell processes (incl. adaptation, protection)"	B Bsu
o0279	b1434	b1434	>	178	"Hypothetical, unclassified, unknown"	B
	b1435	b1435	>	667	Putative enzymes	B
o0280	b1440	b1440	>	381	Putative transport proteins	Eco
	b1441	b1441	>	337	Putative transport proteins	Eco
o0280	b1440	b1440	>	381	Putative transport proteins	Eco
	b1441	b1441	>	337	Putative transport proteins	Eco
	b1442	b1442	>	313	Putative transport proteins	Eco
	b1443	b1443	>	264	Putative transport proteins	Eco
o0280	b1440	b1440	>	381	Putative transport proteins	B
	b1441	b1441	>	337	Putative transport proteins	B
	b1442	b1442	>	313	Putative transport proteins	B
	b1443	b1443	>	264	Putative transport proteins	B
	b1444	b1444	>	474	Putative enzymes	B
o0280	b1441	b1441	>	337	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Sce Syn
	b1442	b1442	>	313	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Sce Syn

operon#	b#	gene	dir	length	function	species
o0280	b1441	b1441	>	337	Putative transport proteins	Bsu Eco Hin Mge Mpn Mth Syn
	b1442	b1442	>	313	Putative transport proteins	Bsu Eco Hin Mge Mpn Mth Syn
	b1443	b1443	>	264	Putative transport proteins	Bsu Eco Hin Mge Mpn Mth Syn
o0280	b1442	b1442	>	313	Putative transport proteins	Bsu Eco Hin Mge Mja Mpn Mth Syn
	b1443	b1443	>	264	Putative transport proteins	Bsu Eco Hin Mge Mja Mpn Mth Syn
o0281	b1447	b1447	<	149	"Hypothetical, unclassified, unknown"	B Bsu
	b1448	b1448	<	172	"Cell processes (incl. adaptation, protection)"	B Bsu
o0282	b1456	rhsE	>	682	"Hypothetical, unclassified, unknown"	B
	b1457	ydcD	>	160	"Hypothetical, unclassified, unknown"	B
o0283	b1458	b1458	>	248	"Hypothetical, unclassified, unknown"	B Eco
	b1459	b1459	>	66	"Hypothetical, unclassified, unknown"	B Eco
o0284	b1465	narV	<	226	Energy metabolism	B Bsu
	b1466	narW	<	231	Energy metabolism	B Bsu
	b1467	narY	<	514	Energy metabolism	B Bsu
	b1468	narZ	<	1246	Energy metabolism	B Bsu
o0284	b1466	narW	<	231	Energy metabolism	Syn
	b1467	narY	<	514	Energy metabolism	Syn
o0284	b1467	narY	<	514	Energy metabolism	Eco Hin Mja
	b1468	narZ	<	1246	Energy metabolism	Eco Hin Mja
o0285	b1470	b1470	<	111	"Hypothetical, unclassified, unknown"	Mge
	b1471	b1471	<	318	Cell structure	Mge

o0285	b1470	b1470	<	111	"Hypothetical, unclassified, unknown"	B
	b1471	b1471	<	318	Cell structure	B
	b1472	b1472	<	96	Membrane proteins	B
o0285	b1471	b1471	<	318	Cell structure	Sce
	b1472	b1472	<	96	Membrane proteins	Sce
o0286	b1474	fdnG	>	1015	Energy metabolism	Bsu Eco Hin Mja Mth
	b1475	fdnH	>	294	Energy metabolism	Bsu Eco Hin Mja Mth
o0286	b1474	fdnG	>	1015	Energy metabolism	B Eco
	b1475	fdnH	>	294	Energy metabolism	B Eco
	b1476	fdnI	>	217	Energy metabolism	B Eco
o0286	b1475	fdnH	>	294	Energy metabolism	Hin
	b1476	fdnI	>	217	Energy metabolism	Hin
o0287	b1483	b1483	<	308	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b1484	b1484	<	328	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0287	b1483	b1483	<	308	Transport and binding proteins	Bsu Eco Mja Syn
	b1484	b1484	<	328	Transport and binding proteins	Bsu Eco Mja Syn
	b1485	b1485	<	298	Transport and binding proteins	Bsu Eco Mja Syn
o0287	b1483	b1483	<	308	Transport and binding proteins	Hin Mge Mpn
	b1484	b1484	<	328	Transport and binding proteins	Hin Mge Mpn
	b1485	b1485	<	298	Transport and binding proteins	Hin Mge Mpn
	b1486	b1486	<	340	Transport and binding proteins	Hin Mge Mpn
o0287	b1483	b1483	<	308	Transport and binding proteins	Bsu Eco Hin Hpy
	b1484	b1484	<	328	Transport and binding proteins	Bsu Eco Hin Hpy
	b1485	b1485	<	298	Transport and binding proteins	Bsu Eco Hin Hpy
	b1486	b1486	<	340	Transport and binding proteins	Bsu Eco Hin Hpy
	b1487	b1487	<	516	Putative transport proteins	Bsu Eco Hin Hpy
o0287	b1483	b1483	<	308	Transport and binding proteins	B
	b1484	b1484	<	328	Transport and binding proteins	B
	b1485	b1485	<	298	Transport and binding proteins	B
	b1486	b1486	<	340	Transport and binding proteins	B
	b1487	b1487	<	516	Putative transport proteins	B
	b1488	b1488	<	193	"Hypothetical, unclassified, unknown"	B
o0287	b1484	b1484	<	328	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Syn
	b1485	b1485	<	298	Transport and binding proteins	Bsu Eco Hin Hpy Mja Mpn Syn
o0287	b1484	b1484	<	328	Transport and binding proteins	Bsu
	b1485	b1485	<	298	Transport and binding proteins	Bsu
	b1486	b1486	<	340	Transport and binding proteins	Bsu
o0287	b1484	b1484	<	328	Transport and binding proteins	Eco
	b1485	b1485	<	298	Transport and binding proteins	Eco
	b1486	b1486	<	340	Transport and binding proteins	Eco
	b1487	b1487	<	516	Putative transport proteins	Eco
o0287	b1485	b1485	<	298	Transport and binding proteins	Eco Hpy Mge Mpn Syn
	b1486	b1486	<	340	Transport and binding proteins	Eco Hpy Mge Mpn Syn
o0287	b1485	b1485	<	298	Transport and binding proteins	Bsu Eco
	b1486	b1486	<	340	Transport and binding proteins	Bsu Eco
	b1487	b1487	<	516	Putative transport proteins	Bsu Eco
o0287	b1486	b1486	<	340	Transport and binding proteins	Eco Hpy
	b1487	b1487	<	516	Putative transport proteins	Eco Hpy
o0288	b1489	b1489	<	807	"Hypothetical, unclassified, unknown"	B Eco Hin Syn
	b1490	b1490	<	460	"Hypothetical, unclassified, unknown"	B Eco Hin Syn

o0289	b1494	yddC	<	931	"Hypothetical, unclassified, unknown"	Eco Hin Sce
	b1495	yddB	<	790	"Hypothetical, unclassified, unknown"	Eco Hin Sce
o0289	b1494	yddC	<	931	"Hypothetical, unclassified, unknown"	B
	b1495	yddB	<	790	"Hypothetical, unclassified, unknown"	B
	b1496	yddA	<	561	Putative transport proteins	B
o0289	b1495	yddB	<	790	"Hypothetical, unclassified, unknown"	Eco Hpy Mpn Syn
	b1496	yddA	<	561	Putative transport proteins	Eco Hpy Mpn Syn
o0290	b1497	b1497	<	390	Putative regulatory proteins	B Eco
	b1498	b1498	<	571	Putative enzymes	B Eco
o0291	b1503	b1503	<	167	"Hypothetical, unclassified, unknown"	Eco
	b1504	b1504	<	176	"Hypothetical, unclassified, unknown"	Eco
o0291	b1503	b1503	<	167	"Hypothetical, unclassified, unknown"	B
	b1504	b1504	<	176	"Hypothetical, unclassified, unknown"	B
	b1505	b1505	<	382	Structural proteins	B
o0291	b1504	b1504	<	176	"Hypothetical, unclassified, unknown"	Eco
	b1505	b1505	<	382	Structural proteins	Eco
o0292	b1507	hipA	<	440	Cell structure	B Eco
	b1508	hipB	<	88	Cell structure	B Eco
o0293	b1509	b1509	<	466	"Hypothetical, unclassified, unknown"	B Eco
	b1510	ydeK	<	1325	"Hypothetical, unclassified, unknown"	B Eco
o0294	b1513	b1513	>	511	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b1514	b1514	>	342	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0294	b1513	b1513	>	511	Putative transport proteins	Eco Hin
	b1514	b1514	>	342	Putative transport proteins	Eco Hin
	b1515	b1515	>	330	Putative transport proteins	Eco Hin
o0294	b1513	b1513	>	511	Putative transport proteins	B
	b1514	b1514	>	342	Putative transport proteins	B
	b1515	b1515	>	330	Putative transport proteins	B
	b1516	b1516	>	340	"Hypothetical, unclassified, unknown"	B
	b1517	b1517	>	291	"Hypothetical, unclassified, unknown"	B
	b1518	b1518	>	96	"Hypothetical, unclassified, unknown"	B
o0294	b1514	b1514	>	342	Putative transport proteins	Eco Hpy Mja Mth Syn
	b1515	b1515	>	330	Putative transport proteins	Eco Hpy Mja Mth Syn
o0294	b1515	b1515	>	330	Putative transport proteins	Eco
	b1516	b1516	>	340	"Hypothetical, unclassified, unknown"	Eco
o0294	b1515	b1515	>	330	Putative transport proteins	Hin
	b1516	b1516	>	340	"Hypothetical, unclassified, unknown"	Hin
	b1517	b1517	>	291	"Hypothetical, unclassified, unknown"	Hin
o0295	b1523	b1523	<	119	"Hypothetical, unclassified, unknown"	B
	b1524	b1524	<	308	Putative enzymes	B
o0296	b1530	marR	>	125	"Cell processes (incl. adaptation, protection)"	B
	b1531	marA	>	129	"Cell processes (incl. adaptation, protection)"	B
	b1532	marB	>	72	"Cell processes (incl. adaptation, protection)"	B
o0297	b1546	b1546	<	191	"Hypothetical, unclassified, unknown"	Eco
	b1547	b1547	<	320	"Hypothetical, unclassified, unknown"	Eco
o0297	b1546	b1546	<	191	"Hypothetical, unclassified, unknown"	B
	b1547	b1547	<	320	"Hypothetical, unclassified, unknown"	B
	b1548	nohA	<	189	"phage, transposon, or plasmid"	B

o0298	b1553	b1553	<	165	"Hypothetical, unclassified, unknown"	B
	b1554	b1554	<	177	"Hypothetical, unclassified, unknown"	B
	b1555	b1555	<	103	"Hypothetical, unclassified, unknown"	B
	b1556	b1556	<	96	"Hypothetical, unclassified, unknown"	B
o0299	b1559	b1559	<	260	"Hypothetical, unclassified, unknown"	B
	b1560	b1560	<	362	"Hypothetical, unclassified, unknown"	B
o0300	b1563	relE	<	95	"Hypothetical, unclassified, unknown"	B
	b1564	relB	<	79	Regulatory function	B
o0301	b1567	b1567	<	49	"Hypothetical, unclassified, unknown"	B
	b1568	b1568	<	96	"Hypothetical, unclassified, unknown"	B
	b1569	dicC	<	76	"Cell processes (incl. adaptation, protection)"	B
o0302	b1571	ydfA	>	51	"Hypothetical, unclassified, unknown"	B
	b1572	ydfB	>	56	"Hypothetical, unclassified, unknown"	B
	b1573	ydfC	>	72	"Hypothetical, unclassified, unknown"	B
o0303	b1577	ydfE	>	306	"Hypothetical, unclassified, unknown"	B
	b1578	b1578	>	218	"Hypothetical, unclassified, unknown"	B
	b1579	b1579	>	398	"phage, transposon, or plasmid"	B
o0304	b1580	rspB	<	339	Regulatory function	B
	b1581	rspA	<	404	Regulatory function	B
o0305	b1583	b1583	>	113	"Hypothetical, unclassified, unknown"	B
	b1584	speG	>	186	Central intermediary metabolism	B
o0306	b1588	b1588	>	808	Energy metabolism	Bsu Eco Mja Mth
	b1589	b1589	>	205	"Hypothetical, unclassified, unknown"	Bsu Eco Mja Mth
o0306	b1588	b1588	>	808	Energy metabolism	Eco
	b1589	b1589	>	205	"Hypothetical, unclassified, unknown"	Eco
	b1590	b1590	>	284	Energy metabolism	Eco
o0306	b1588	b1588	>	808	Energy metabolism	B Hin
	b1589	b1589	>	205	"Hypothetical, unclassified, unknown"	B Hin
	b1590	b1590	>	284	Energy metabolism	B Hin
	b1591	b1591	>	207	"Hypothetical, unclassified, unknown"	B Hin
o0306	b1590	b1590	>	284	Energy metabolism	Eco
	b1591	b1591	>	207	"Hypothetical, unclassified, unknown"	Eco
o0307	b1599	b1599	<	109	"Hypothetical, unclassified, unknown"	B Bsu Eco
	b1600	b1600	<	121	"Hypothetical, unclassified, unknown"	B Bsu Eco
o0308	b1602	pntB	<	462	Central intermediary metabolism	B Hin
	b1603	pntA	<	510	Central intermediary metabolism	B Hin
o0309	b1605	b1605	>	460	Amino acid biosynthesis and metabolism	B Hin
	b1606	b1606	>	240	"Hypothetical, unclassified, unknown"	B Hin
o0310	b1608	rstA	>	242	Putative regulatory proteins	B Bsu Eco Hin Mth Syn
	b1609	rstB	>	433	Regulatory function	B Bsu Eco Hin Mth Syn
o0311	b1616	uidB	<	457	Transport and binding proteins	B Eco
	b1617	uidA	<	603	Carbon compound catabolism	B Eco
o0312	b1621	malX	>	530	Transport and binding proteins	B
	b1622	malY	>	390	Carbon compound catabolism	B
o0313	b1627	b1627	>	193	"Hypothetical, unclassified, unknown"	Eco
	b1628	b1628	>	192	"Hypothetical, unclassified, unknown"	Eco

o0313	b1627	b1627	>	193	"Hypothetical, unclassified, unknown"	B Hin
	b1628	b1628	>	192	"Hypothetical, unclassified, unknown"	B Hin
	b1629	b1629	>	740	"Hypothetical, unclassified, unknown"	B Hin
	b1630	b1630	>	352	"Hypothetical, unclassified, unknown"	B Hin
	b1631	b1631	>	206	"Hypothetical, unclassified, unknown"	B Hin
	b1632	b1632	>	231	"Hypothetical, unclassified, unknown"	B Hin
	b1633	nth	>	211	"Transcription, RNA processing and degradation"	B Hin
o0313	b1628	b1628	>	192	"Hypothetical, unclassified, unknown"	Eco Hin Mja Mth
	b1629	b1629	>	740	"Hypothetical, unclassified, unknown"	Eco Hin Mja Mth
o0313	b1629	b1629	>	740	"Hypothetical, unclassified, unknown"	Eco Hin
	b1630	b1630	>	352	"Hypothetical, unclassified, unknown"	Eco Hin
o0313	b1629	b1629	>	740	"Hypothetical, unclassified, unknown"	Hin
	b1630	b1630	>	352	"Hypothetical, unclassified, unknown"	Hin
	b1631	b1631	>	206	"Hypothetical, unclassified, unknown"	Hin
	b1632	b1632	>	231	"Hypothetical, unclassified, unknown"	Hin
o0313	b1631	b1631	>	206	"Hypothetical, unclassified, unknown"	Hin
	b1632	b1632	>	231	"Hypothetical, unclassified, unknown"	Hin
o0314	b1643	b1643	>	78	"Hypothetical, unclassified, unknown"	B Eco
	b1644	b1644	>	299	"Hypothetical, unclassified, unknown"	B Eco
	b1645	b1645	>	670	"Hypothetical, unclassified, unknown"	B Eco
o0314	b1644	b1644	>	299	"Hypothetical, unclassified, unknown"	Eco
	b1645	b1645	>	670	"Hypothetical, unclassified, unknown"	Eco
o0315	b1647	b1647	<	298	"Hypothetical, unclassified, unknown"	B
	b1648	b1648	<	125	"Hypothetical, unclassified, unknown"	B
o0316	b1649	b1649	>	199	"Hypothetical, unclassified, unknown"	B
	b1650	b1650	>	365	Energy metabolism	B
o0317	b1652	rnt	>	215	"DNA replication, recombination, modification and repair"	B
	b1653	lhr	>	1538	"DNA replication, recombination, modification and repair"	B
o0318	b1665	valV	>		tRNA	B
	b1666	valW	>		tRNA	B
o0319	b1669	b1669	<	270	"Hypothetical, unclassified, unknown"	B
	b1670	b1670	<	261	"Hypothetical, unclassified, unknown"	B
	b1671	b1671	<	239	"Hypothetical, unclassified, unknown"	B
	b1672	b1672	<	215	"Hypothetical, unclassified, unknown"	B
	b1673	b1673	<	700	"Hypothetical, unclassified, unknown"	B
	b1674	b1674	<	208	"Hypothetical, unclassified, unknown"	B
o0319	b1673	b1673	<	700	"Hypothetical, unclassified, unknown"	Syn
	b1674	b1674	<	208	"Hypothetical, unclassified, unknown"	Syn
o0320	b1679	b1679	<	138	"Hypothetical, unclassified, unknown"	Eco Hin
	b1680	b1680	<	406	Putative enzymes	Eco Hin
o0320	b1679	b1679	<	138	"Hypothetical, unclassified, unknown"	B
	b1680	b1680	<	406	Putative enzymes	B
	b1681	b1681	<	423	"Hypothetical, unclassified, unknown"	B
	b1682	b1682	<	248	"Hypothetical, unclassified, unknown"	B
	b1683	b1683	<	508	"Hypothetical, unclassified, unknown"	B
	b1684	b1684	<	122	"Hypothetical, unclassified, unknown"	B
o0320	b1680	b1680	<	406	Putative enzymes	Bsu
	b1681	b1681	<	423	"Hypothetical, unclassified, unknown"	Bsu
	b1682	b1682	<	248	"Hypothetical, unclassified, unknown"	Bsu

o0320	b1680	b1680	<	406	Putative enzymes	Syn
	b1681	b1681	<	423	"Hypothetical, unclassified, unknown"	Syn
	b1682	b1682	<	248	"Hypothetical, unclassified, unknown"	Syn
	b1683	b1683	<	508	"Hypothetical, unclassified, unknown"	Syn
o0320	b1681	b1681	<	423	"Hypothetical, unclassified, unknown"	Mth Syn
	b1682	b1682	<	248	"Hypothetical, unclassified, unknown"	Mth Syn
o0320	b1681	b1681	<	423	"Hypothetical, unclassified, unknown"	Syn
	b1682	b1682	<	248	"Hypothetical, unclassified, unknown"	Syn
	b1683	b1683	<	508	"Hypothetical, unclassified, unknown"	Syn
o0320	b1682	b1682	<	248	"Hypothetical, unclassified, unknown"	Bsu Eco Mja Mth
	b1683	b1683	<	508	"Hypothetical, unclassified, unknown"	Bsu Eco Mja Mth
o0321	b1685	b1685	<	89	"Hypothetical, unclassified, unknown"	B
	b1686	b1686	<	136	"Hypothetical, unclassified, unknown"	B
	b1687	b1687	<	1018	"Hypothetical, unclassified, unknown"	B
o0322	b1691	b1691	>	423	Putative transport proteins	B
	b1692	ydiB	>	288	Putative enzymes	B
	b1693	aroD	>	252	Amino acid biosynthesis and metabolism	B
o0323	b1694	ydiF	>	531	"Hypothetical, unclassified, unknown"	B
	b1695	b1695	>	401	Putative enzymes	B
o0324	b1697	b1697	>	254	Energy metabolism	B Bsu
	b1698	b1698	>	312	Energy metabolism	B Bsu
o0325	b1699	b1699	>	429	"Hypothetical, unclassified, unknown"	Eco Mth
	b1700	b1700	>	97	"Hypothetical, unclassified, unknown"	Eco Mth
o0325	b1699	b1699	>	429	"Hypothetical, unclassified, unknown"	B
	b1700	b1700	>	97	"Hypothetical, unclassified, unknown"	B
	b1701	ydiD	>	566	Central intermediary metabolism	B
o0325	b1700	b1700	>	97	"Hypothetical, unclassified, unknown"	Eco
	b1701	ydiD	>	566	Central intermediary metabolism	Eco
o0326	b1709	btuD	<	249	Transport and binding proteins	B
	b1710	btuE	<	183	Transport and binding proteins	B
	b1711	btuC	<	326	Transport and binding proteins	B
o0327	b1713	pheT	<	795	"Translation, post-translational modification"	Bsu Hpy Mge Mpn
	b1714	pheS	<	327	"Translation, post-translational modification"	Bsu Hpy Mge Mpn
o0327	b1713	pheT	<	795	"Translation, post-translational modification"	B
	b1714	pheS	<	327	"Translation, post-translational modification"	B
	b1715	pheM	<	14	"Translation, post-translational modification"	B
o0328	b1716	rplT	<	118	"Translation, post-translational modification"	Syn
	b1717	rpmI	<	65	"Translation, post-translational modification"	Syn
o0328	b1716	rplT	<	118	"Translation, post-translational modification"	Bsu Hin Mge Mpn
	b1717	rpmI	<	65	"Translation, post-translational modification"	Bsu Hin Mge Mpn
	b1718	infC	<	180	"Translation, post-translational modification"	Bsu Hin Mge Mpn
o0328	b1716	rplT	<	118	"Translation, post-translational modification"	B Hpy
	b1717	rpmI	<	65	"Translation, post-translational modification"	B Hpy
	b1718	infC	<	180	"Translation, post-translational modification"	B Hpy
	b1719	thrS	<	642	"Translation, post-translational modification"	B Hpy
o0329	b1720	b1720	>	157	"Hypothetical, unclassified, unknown"	B
	b1721	b1721	>	471	"Hypothetical, unclassified, unknown"	B
o0330	b1734	celF	<	450	Carbon compound catabolism	Eco
	b1735	celD	<	280	Carbon compound catabolism	Eco

o0330	b1734	celF	<	450	Carbon compound catabolism	B
	b1735	celD	<	280	Carbon compound catabolism	B
	b1736	celC	<	116	Transport and binding proteins	B
	b1737	celB	<	452	Transport and binding proteins	B
	b1738	celA	<	106	Transport and binding proteins	B

operon#	b#	gene	dir	length	function	species
o0330	b1736	celC	<	116	Transport and binding proteins	Bsu
	b1737	celB	<	452	Transport and binding proteins	Bsu
o0330	b1736	celC	<	116	Transport and binding proteins	Bsu
	b1737	celB	<	452	Transport and binding proteins	Bsu
	b1738	celA	<	106	Transport and binding proteins	Bsu
o0331	b1744	b1744	<	322	"Hypothetical, unclassified, unknown"	B
	b1745	b1745	<	447	"Hypothetical, unclassified, unknown"	B
	b1746	b1746	<	492	Putative enzymes	B
	b1747	b1747	<	344	"Hypothetical, unclassified, unknown"	B
	b1748	b1748	<	406	Amino acid biosynthesis and metabolism	B
o0331	b1745	b1745	<	447	"Hypothetical, unclassified, unknown"	Syn
	b1746	b1746	<	492	Putative enzymes	Syn
o0331	b1746	b1746	<	492	Putative enzymes	Syn
	b1747	b1747	<	344	"Hypothetical, unclassified, unknown"	Syn
o0332	b1750	b1750	>	252	"Hypothetical, unclassified, unknown"	B
	b1751	b1751	>	279	"Hypothetical, unclassified, unknown"	B
	b1752	b1752	>	235	"Hypothetical, unclassified, unknown"	B
	b1753	b1753	>	182	"Hypothetical, unclassified, unknown"	B
	b1754	b1754	>	389	"Hypothetical, unclassified, unknown"	B
	b1755	b1755	>	496	"Hypothetical, unclassified, unknown"	B
	b1756	b1756	>	217	Putative transport proteins	B
o0332	b1751	b1751	>	279	"Hypothetical, unclassified, unknown"	Eco
	b1752	b1752	>	235	"Hypothetical, unclassified, unknown"	Eco
o0332	b1754	b1754	>	389	"Hypothetical, unclassified, unknown"	Eco
	b1755	b1755	>	496	"Hypothetical, unclassified, unknown"	Eco
o0332	b1755	b1755	>	496	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Hpy Mja Mth Sce Syn
	b1756	b1756	>	217	Putative transport proteins	Bsu Eco Hin Hpy Mja Mth Sce Syn
o0333	b1762	b1762	<	387	"Hypothetical, unclassified, unknown"	B
	b1763	topB	<	653	"DNA replication, recombination, modification and repair"	B
o0334	b1771	b1771	<	326	"Hypothetical, unclassified, unknown"	B
	b1772	b1772	<	322	Carbon compound catabolism	B
	b1773	b1773	<	278	Energy metabolism	B
	b1774	b1774	<	347	Putative enzymes	B
	b1775	b1775	<	459	"Hypothetical, unclassified, unknown"	B
	b1776	b1776	<	358	Putative enzymes	B
o0334	b1774	b1774	<	347	Putative enzymes	Bsu Sce Syn
	b1775	b1775	<	459	"Hypothetical, unclassified, unknown"	Bsu Sce Syn
o0334	b1775	b1775	<	459	"Hypothetical, unclassified, unknown"	Bsu Eco Sce
	b1776	b1776	<	358	Putative enzymes	Bsu Eco Sce
o0335	b1777	b1777	<	105	"Hypothetical, unclassified, unknown"	B
	b1778	b1778	<	137	"Hypothetical, unclassified, unknown"	B
o0336	b1785	b1785	>	491	"Hypothetical, unclassified, unknown"	Eco
	b1786	b1786	>	556	"Hypothetical, unclassified, unknown"	Eco

o0336	b1785	b1785	>	491	"Hypothetical, unclassified, unknown"	B
	b1786	b1786	>	556	"Hypothetical, unclassified, unknown"	B
	b1787	b1787	>	167	"Hypothetical, unclassified, unknown"	B
o0337	b1791	b1791	>	393	"Hypothetical, unclassified, unknown"	B
	b1792	b1792	>	122	"Hypothetical, unclassified, unknown"	B
o0338	b1796	b1796	<	60	"Hypothetical, unclassified, unknown"	B
	b1797	b1797	<	119	"Hypothetical, unclassified, unknown"	B
o0339	b1801	b1801	>	481	Putative transport proteins	B Eco
	b1802	b1802	>	374	"Hypothetical, unclassified, unknown"	B Eco
o0340	b1806	b1806	<	193	"Hypothetical, unclassified, unknown"	B
	b1807	b1807	<	231	"Hypothetical, unclassified, unknown"	B
o0341	b1812	pabB	>	453	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1813	yeaB	>	192	"Hypothetical, unclassified, unknown"	B
o0342	b1817	manX	>	323	Transport and binding proteins	Eco Mpn
	b1818	manY	>	266	Transport and binding proteins	Eco Mpn
o0342	b1817	manX	>	323	Transport and binding proteins	B Bsu Eco
	b1818	manY	>	266	Transport and binding proteins	B Bsu Eco
	b1819	manZ	>	286	Transport and binding proteins	B Bsu Eco
o0343	b1823	cspC	<	69	Other known genes	B
	b1824	b1824	<	47	"Hypothetical, unclassified, unknown"	B
o0344	b1830	prc	<	682	"Translation, post-translational modification"	B Hin
	b1831	yebJ	<	39	"Hypothetical, unclassified, unknown"	B Hin
o0345	b1833	b1833	>	427	"Hypothetical, unclassified, unknown"	B Eco Hin
	b1834	b1834	>	879	"Hypothetical, unclassified, unknown"	B Eco Hin
o0346	b1839	b1839	<	113	"Hypothetical, unclassified, unknown"	B
	b1840	b1840	<	290	"Cell processes (incl. adaptation, protection)"	B
	b1841	b1841	<	124	"Hypothetical, unclassified, unknown"	B
o0347	b1843	b1843	>	218	"Hypothetical, unclassified, unknown"	B
	b1844	b1844	>	220	"Hypothetical, unclassified, unknown"	B
o0348	b1850	eda	<	213	Central intermediary metabolism	B
	b1851	edd	<	603	Central intermediary metabolism	B
o0349	b1858	b1858	>	251	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Hpy Mge Mja Syn
	b1859	yebI	>	261	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Hpy Mge Mja Syn
o0350	b1860	ruvB	<	336	"DNA replication, recombination, modification and repair"	B Bsu Hin Mge Mpn
	b1861	ruvA	<	203	"DNA replication, recombination, modification and repair"	B Bsu Hin Mge Mpn
o0351	b1863	ruvC	<	173	"DNA replication, recombination, modification and repair"	B
	b1864	yebC	<	246	"Hypothetical, unclassified, unknown"	B
	b1865	ntpA	<	150	Central intermediary metabolism	B
o0352	b1867	yecD	>	199	"Hypothetical, unclassified, unknown"	B
	b1868	yecE	>	272	"Hypothetical, unclassified, unknown"	B
	b1869	b1869	>	141	"Hypothetical, unclassified, unknown"	B
	b1870	b1870	>	247	"Hypothetical, unclassified, unknown"	B
	b1871	b1871	>	323	"Hypothetical, unclassified, unknown"	B
o0353	b1872	bisZ	<	815	Central intermediary metabolism	B Eco Hin
	b1873	b1873	<	366	Energy metabolism	B Eco Hin
o0354	b1878	b1878	<	130	"Hypothetical, unclassified, unknown"	B
	b1879	flhA	<	692	Cell structure	B
	b1880	b1880	<	382	"Cell processes (incl. adaptation, protection)"	B
o0354	b1879	flhA	<	692	Cell structure	Bsu
	b1880	b1880	<	382	"Cell processes (incl. adaptation, protection)"	Bsu

o0355	b1881	cheZ	<	214	"Cell processes (incl. adaptation, protection)"	Bsu Eco Syn
	b1882	cheY	<	129	"Cell processes (incl. adaptation, protection)"	Bsu Eco Syn
o0355	b1881	cheZ	<	214	"Cell processes (incl. adaptation, protection)"	B
	b1882	cheY	<	129	"Cell processes (incl. adaptation, protection)"	B
	b1883	cheB	<	349	"Cell processes (incl. adaptation, protection)"	B
	b1884	cheR	<	286	"Cell processes (incl. adaptation, protection)"	B
	b1885	tap	<	533	"Cell processes (incl. adaptation, protection)"	B
	b1886	tar	<	553	"Cell processes (incl. adaptation, protection)"	B
o0355	b1882	cheY	<	129	"Cell processes (incl. adaptation, protection)"	Eco Hpy Mth Syn
	b1883	cheB	<	349	"Cell processes (incl. adaptation, protection)"	Eco Hpy Mth Syn
o0355	b1884	cheR	<	286	"Cell processes (incl. adaptation, protection)"	Eco
	b1885	tap	<	533	"Cell processes (incl. adaptation, protection)"	Eco
o0355	b1885	tap	<	533	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hin Sce Syn
	b1886	tar	<	553	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hin Sce Syn
o0356	b1887	cheW	<	167	"Cell processes (incl. adaptation, protection)"	Bsu Hpy
	b1888	cheA	<	654	"Cell processes (incl. adaptation, protection)"	Bsu Hpy
o0356	b1887	cheW	<	167	"Cell processes (incl. adaptation, protection)"	B
	b1888	cheA	<	654	"Cell processes (incl. adaptation, protection)"	B
	b1889	motB	<	308	"Cell processes (incl. adaptation, protection)"	B
	b1890	motA	<	295	"Cell processes (incl. adaptation, protection)"	B
o0356	b1889	motB	<	308	"Cell processes (incl. adaptation, protection)"	Bsu Hpy
	b1890	motA	<	295	"Cell processes (incl. adaptation, protection)"	Bsu Hpy
o0357	b1891	flhC	<	192	Cell structure	B
	b1892	flhD	<	119	Cell structure	B
o0358	b1893	insB_5	<	167	"phage, transposon, or plasmid"	B Eco Syn
	b1894	insA_5	<	91	"phage, transposon, or plasmid"	B Eco Syn
o0359	b1896	otsA	<	474	"Cell processes (incl. adaptation, protection)"	B
	b1897	otsB	<	266	"Cell processes (incl. adaptation, protection)"	B
o0360	b1898	araH	<	86	Transport and binding proteins	Eco
	b1899	b1899	<	234	"Hypothetical, unclassified, unknown"	Eco
o0360	b1898	araH	<	86	Transport and binding proteins	Eco
	b1899	b1899	<	234	"Hypothetical, unclassified, unknown"	Eco
	b1900	araG	<	504	Transport and binding proteins	Eco
o0360	b1898	araH	<	86	Transport and binding proteins	B
	b1899	b1899	<	234	"Hypothetical, unclassified, unknown"	B
	b1900	araG	<	504	Transport and binding proteins	B
	b1901	araF	<	329	Transport and binding proteins	B
o0360	b1899	b1899	<	234	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Mpn Syn
	b1900	araG	<	504	Transport and binding proteins	Bsu Eco Hin Mpn Syn
o0360	b1899	b1899	<	234	"Hypothetical, unclassified, unknown"	Eco
	b1900	araG	<	504	Transport and binding proteins	Eco
	b1901	araF	<	329	Transport and binding proteins	Eco
o0360	b1900	araG	<	504	Transport and binding proteins	Eco
	b1901	araF	<	329	Transport and binding proteins	Eco
o0361	b1902	yecI	>	167	"Hypothetical, unclassified, unknown"	B
	b1903	b1903	>	112	"Hypothetical, unclassified, unknown"	B
o0362	b1909	leuZ	<		tRNA	B
	b1910	cysT	<		tRNA	B
	b1911	glyW	<		tRNA	B
o0363	b1917	b1917	<	250	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Hpy Syn
	b1918	yecC	<	222	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Hpy Syn

o0363	b1917	b1917	<	250	"Hypothetical, unclassified, unknown"	B
	b1918	yecC	<	222	"Hypothetical, unclassified, unknown"	B
	b1919	b1919	<	360	Putative enzymes	B
	b1920	fliY	<	266	"Cell processes (incl. adaptation, protection)"	B
o0363	b1919	b1919	<	360	Putative enzymes	Mth
	b1920	fliY	<	266	"Cell processes (incl. adaptation, protection)"	Mth
o0364	b1921	fliZ	<	195	"Hypothetical, unclassified, unknown"	B
	b1922	fliA	<	239	Cell structure	B
	b1923	fliC	<	498	Cell structure	B
o0364	b1922	fliA	<	239	Cell structure	Syn
	b1923	fliC	<	498	Cell structure	Syn
o0365	b1924	fliD	>	468	Cell structure	Bsu Hpy
	b1925	fliS	>	136	Cell structure	Bsu Hpy
o0365	b1924	fliD	>	468	Cell structure	B
	b1925	fliS	>	136	Cell structure	B
	b1926	fliT	>	121	Cell structure	B
o0366	b1929	yedE	>	401	"Hypothetical, unclassified, unknown"	B Eco
	b1930	yedF	>	77	"Hypothetical, unclassified, unknown"	B Eco
o0367	b1933	b1933	<	63	"Hypothetical, unclassified, unknown"	B
	b1934	b1934	<	106	"Hypothetical, unclassified, unknown"	B
o0368	b1938	fliF	>	552	Cell structure	Mpn Syn
	b1939	fliG	>	331	Cell structure	Mpn Syn
o0368	b1938	fliF	>	552	Cell structure	Hpy
	b1939	fliG	>	331	Cell structure	Hpy
	b1940	fliH	>	235	Cell structure	Hpy
o0368	b1938	fliF	>	552	Cell structure	B
	b1939	fliG	>	331	Cell structure	B
	b1940	fliH	>	235	Cell structure	B
	b1941	fliI	>	457	"Cell processes (incl. adaptation, protection)"	B
	b1942	fliJ	>	147	"Cell processes (incl. adaptation, protection)"	B
	b1943	fliK	>	375	"Cell processes (incl. adaptation, protection)"	B
o0368	b1940	fliH	>	235	Cell structure	Eco Sce Syn
	b1941	fliI	>	457	"Cell processes (incl. adaptation, protection)"	Eco Sce Syn
o0368	b1942	fliJ	>	147	"Cell processes (incl. adaptation, protection)"	Syn
	b1943	fliK	>	375	"Cell processes (incl. adaptation, protection)"	Syn
o0369	b1944	fliL	>	154	Cell structure	B
	b1945	fliM	>	334	Cell structure	B
	b1946	fliN	>	137	Cell structure	B
	b1947	fliO	>	101	Cell structure	B
	b1948	fliP	>	245	Cell structure	B
	b1949	fliQ	>	89	Cell structure	B
	b1950	fliR	>	261	Cell structure	B
o0369	b1945	fliM	>	334	Cell structure	Bsu Hpy
	b1946	fliN	>	137	Cell structure	Bsu Hpy
o0369	b1948	fliP	>	245	Cell structure	Bsu
	b1949	fliQ	>	89	Cell structure	Bsu
	b1950	fliR	>	261	Cell structure	Bsu
o0370	b1960	vsr	<	156	"Transcription, RNA processing and degradation"	B
	b1961	dcm	<	472	"DNA replication, recombination, modification and repair"	B
o0371	b1962	yedJ	<	231	"Hypothetical, unclassified, unknown"	B
	b1963	b1963	<	127	"Hypothetical, unclassified, unknown"	B

o0372	b1964	b1964	>	171	"Hypothetical, unclassified, unknown"	B
	b1965	b1965	>	69	"Hypothetical, unclassified, unknown"	B
o0373	b1968	b1968	<	452	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Hpy Mth Syn
	b1969	b1969	<	239	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Hpy Mth Syn
o0374	b1971	b1971	>	334	Putative enzymes	B
	b1972	b1972	>	211	"Hypothetical, unclassified, unknown"	B
o0375	b1979	b1979	<	108	"Hypothetical, unclassified, unknown"	B
	b1980	b1980	<	234	"Hypothetical, unclassified, unknown"	B
o0376	b1991	cobT	<	359	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1992	cobS	<	247	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b1993	cobU	<	181	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0377	b1996	yi22_3	<	301	"Hypothetical, unclassified, unknown"	B Eco
	b1997	yi21_3	<	136	"Hypothetical, unclassified, unknown"	B Eco
o0378	b1998	b1998	>	86	"Hypothetical, unclassified, unknown"	B Eco
	b1999	b1999	>	236	Structural proteins	B Eco
o0379	b2001	b2001	>	512	"Hypothetical, unclassified, unknown"	B
	b2002	b2002	>	148	"DNA replication, recombination, modification and repair"	B
o0380	b2005	b2005	>	124	"Hypothetical, unclassified, unknown"	B
	b2006	b2006	>	64	"Hypothetical, unclassified, unknown"	B
o0381	b2012	yeeD	<	75	"Hypothetical, unclassified, unknown"	B Eco
	b2013	yeeE	<	352	"Hypothetical, unclassified, unknown"	B Eco
o0382	b2015	b2015	<	316	Putative regulatory proteins	B Bsu
	b2016	b2016	<	274	Putative enzymes	B Bsu
o0383	b2019	hisG	>	299	Amino acid biosynthesis and metabolism	Bsu
	b2020	hisD	>	434	Amino acid biosynthesis and metabolism	Bsu
o0383	b2019	hisG	>	299	Amino acid biosynthesis and metabolism	B Hin
	b2020	hisD	>	434	Amino acid biosynthesis and metabolism	B Hin
	b2021	hisC	>	356	Amino acid biosynthesis and metabolism	B Hin
	b2022	hisB	>	356	Amino acid biosynthesis and metabolism	B Hin
	b2023	hisH	>	196	Amino acid biosynthesis and metabolism	B Hin
	b2024	hisA	>	246	Amino acid biosynthesis and metabolism	B Hin
	b2025	hisF	>	258	Amino acid biosynthesis and metabolism	B Hin
	b2026	hisI	>	203	Amino acid biosynthesis and metabolism	B Hin
o0383	b2020	hisD	>	434	Amino acid biosynthesis and metabolism	Syn
	b2021	hisC	>	356	Amino acid biosynthesis and metabolism	Syn
o0383	b2022	hisB	>	356	Amino acid biosynthesis and metabolism	Syn
	b2023	hisH	>	196	Amino acid biosynthesis and metabolism	Syn
o0383	b2022	hisB	>	356	Amino acid biosynthesis and metabolism	Bsu
	b2023	hisH	>	196	Amino acid biosynthesis and metabolism	Bsu
	b2024	hisA	>	246	Amino acid biosynthesis and metabolism	Bsu
	b2025	hisF	>	258	Amino acid biosynthesis and metabolism	Bsu
	b2026	hisI	>	203	Amino acid biosynthesis and metabolism	Bsu
o0383	b2023	hisH	>	196	Amino acid biosynthesis and metabolism	Eco Hin Sce
	b2024	hisA	>	246	Amino acid biosynthesis and metabolism	Eco Hin Sce
o0383	b2024	hisA	>	246	Amino acid biosynthesis and metabolism	Bsu Eco Hin
	b2025	hisF	>	258	Amino acid biosynthesis and metabolism	Bsu Eco Hin
o0383	b2025	hisF	>	258	Amino acid biosynthesis and metabolism	Mth
	b2026	hisI	>	203	Amino acid biosynthesis and metabolism	Mth

o0384	b2030	yi52_7	<	338	"phage, transposon, or plasmid"	B
	b2031	yefJ	<	157	Putative enzymes	B
	b2032	yefI	<	372	"Hypothetical, unclassified, unknown"	B
	b2033	yefH	<	196	Putative enzymes	B
	b2034	yefG	<	330	"Hypothetical, unclassified, unknown"	B
	b2035	rfc	<	388	Cell structure	B
	b2036	yefE	<	367	"Hypothetical, unclassified, unknown"	B
o0384	b2031	yefJ	<	157	Putative enzymes	Syn
	b2032	yefI	<	372	"Hypothetical, unclassified, unknown"	Syn
o0384	b2032	yefI	<	372	"Hypothetical, unclassified, unknown"	Eco Syn
	b2033	yefH	<	196	Putative enzymes	Eco Syn
o0385	b2037	rfbX	<	415	Cell structure	B
	b2038	rfbC	<	185	Central intermediary metabolism	B
	b2039	rfbA	<	293	Central intermediary metabolism	B
	b2040	rfbD	<	299	Central intermediary metabolism	B
	b2041	rfbB	<	361	Central intermediary metabolism	B
o0385	b2038	rfbC	<	185	Central intermediary metabolism	Mth
	b2039	rfbA	<	293	Central intermediary metabolism	Mth
	b2040	rfbD	<	299	Central intermediary metabolism	Mth
o0385	b2039	rfbA	<	293	Central intermediary metabolism	Bsu Syn
	b2040	rfbD	<	299	Central intermediary metabolism	Bsu Syn
o0385	b2040	rfbD	<	299	Central intermediary metabolism	Bsu Hpy
	b2041	rfbB	<	361	Central intermediary metabolism	Bsu Hpy

operon#	b#	gene	dir	length	function	species
o0386	b2043	b2043	<	464	"Hypothetical, unclassified, unknown"	B
	b2044	b2044	<	406	Putative enzymes	B
	b2045	b2045	<	426	Carbon compound catabolism	B
o0387	b2046	b2046	<	492	"Hypothetical, unclassified, unknown"	B Bsu
	b2047	b2047	<	464	Putative enzymes	B Bsu
o0388	b2048	cpsG	<	456	Central intermediary metabolism	B Mth
	b2049	cpsB	<	478	Central intermediary metabolism	B Mth
o0389	b2050	yefD	<	407	"Hypothetical, unclassified, unknown"	B
	b2051	yefC	<	160	"Hypothetical, unclassified, unknown"	B
	b2052	yefB	<	321	"Hypothetical, unclassified, unknown"	B
	b2053	yefA	<	373	Putative enzymes	B
	b2054	b2054	<	182	Putative enzymes	B
	b2055	b2055	<	248	Putative enzymes	B
	b2056	b2056	<	405	Putative regulatory proteins	B
	b2057	b2057	<	405	"Hypothetical, unclassified, unknown"	B
	b2058	wcaB	<	162	Amino acid biosynthesis and metabolism	B
	b2059	b2059	<	279	Cell structure	B
o0389	b2052	yefB	<	321	"Hypothetical, unclassified, unknown"	Bsu Hpy Syn
	b2053	yefA	<	373	Putative enzymes	Bsu Hpy Syn
o0389	b2055	b2055	<	248	Putative enzymes	Bsu Hin
	b2056	b2056	<	405	Putative regulatory proteins	Bsu Hin
o0389	b2056	b2056	<	405	Putative regulatory proteins	Mth
	b2057	b2057	<	405	"Hypothetical, unclassified, unknown"	Mth
o0389	b2057	b2057	<	405	"Hypothetical, unclassified, unknown"	Eco
	b2058	wcaB	<	162	Amino acid biosynthesis and metabolism	Eco

o0390	b2060	b2060	<	732	"Hypothetical, unclassified, unknown"	B Eco
	b2061	b2061	<	147	Putative regulatory proteins	B Eco
	b2062	b2062	<	379	Cell structure	B Eco
o0391	b2065	dcd	<	193	Nucleotide biosynthesis and metabolism	B Hin
	b2066	udk	<	231	Central intermediary metabolism	B Hin
o0392	b2072	b2072	<	253	"Hypothetical, unclassified, unknown"	B
	b2073	b2073	<	219	"Hypothetical, unclassified, unknown"	B
o0393	b2074	b2074	>	464	Putative transport proteins	Eco Hin Hpy Syn
	b2075	b2075	>	1040	"Hypothetical, unclassified, unknown"	Eco Hin Hpy Syn
o0393	b2074	b2074	>	464	Putative transport proteins	B
	b2075	b2075	>	1040	"Hypothetical, unclassified, unknown"	B
	b2076	b2076	>	1025	"Hypothetical, unclassified, unknown"	B
	b2077	b2077	>	471	Putative transport proteins	B
o0393	b2075	b2075	>	1040	"Hypothetical, unclassified, unknown"	Eco Hin Syn
	b2076	b2076	>	1025	"Hypothetical, unclassified, unknown"	Eco Hin Syn
o0393	b2076	b2076	>	1025	"Hypothetical, unclassified, unknown"	Bsu Eco Sce Syn
	b2077	b2077	>	471	Putative transport proteins	Bsu Eco Sce Syn
o0394	b2078	baeS	>	467	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Mth Syn
	b2079	baeR	>	240	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Mth Syn
o0395	b2083	b2083	<	48	"Hypothetical, unclassified, unknown"	B
	b2084	b2084	<	88	"Hypothetical, unclassified, unknown"	B
	b2085	b2085	<	125	"Hypothetical, unclassified, unknown"	B
o0396	b2086	b2086	>	299	"Hypothetical, unclassified, unknown"	B
	b2088	b2088	>	102	Carbon compound catabolism	B
	b2089	tra5_4	>	288	"phage, transposon, or plasmid"	B
o0396	b2088	b2088	>	102	Carbon compound catabolism	Eco
	b2089	tra5_4	>	288	"phage, transposon, or plasmid"	Eco
o0397	b2090	gatR_2	<	112	Carbon compound catabolism	B
	b2091	gatD	<	346	Carbon compound catabolism	B
	b2092	gatC	<	451	Transport and binding proteins	B
	b2093	gatB	<	94	Transport and binding proteins	B
	b2094	gatA	<	150	Transport and binding proteins	B
	b2095	gatZ	<	420	Carbon compound catabolism	B
	b2096	gatY	<	286	Carbon compound catabolism	B
o0397	b2091	gatD	<	346	Carbon compound catabolism	Bsu
	b2092	gatC	<	451	Transport and binding proteins	Bsu
o0397	b2093	gatB	<	94	Transport and binding proteins	Eco
	b2094	gatA	<	150	Transport and binding proteins	Eco
o0398	b2098	b2098	>	425	Putative transport proteins	Sce
	b2099	b2099	>	334	"Hypothetical, unclassified, unknown"	Sce
o0398	b2098	b2098	>	425	Putative transport proteins	B
	b2099	b2099	>	334	"Hypothetical, unclassified, unknown"	B
	b2100	b2100	>	321	Putative enzymes	B
o0399	b2103	b2103	<	266	"Hypothetical, unclassified, unknown"	B Eco Hin Hpy Syn
	b2104	b2104	<	262	Putative enzymes	B Eco Hin Hpy Syn
o0400	b2106	b2106	>	274	"Hypothetical, unclassified, unknown"	B
	b2107	b2107	>	172	"Hypothetical, unclassified, unknown"	B
o0401	b2108	yehA	<	344	Cell structure	Eco
	b2109	yehB	<	826	"Hypothetical, unclassified, unknown"	Eco
	b2110	yehC	<	239	Putative chaperones	Eco

o0401	b2108	yehA	<	344	Cell structure	B
	b2109	yehB	<	826	"Hypothetical, unclassified, unknown"	B
	b2110	yehC	<	239	Putative chaperones	B
	b2111	yehD	<	180	Cell structure	B
o0401	b2109	yehB	<	826	"Hypothetical, unclassified, unknown"	Eco
	b2110	yehC	<	239	Putative chaperones	Eco
o0401	b2109	yehB	<	826	"Hypothetical, unclassified, unknown"	Eco
	b2110	yehC	<	239	Putative chaperones	Eco
	b2111	yehD	<	180	Cell structure	Eco
o0402	b2115	molR_1	>	274	Transport and binding proteins	B
	b2116	molR_2	>	645	Transport and binding proteins	B
	b2117	molR_3	>	333	Transport and binding proteins	B
	b2118	yehI	>	1210	"Hypothetical, unclassified, unknown"	B
o0402	b2117	molR_3	>	333	Transport and binding proteins	Eco Syn
	b2118	yehI	>	1210	"Hypothetical, unclassified, unknown"	Eco Syn
o0403	b2119	yehL	>	384	"Hypothetical, unclassified, unknown"	Eco
	b2120	b2120	>	759	"Hypothetical, unclassified, unknown"	Eco
o0403	b2119	yehL	>	384	"Hypothetical, unclassified, unknown"	B
	b2120	b2120	>	759	"Hypothetical, unclassified, unknown"	B
	b2121	yehP	>	378	"Hypothetical, unclassified, unknown"	B
	b2122	yehQ	>	622	"Hypothetical, unclassified, unknown"	B
o0403	b2120	b2120	>	759	"Hypothetical, unclassified, unknown"	Eco Syn
	b2121	yehP	>	378	"Hypothetical, unclassified, unknown"	Eco Syn
o0404	b2124	yehS	<	156	"Hypothetical, unclassified, unknown"	B
	b2125	yehT	<	244	"Hypothetical, unclassified, unknown"	B
	b2126	yehU	<	561	"Hypothetical, unclassified, unknown"	B
o0404	b2125	yehT	<	244	"Hypothetical, unclassified, unknown"	Bsu Eco Mth Syn
	b2126	yehU	<	561	"Hypothetical, unclassified, unknown"	Bsu Eco Mth Syn
o0405	b2128	yehW	<	243	Putative transport proteins	Bsu Eco Hin Hpy Mth Syn
	b2129	yehX	<	308	Putative transport proteins	Bsu Eco Hin Hpy Mth Syn
o0405	b2128	yehW	<	243	Putative transport proteins	B
	b2129	yehX	<	308	Putative transport proteins	B
	b2130	yehY	<	385	"Hypothetical, unclassified, unknown"	B
	b2131	yehZ	<	305	Putative transport proteins	B
o0405	b2129	yehX	<	308	Putative transport proteins	Bsu Eco Hin Hpy Mge Mpn Syn
	b2130	yehY	<	385	"Hypothetical, unclassified, unknown"	Bsu Eco Hin Hpy Mge Mpn Syn
o0405	b2129	yehX	<	308	Putative transport proteins	Bsu
	b2130	yehY	<	385	"Hypothetical, unclassified, unknown"	Bsu
	b2131	yehZ	<	305	Putative transport proteins	Bsu
o0405	b2130	yehY	<	385	"Hypothetical, unclassified, unknown"	Bsu Eco
	b2131	yehZ	<	305	Putative transport proteins	Bsu Eco
o0406	b2138	yohG	<	398	Putative transport proteins	B
	b2139	yohH	<	96	"Hypothetical, unclassified, unknown"	B
o0407	b2141	yohJ	>	132	"Hypothetical, unclassified, unknown"	B Bsu Hin
	b2142	yohK	>	231	Putative transport proteins	B Bsu Hin
o0408	b2144	sanA	>	239	"Cell processes (incl. adaptation, protection)"	B
	b2145	b2145	>	79	"Hypothetical, unclassified, unknown"	B
o0409	b2146	b2146	>	412	Putative enzymes	B Eco Hin Mja Mth Syn
	b2147	yeiA	>	413	Putative enzymes	B Eco Hin Mja Mth Syn
o0410	b2148	mglC	<	336	Transport and binding proteins	Bsu Eco Hin Mge Mja Syn
	b2149	mglA	<	506	Transport and binding proteins	Bsu Eco Hin Mge Mja Syn

o0410	b2148	mglC	<	336	Transport and binding proteins	B Eco Hin
	b2149	mglA	<	506	Transport and binding proteins	B Eco Hin
	b2150	mglB	<	332	Transport and binding proteins	B Eco Hin
o0410	b2149	mglA	<	506	Transport and binding proteins	Eco Sce
	b2150	mglB	<	332	Transport and binding proteins	Eco Sce
o0411	b2152	yeiB	<	385	"Hypothetical, unclassified, unknown"	B Syn
	b2153	folE	<	222	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Syn
o0412	b2165	yeiN	<	312	"Hypothetical, unclassified, unknown"	B
	b2166	yeiC	<	313	Putative enzymes	B
o0413	b2167	fruA	<	563	Carbon compound catabolism	Bsu Eco Mge Mpn
	b2168	fruK	<	312	Energy metabolism	Bsu Eco Mge Mpn
o0413	b2167	fruA	<	563	Carbon compound catabolism	B Hin
	b2168	fruK	<	312	Energy metabolism	B Hin
	b2169	fruB	<	376	Transport and binding proteins	B Hin
o0413	b2168	fruK	<	312	Energy metabolism	Bsu Eco Mge Mpn
	b2169	fruB	<	376	Transport and binding proteins	Bsu Eco Mge Mpn
o0414	b2173	yeiR	>	328	"Hypothetical, unclassified, unknown"	B Hpy
	b2174	b2174	>	249	"Hypothetical, unclassified, unknown"	B Hpy
o0415	b2177	yejA	>	606	"Hypothetical, unclassified, unknown"	Hin Hpy
	b2178	yejB	>	364	"Hypothetical, unclassified, unknown"	Hin Hpy
o0415	b2177	yejA	>	606	"Hypothetical, unclassified, unknown"	Bsu Eco
	b2178	yejB	>	364	"Hypothetical, unclassified, unknown"	Bsu Eco
	b2179	yejE	>	341	Transport and binding proteins	Bsu Eco
o0415	b2177	yejA	>	606	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Hpy
	b2178	yejB	>	364	"Hypothetical, unclassified, unknown"	B Bsu Eco Hin Hpy
	b2179	yejE	>	341	Transport and binding proteins	B Bsu Eco Hin Hpy
	b2180	yejF	>	529	Transport and binding proteins	B Bsu Eco Hin Hpy
o0415	b2178	yejB	>	364	"Hypothetical, unclassified, unknown"	Bsu Eco Mpn
	b2179	yejE	>	341	Transport and binding proteins	Bsu Eco Mpn
o0415	b2178	yejB	>	364	"Hypothetical, unclassified, unknown"	Bsu Hin Mge Mpn
	b2179	yejE	>	341	Transport and binding proteins	Bsu Hin Mge Mpn
	b2180	yejF	>	529	Transport and binding proteins	Bsu Hin Mge Mpn
o0415	b2179	yejE	>	341	Transport and binding proteins	Bsu Eco Hpy Mpn Syn
	b2180	yejF	>	529	Transport and binding proteins	Bsu Eco Hpy Mpn Syn
o0416	b2182	bcr	<	396	"Cell processes (incl. adaptation, protection)"	B Hin Sce
	b2183	yejD	<	231	"Hypothetical, unclassified, unknown"	B Hin Sce
o0417	b2187	yejL	>	75	"Hypothetical, unclassified, unknown"	B
	b2188	yejM	>	586	Central intermediary metabolism	B
o0418	b2194	ccmH	<	350	Energy metabolism	Hin
	b2195	dsbE	<	185	Energy metabolism	Hin
	b2196	ccmF	<	647	Energy metabolism	Hin

o0418	b2194	ccmH	<	350	Energy metabolism	B
	b2195	dsbE	<	185	Energy metabolism	B
	b2196	ccmF	<	647	Energy metabolism	B
	b2197	ccmE	<	159	Energy metabolism	B
	b2198	ccmD	<	69	Energy metabolism	B
	b2199	ccmC	<	245	Energy metabolism	B
	b2200	ccmB	<	220	Energy metabolism	B
	b2201	ccmA	<	205	Energy metabolism	B
	b2202	napC	<	200	Energy metabolism	B
	b2203	napB	<	156	Energy metabolism	B
	b2204	napH	<	287	Energy metabolism	B
	b2205	napG	<	231	Energy metabolism	B
	b2206	napA	<	828	Energy metabolism	B
	b2207	yojF	<	87	"Hypothetical, unclassified, unknown"	B
	b2208	napF	<	164	Energy metabolism	B
o0418	b2195	dsbE	<	185	Energy metabolism	Bsu
	b2196	ccmF	<	647	Energy metabolism	Bsu
o0418	b2195	dsbE	<	185	Energy metabolism	Hin
	b2196	ccmF	<	647	Energy metabolism	Hin
	b2197	ccmE	<	159	Energy metabolism	Hin
	b2198	ccmD	<	69	Energy metabolism	Hin
	b2199	ccmC	<	245	Energy metabolism	Hin
	b2200	ccmB	<	220	Energy metabolism	Hin
	b2201	ccmA	<	205	Energy metabolism	Hin
o0418	b2200	ccmB	<	220	Energy metabolism	Bsu Eco Hin Mth Syn
	b2201	ccmA	<	205	Energy metabolism	Bsu Eco Hin Mth Syn
o0418	b2201	ccmA	<	205	Energy metabolism	Hin
	b2202	napC	<	200	Energy metabolism	Hin
o0418	b2202	napC	<	200	Energy metabolism	Hin
	b2203	napB	<	156	Energy metabolism	Hin
	b2204	napH	<	287	Energy metabolism	Hin
	b2205	napG	<	231	Energy metabolism	Hin
o0418	b2203	napB	<	156	Energy metabolism	Mth
	b2204	napH	<	287	Energy metabolism	Mth
o0418	b2204	napH	<	287	Energy metabolism	Eco Hin Mja Mth
	b2205	napG	<	231	Energy metabolism	Eco Hin Mja Mth
o0418	b2204	napH	<	287	Energy metabolism	Mja
	b2205	napG	<	231	Energy metabolism	Mja
	b2206	napA	<	828	Energy metabolism	Mja
o0418	b2205	napG	<	231	Energy metabolism	Eco Mja
	b2206	napA	<	828	Energy metabolism	Eco Mja
o0418	b2207	yojF	<	87	"Hypothetical, unclassified, unknown"	Hin
	b2208	napF	<	164	Energy metabolism	Hin
o0419	b2212	alkB	<	216	"DNA replication, recombination, modification and repair"	B
	b2213	ada	<	354	"DNA replication, recombination, modification and repair"	B
o0420	b2219	atoS	>	608	Putative regulatory proteins	B Bsu Eco Hin Mja Mth Syn
	b2220	atoC	>	461	Fatty acid and phospholipid metabolism	B Bsu Eco Hin Mja Mth Syn
o0421	b2221	atoD	>	220	Putative enzymes	Bsu Eco
	b2222	atoA	>	216	Putative enzymes	Bsu Eco

o0421	b2221	atoD	>	220	Putative enzymes	Hpy
	b2222	atoA	>	216	Putative enzymes	Hpy
	b2223	atoB	>	440	"Hypothetical, unclassified, unknown"	Hpy
o0421	b2221	atoD	>	220	Putative enzymes	B Hin
	b2222	atoA	>	216	Putative enzymes	B Hin
	b2223	atoB	>	440	"Hypothetical, unclassified, unknown"	B Hin
	b2224	b2224	>	394	Putative enzymes	B Hin
o0421	b2222	atoA	>	216	Putative enzymes	Hin
	b2223	atoB	>	440	"Hypothetical, unclassified, unknown"	Hin
o0421	b2223	atoB	>	440	"Hypothetical, unclassified, unknown"	Sce
	b2224	b2224	>	394	Putative enzymes	Sce
o0422	b2225	b2225	<	258	"Hypothetical, unclassified, unknown"	B
	b2226	b2226	<	549	"Hypothetical, unclassified, unknown"	B
	b2227	b2227	<	161	"Hypothetical, unclassified, unknown"	B
	b2228	b2228	<	1337	"Hypothetical, unclassified, unknown"	B
	b2229	b2229	<	216	"Hypothetical, unclassified, unknown"	B
	b2230	yfaA	<	578	"Hypothetical, unclassified, unknown"	B
o0423	b2234	nrdA	>	761	Nucleotide biosynthesis and metabolism	B Bsu Eco Hin
	b2235	nrdB	>	376	Nucleotide biosynthesis and metabolism	B Bsu Eco Hin
o0424	b2239	glpQ	<	358	Central intermediary metabolism	B Bsu
	b2240	glpT	<	452	Transport and binding proteins	B Bsu
o0425	b2241	glpA	>	542	Energy metabolism	Mth
	b2242	glpB	>	419	Energy metabolism	Mth
o0425	b2241	glpA	>	542	Energy metabolism	B
	b2242	glpB	>	419	Energy metabolism	B
	b2243	glpC	>	396	Energy metabolism	B
o0425	b2242	glpB	>	419	Energy metabolism	Eco
	b2243	glpC	>	396	Energy metabolism	Eco
o0426	b2245	b2245	<	267	"Hypothetical, unclassified, unknown"	Bsu Eco
	b2246	b2246	<	442	Putative transport proteins	Bsu Eco
o0426	b2245	b2245	<	267	"Hypothetical, unclassified, unknown"	B
	b2246	b2246	<	442	Putative transport proteins	B
	b2247	b2247	<	405	Putative enzymes	B
	b2248	b2248	<	260	Putative regulatory proteins	B
o0426	b2246	b2246	<	442	Putative transport proteins	Bsu Eco
	b2247	b2247	<	405	Putative enzymes	Bsu Eco
o0427	b2253	b2253	>	390	Cell structure	B
	b2254	b2254	>	322	Putative enzymes	B
	b2255	b2255	>	660	Putative enzymes	B
	b2256	b2256	>	296	"Hypothetical, unclassified, unknown"	B
	b2257	b2257	>	550	"Hypothetical, unclassified, unknown"	B
	b2258	b2258	>	222	Putative transport proteins	B
o0427	b2254	b2254	>	322	Putative enzymes	Mth
	b2255	b2255	>	660	Putative enzymes	Mth
o0427	b2256	b2256	>	296	"Hypothetical, unclassified, unknown"	Syn
	b2257	b2257	>	550	"Hypothetical, unclassified, unknown"	Syn

o0428	b2260	menE	<	451	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2261	menC	<	320	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2262	menB	<	285	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2263	yfbB	<	252	Putative enzymes	B
	b2264	menD	<	556	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2265	menF	<	356	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0428	b2261	menC	<	320	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin
	b2262	menB	<	285	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin
o0428	b2262	menB	<	285	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b2263	yfbB	<	252	Putative enzymes	Bsu
	b2264	menD	<	556	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b2265	menF	<	356	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0428	b2263	yfbB	<	252	Putative enzymes	Hin
	b2264	menD	<	556	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin
o0428	b2264	menD	<	556	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hpy
	b2265	menF	<	356	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hpy
o0429	b2276	nuoN	<	425	Energy metabolism	Eco Hpy Mja Syn
	b2277	nuoM	<	509	Energy metabolism	Eco Hpy Mja Syn

operon#	b#	gene	dir	length	function	species
o0429	b2276	nuoN	<	425	Energy metabolism	Hpy
	b2277	nuoM	<	509	Energy metabolism	Hpy
	b2278	nuoL	<	613	Energy metabolism	Hpy
o0429	b2276	nuoN	<	425	Energy metabolism	Hpy
	b2277	nuoM	<	509	Energy metabolism	Hpy
	b2278	nuoL	<	613	Energy metabolism	Hpy
	b2279	nuoK	<	100	Energy metabolism	Hpy
	b2280	nuoJ	<	184	Energy metabolism	Hpy
	b2281	nuoI	<	180	Energy metabolism	Hpy
	b2282	nuoH	<	325	Energy metabolism	Hpy
	b2283	nuoG	<	910	Energy metabolism	Hpy
o0429	b2276	nuoN	<	425	Energy metabolism	B
	b2277	nuoM	<	509	Energy metabolism	B
	b2278	nuoL	<	613	Energy metabolism	B
	b2279	nuoK	<	100	Energy metabolism	B
	b2280	nuoJ	<	184	Energy metabolism	B
	b2281	nuoI	<	180	Energy metabolism	B
	b2282	nuoH	<	325	Energy metabolism	B
	b2283	nuoG	<	910	Energy metabolism	B
	b2284	nuoF	<	445	Energy metabolism	B
	b2285	nuoE	<	166	Energy metabolism	B
	b2286	b2286	<	600	"Hypothetical, unclassified, unknown"	B
	b2287	nuoB	<	220	Energy metabolism	B
	b2288	nuoA	<	147	Energy metabolism	B
o0429	b2277	nuoM	<	509	Energy metabolism	Eco Hpy Syn
	b2278	nuoL	<	613	Energy metabolism	Eco Hpy Syn
o0429	b2278	nuoL	<	613	Energy metabolism	Eco Mja Syn
	b2279	nuoK	<	100	Energy metabolism	Eco Mja Syn

o0429	b2279	nuoK	<	100	Energy metabolism	Syn
	b2280	nuoJ	<	184	Energy metabolism	Syn
	b2281	nuoI	<	180	Energy metabolism	Syn
	b2282	nuoH	<	325	Energy metabolism	Syn
o0429	b2281	nuoI	<	180	Energy metabolism	Eco Hin
	b2282	nuoH	<	325	Energy metabolism	Eco Hin
o0429	b2282	nuoH	<	325	Energy metabolism	Bsu Syn
	b2283	nuoG	<	910	Energy metabolism	Bsu Syn
o0429	b2283	nuoG	<	910	Energy metabolism	Bsu
	b2284	nuoF	<	445	Energy metabolism	Bsu
o0429	b2284	nuoF	<	445	Energy metabolism	Mth Syn
	b2285	nuoE	<	166	Energy metabolism	Mth Syn
o0429	b2285	nuoE	<	166	Energy metabolism	Eco
	b2286	b2286	<	600	"Hypothetical, unclassified, unknown"	Eco
o0429	b2286	b2286	<	600	"Hypothetical, unclassified, unknown"	Eco Mja Mth
	b2287	nuoB	<	220	Energy metabolism	Eco Mja Mth
o0429	b2286	b2286	<	600	"Hypothetical, unclassified, unknown"	Hpy Syn
	b2287	nuoB	<	220	Energy metabolism	Hpy Syn
	b2288	nuoA	<	147	Energy metabolism	Hpy Syn
o0430	b2293	b2293	<	222	Putative enzymes	B
	b2294	b2294	<	170	"Hypothetical, unclassified, unknown"	B
o0431	b2303	b2303	>	120	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2304	b2304	>	297	Putative enzymes	B
o0432	b2306	hisP	<	257	Transport and binding proteins	Bsu Eco Hin Hpy Sce Syn
	b2307	hisM	<	238	Transport and binding proteins	Bsu Eco Hin Hpy Sce Syn
o0432	b2306	hisP	<	257	Transport and binding proteins	B Bsu Eco Hpy Syn
	b2307	hisM	<	238	Transport and binding proteins	B Bsu Eco Hpy Syn
	b2308	hisQ	<	228	Central intermediary metabolism	B Bsu Eco Hpy Syn
o0432	b2307	hisM	<	238	Transport and binding proteins	Bsu Eco Hin Hpy Syn
	b2308	hisQ	<	228	Central intermediary metabolism	Bsu Eco Hin Hpy Syn
o0433	b2311	ubiX	<	189	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2312	purF	<	505	Nucleotide biosynthesis and metabolism	B
	b2313	cvpA	<	162	"phage, transposon, or plasmid"	B
	b2314	dedD	<	211	"Hypothetical, unclassified, unknown"	B
o0433	b2312	purF	<	505	Nucleotide biosynthesis and metabolism	Hin
	b2313	cvpA	<	162	"phage, transposon, or plasmid"	Hin
o0434	b2318	truA	<	270	"Translation, post-translational modification"	B
	b2319	usg	<	337	"Cell processes (incl. adaptation, protection)"	B
o0435	b2325	b2325	<	92	"Hypothetical, unclassified, unknown"	B
	b2326	b2326	<	182	Putative regulatory proteins	B
	b2327	yfcA	<	269	Structural proteins	B
	b2328	mepA	<	274	Cell structure	B
	b2329	aroC	<	361	Amino acid biosynthesis and metabolism	B
	b2330	yfcB	<	421	Putative enzymes	B
o0435	b2327	yfcA	<	269	Structural proteins	Syn
	b2328	mepA	<	274	Cell structure	Syn
o0435	b2327	yfcA	<	269	Structural proteins	Hin
	b2328	mepA	<	274	Cell structure	Hin
	b2329	aroC	<	361	Amino acid biosynthesis and metabolism	Hin

o0436	b2332	b2332	<	278	"Hypothetical, unclassified, unknown"	B
	b2333	b2333	<	179	Cell structure	B
	b2334	b2334	<	162	"Hypothetical, unclassified, unknown"	B
	b2335	b2335	<	170	Cell structure	B
	b2336	b2336	<	250	Putative chaperones	B
	b2337	b2337	<	298	"Hypothetical, unclassified, unknown"	B
	b2338	b2338	<	578	Structural proteins	B
o0436	b2333	b2333	<	179	Cell structure	Eco
	b2334	b2334	<	162	"Hypothetical, unclassified, unknown"	Eco
o0436	b2334	b2334	<	162	"Hypothetical, unclassified, unknown"	Eco
	b2335	b2335	<	170	Cell structure	Eco
o0436	b2336	b2336	<	250	Putative chaperones	Eco Sce
	b2337	b2337	<	298	"Hypothetical, unclassified, unknown"	Eco Sce
o0437	b2341	b2341	<	714	Fatty acid and phospholipid metabolism	B Bsu Eco Syn
	b2342	b2342	<	436	Central intermediary metabolism	B Bsu Eco Syn
o0438	b2350	b2350	>	120	"Hypothetical, unclassified, unknown"	B
	b2351	b2351	>	306	Cell structure	B
	b2352	b2352	>	443	"Hypothetical, unclassified, unknown"	B
o0439	b2354	b2354	<	146	"Hypothetical, unclassified, unknown"	B
	b2355	b2355	<	172	Putative enzymes	B
	b2356	b2356	<	102	"Hypothetical, unclassified, unknown"	B
	b2357	b2357	<	164	"Hypothetical, unclassified, unknown"	B
	b2358	b2358	<	122	"Hypothetical, unclassified, unknown"	B
o0440	b2361	b2361	>	187	"Hypothetical, unclassified, unknown"	B
	b2362	b2362	>	120	"Hypothetical, unclassified, unknown"	B
	b2363	b2363	>	101	"Hypothetical, unclassified, unknown"	B
o0441	b2365	dsdX	>	445	Putative transport proteins	B Syn
	b2366	dsdA	>	442	Amino acid biosynthesis and metabolism	B Syn
o0442	b2367	emrY	<	512	"Cell processes (incl. adaptation, protection)"	B Bsu Eco Hin
	b2368	emrK	<	387	"Cell processes (incl. adaptation, protection)"	B Bsu Eco Hin
o0443	b2369	evgA	>	204	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Mth Syn
	b2370	evgS	>	1197	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Mth Syn
o0444	b2371	b2371	<	394	"Hypothetical, unclassified, unknown"	B
	b2372	b2372	<	314	Putative transport proteins	B
o0445	b2380	b2380	>	565	Putative regulatory proteins	Bsu Eco Mth Syn
	b2381	b2381	>	244	"Hypothetical, unclassified, unknown"	Bsu Eco Mth Syn
o0445	b2380	b2380	>	565	Putative regulatory proteins	B
	b2381	b2381	>	244	"Hypothetical, unclassified, unknown"	B
	b2382	b2382	>	285	Putative regulatory proteins	B
o0446	b2383	b2383	<	831	Central intermediary metabolism	B
	b2384	b2384	<	345	"Hypothetical, unclassified, unknown"	B
	b2385	b2385	<	361	"Translation, post-translational modification"	B
	b2386	b2386	<	415	"Hypothetical, unclassified, unknown"	B
	b2387	b2387	<	108	Transport and binding proteins	B
o0446	b2385	b2385	<	361	"Translation, post-translational modification"	Bsu Mth
	b2386	b2386	<	415	"Hypothetical, unclassified, unknown"	Bsu Mth
o0446	b2386	b2386	<	415	"Hypothetical, unclassified, unknown"	Eco
	b2387	b2387	<	108	Transport and binding proteins	Eco
o0447	b2390	b2390	>	108	"Hypothetical, unclassified, unknown"	B
	b2391	b2391	>	114	"Hypothetical, unclassified, unknown"	B

o0448	b2396	alaX	<		tRNA	B
	b2397	alaW	<		tRNA	B
o0449	b2398	yfeC	>	119	"Hypothetical, unclassified, unknown"	B Eco
	b2399	yfeD	>	130	"Hypothetical, unclassified, unknown"	B Eco
o0450	b2401	valU	>		tRNA	B
	b2402	valX	>		tRNA	B
	b2403	valY	>		tRNA	B
	b2404	lysV	>		tRNA	B
o0451	b2405	xapR	<	294	Central intermediary metabolism	B
	b2406	xapB	<	418	Transport and binding proteins	B
	b2407	xapA	<	277	Central intermediary metabolism	B
o0452	b2416	ptsI	>	575	Transport and binding proteins	B
	b2417	crr	>	169	Transport and binding proteins	B
o0453	b2419	b2419	>	124	"Hypothetical, unclassified, unknown"	B
	b2420	b2420	>	244	"Hypothetical, unclassified, unknown"	B
o0454	b2421	cysM	<	303	Amino acid biosynthesis and metabolism	Bsu Mth
	b2422	cysA	<	365	Transport and binding proteins	Bsu Mth
o0454	b2421	cysM	<	303	Amino acid biosynthesis and metabolism	B
	b2422	cysA	<	365	Transport and binding proteins	B
	b2423	cysW	<	149	Transport and binding proteins	B
	b2424	cysU	<	277	Transport and binding proteins	B
	b2425	cysP	<	338	Transport and binding proteins	B
o0454	b2422	cysA	<	365	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth
	b2423	cysW	<	149	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth
o0454	b2422	cysA	<	365	Transport and binding proteins	Bsu Eco Hin Mth Syn
	b2423	cysW	<	149	Transport and binding proteins	Bsu Eco Hin Mth Syn
	b2424	cysU	<	277	Transport and binding proteins	Bsu Eco Hin Mth Syn
o0454	b2423	cysW	<	149	Transport and binding proteins	Bsu Eco Hin Mge Mja Mpn Mth Syn
	b2424	cysU	<	277	Transport and binding proteins	Bsu Eco Hin Mge Mja Mpn Mth Syn
o0454	b2424	cysU	<	277	Transport and binding proteins	Bsu
	b2425	cysP	<	338	Transport and binding proteins	Bsu
o0455	b2428	b2428	>	298	Putative regulatory proteins	Eco
	b2429	b2429	>	474	Putative enzymes	Eco
o0455	b2428	b2428	>	298	Putative regulatory proteins	B
	b2429	b2429	>	474	Putative enzymes	B
	b2430	b2430	>	463	"phage, transposon, or plasmid"	B
o0455	b2429	b2429	>	474	Putative enzymes	Bsu
	b2430	b2430	>	463	"phage, transposon, or plasmid"	Bsu
o0456	b2433	b2433	<	151	"Hypothetical, unclassified, unknown"	B
	b2434	b2434	<	178	"Hypothetical, unclassified, unknown"	B
o0457	b2435	amiA	>	289	Cell structure	B
	b2436	hemF	>	299	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0458	b2437	yfeG	<	350	"Hypothetical, unclassified, unknown"	B
	b2438	b2438	<	168	Structural proteins	B
	b2439	b2439	<	219	"Hypothetical, unclassified, unknown"	B
	b2440	eutC	<	295	Carbon compound catabolism	B
	b2441	eutB	<	467	Carbon compound catabolism	B
o0459	b2444	b2444	>	81	"Hypothetical, unclassified, unknown"	B
	b2445	b2445	>	127	"Hypothetical, unclassified, unknown"	B
o0460	b2446	b2446	>	138	"Hypothetical, unclassified, unknown"	B
	b2447	b2447	>	197	"Hypothetical, unclassified, unknown"	B

o0461	b2448	b2448	>	130	"Hypothetical, unclassified, unknown"	B
	b2449	b2449	>	130	"Hypothetical, unclassified, unknown"	B
o0462	b2451	b2451	<	467	"Hypothetical, unclassified, unknown"	Eco
	b2452	eutH	<	408	Carbon compound catabolism	Eco
o0462	b2451	b2451	<	467	"Hypothetical, unclassified, unknown"	B
	b2452	eutH	<	408	Carbon compound catabolism	B
	b2453	eutG	<	404	Carbon compound catabolism	B
	b2454	eutJ	<	278	Carbon compound catabolism	B
	b2455	eutE	<	467	Carbon compound catabolism	B
	b2456	cchB	<	95	"Hypothetical, unclassified, unknown"	B
o0462	b2452	eutH	<	408	Carbon compound catabolism	Hin
	b2453	eutG	<	404	Carbon compound catabolism	Hin
o0463	b2457	cchA	<	111	"Hypothetical, unclassified, unknown"	B
	b2458	eutI	<	338	Carbon compound catabolism	B
	b2459	b2459	<	267	"Hypothetical, unclassified, unknown"	B
	b2460	b2460	<	233	"Hypothetical, unclassified, unknown"	B
	b2461	b2461	<	159	"Hypothetical, unclassified, unknown"	B
	b2462	b2462	<	135	"Hypothetical, unclassified, unknown"	B
o0464	b2464	b2464	>	316	Central intermediary metabolism	B
	b2465	tktB	>	667	Energy metabolism	B
o0465	b2471	yffB	>	118	"Hypothetical, unclassified, unknown"	B Hin
	b2472	dapE	>	375	Amino acid biosynthesis and metabolism	B Hin
o0466	b2473	b2473	<	240	"Hypothetical, unclassified, unknown"	B
	b2474	b2474	<	671	"Hypothetical, unclassified, unknown"	B
	b2475	b2475	<	287	"Hypothetical, unclassified, unknown"	B
o0467	b2477	nlpB	<	345	Membrane proteins	B Hin Mth
	b2478	dapA	<	292	Amino acid biosynthesis and metabolism	B Hin Mth
o0468	b2479	gcvR	>	212	Central intermediary metabolism	B
	b2480	bcp	>	156	Transport and binding proteins	B
o0469	b2481	yffE	>	218	Energy metabolism	Eco Syn
	b2482	b2482	>	672	Energy metabolism	Eco Syn
o0469	b2481	yffE	>	218	Energy metabolism	Eco
	b2482	b2482	>	672	Energy metabolism	Eco
	b2483	b2483	>	322	Energy metabolism	Eco
o0469	b2481	yffE	>	218	Energy metabolism	B
	b2482	b2482	>	672	Energy metabolism	B
	b2483	b2483	>	322	Energy metabolism	B
	b2484	b2484	>	479	Central intermediary metabolism	B
	b2485	b2485	>	216	"Hypothetical, unclassified, unknown"	B
	b2486	b2486	>	526	Energy metabolism	B
	b2487	b2487	>	555	Energy metabolism	B
	b2488	b2488	>	181	Energy metabolism	B
	b2489	b2489	>	252	Energy metabolism	B
	b2490	b2490	>	158	"Translation, post-translational modification"	B
o0469	b2482	b2482	>	672	Energy metabolism	Eco Syn
	b2483	b2483	>	322	Energy metabolism	Eco Syn
o0469	b2483	b2483	>	322	Energy metabolism	Eco Mth
	b2484	b2484	>	479	Central intermediary metabolism	Eco Mth
o0469	b2484	b2484	>	479	Central intermediary metabolism	Eco Hpy Syn
	b2485	b2485	>	216	"Hypothetical, unclassified, unknown"	Eco Hpy Syn

o0469	b2485	b2485	>	216	"Hypothetical, unclassified, unknown"	Eco Hpy Syn
	b2486	b2486	>	526	Energy metabolism	Eco Hpy Syn
o0469	b2486	b2486	>	526	Energy metabolism	Syn
	b2487	b2487	>	555	Energy metabolism	Syn
o0469	b2487	b2487	>	555	Energy metabolism	Mja Mth
	b2488	b2488	>	181	Energy metabolism	Mja Mth
o0469	b2487	b2487	>	555	Energy metabolism	Eco
	b2488	b2488	>	181	Energy metabolism	Eco
	b2489	b2489	>	252	Energy metabolism	Eco
	b2490	b2490	>	158	"Translation, post-translational modification"	Eco
o0469	b2488	b2488	>	181	Energy metabolism	Eco Mja Mth
	b2489	b2489	>	252	Energy metabolism	Eco Mja Mth
o0470	b2491	b2491	>	663	Central intermediary metabolism	B Bsu
	b2492	b2492	>	282	Putative transport proteins	B Bsu
o0471	b2494	b2494	>	487	"Hypothetical, unclassified, unknown"	B
	b2495	b2495	>	119	Putative enzymes	B
o0472	b2496	b2496	<	248	"DNA replication, recombination, modification and repair"	B
	b2497	uraA	<	429	Transport and binding proteins	B
o0473	b2499	purM	>	345	Nucleotide biosynthesis and metabolism	B Bsu Hin
	b2500	purN	>	212	Nucleotide biosynthesis and metabolism	B Bsu Hin
o0474	b2505	b2505	>	172	Cell structure	B
	b2506	b2506	>	179	Structural proteins	B
o0475	b2507	guaA	<	525	Nucleotide biosynthesis and metabolism	B Eco Hin Mja
	b2508	guaB	<	488	Nucleotide biosynthesis and metabolism	B Eco Hin Mja
o0476	b2510	b2510	<	83	"Hypothetical, unclassified, unknown"	B
	b2511	b2511	<	503	Putative enzymes	B
o0477	b2512	b2512	<	392	Putative enzymes	Eco
	b2513	b2513	<	206	"Hypothetical, unclassified, unknown"	Eco
o0477	b2512	b2512	<	392	Putative enzymes	B
	b2513	b2513	<	206	"Hypothetical, unclassified, unknown"	B
	b2514	hisS	<	424	"Translation, post-translational modification"	B
o0478	b2515	gcpE	<	372	"Hypothetical, unclassified, unknown"	B Eco Syn
	b2516	yfgA	<	337	Cell structure	B Eco Syn
o0479	b2519	b2519	<	770	Cell structure	B
	b2520	b2520	<	1653	"Hypothetical, unclassified, unknown"	B
o0480	b2524	yfhJ	<	66	"Hypothetical, unclassified, unknown"	Hin
	b2525	fdx	<	111	Energy metabolism	Hin
	b2526	hscA	<	616	"Cell processes (incl. adaptation, protection)"	Hin
o0480	b2524	yfhJ	<	66	"Hypothetical, unclassified, unknown"	B
	b2525	fdx	<	111	Energy metabolism	B
	b2526	hscA	<	616	"Cell processes (incl. adaptation, protection)"	B
	b2527	yfhE	<	171	"Hypothetical, unclassified, unknown"	B
o0480	b2526	hscA	<	616	"Cell processes (incl. adaptation, protection)"	Mth Syn
	b2527	yfhE	<	171	"Hypothetical, unclassified, unknown"	Mth Syn
o0481	b2528	yfhF	<	107	"Hypothetical, unclassified, unknown"	B
	b2529	b2529	<	128	"Hypothetical, unclassified, unknown"	B
	b2530	b2530	<	412	Central intermediary metabolism	B
o0481	b2529	b2529	<	128	"Hypothetical, unclassified, unknown"	Bsu Hpy
	b2530	b2530	<	412	Central intermediary metabolism	Bsu Hpy

o0482	b2538	b2538	>	453	Central intermediary metabolism	B
	b2539	b2539	>	172	Central intermediary metabolism	B
	b2540	b2540	>	106	Central intermediary metabolism	B
	b2541	b2541	>	270	Putative enzymes	B
	b2542	b2542	>	400	Putative enzymes	B
	b2543	b2543	>	164	"Hypothetical, unclassified, unknown"	B

operon#	b#	gene	dir	length	function	species
o0482	b2541	b2541	>	270	Putative enzymes	Hin
	b2542	b2542	>	400	Putative enzymes	Hin
o0482	b2542	b2542	>	400	Putative enzymes	Syn
	b2543	b2543	>	164	"Hypothetical, unclassified, unknown"	Syn
o0483	b2544	b2544	<	290	"Hypothetical, unclassified, unknown"	B
	b2545	b2545	<	364	Putative enzymes	B
	b2546	b2546	<	332	Putative transport proteins	B
	b2547	b2547	<	503	Putative transport proteins	B
	b2548	b2548	<	327	"Hypothetical, unclassified, unknown"	B
o0483	b2545	b2545	<	364	Putative enzymes	Mja
	b2546	b2546	<	332	Putative transport proteins	Mja
o0483	b2546	b2546	<	332	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
	b2547	b2547	<	503	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
o0483	b2546	b2546	<	332	Putative transport proteins	Eco Hin
	b2547	b2547	<	503	Putative transport proteins	Eco Hin
	b2548	b2548	<	327	"Hypothetical, unclassified, unknown"	Eco Hin
o0483	b2547	b2547	<	503	Putative transport proteins	Eco
	b2548	b2548	<	327	"Hypothetical, unclassified, unknown"	Eco
o0484	b2554	yfhA	<	444	Central intermediary metabolism	B Eco
	b2555	yfhG	<	237	Structural proteins	B Eco
o0485	b2559	yfhC	<	178	Putative enzymes	B Sce
	b2560	yfhB	<	190	"Hypothetical, unclassified, unknown"	B Sce
o0486	b2563	acpS	<	126	Fatty acid and phospholipid metabolism	B
	b2564	pdxJ	<	243	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0487	b2565	recO	<	242	"DNA replication, recombination, modification and repair"	Bsu
	b2566	era	<	301	Regulatory function	Bsu
o0487	b2565	recO	<	242	"DNA replication, recombination, modification and repair"	B
	b2566	era	<	301	Regulatory function	B
	b2567	rnc	<	226	"DNA replication, recombination, modification and repair"	B
o0488	b2570	rseC	<	159	Regulatory function	B
	b2571	rseB	<	318	Regulatory function	B
o0489	b2572	rseA	<	216	Regulatory function	B
	b2573	rpoE	<	191	Regulatory function	B
o0490	b2582	yfiG	>	139	Energy metabolism	B
	b2583	b2583	>	240	"Hypothetical, unclassified, unknown"	B
	b2584	b2584	>	886	"Hypothetical, unclassified, unknown"	B
o0491	b2588	rrfG	<		rRNA	B
	b2589	rrlG	<		rRNA	B
	b2590	gltW	<		tRNA	B
	b2591	rrsG	<		rRNA	B
o0492	b2593	yfiH	<	243	"Hypothetical, unclassified, unknown"	B
	b2594	sfhB	<	326	Putative enzymes	B

o0493	b2595	b2595	>	245	"Hypothetical, unclassified, unknown"	B
	b2596	b2596	>	68	"Hypothetical, unclassified, unknown"	B
	b2597	yfiA	>	113	"Transcription, RNA processing and degradation"	B
o0494	b2600	tyrA	<	373	Amino acid biosynthesis and metabolism	B Syn
	b2601	aroF	<	356	Amino acid biosynthesis and metabolism	B Syn
o0495	b2603	b2603	>	172	"Hypothetical, unclassified, unknown"	B
	b2604	yfiN	>	408	"Hypothetical, unclassified, unknown"	B
	b2605	yfiB	>	160	Structural proteins	B
o0496	b2608	yfjA	<	185	"Hypothetical, unclassified, unknown"	B
	b2609	rpsP	<	82	"Translation, post-translational modification"	B
o0497	b2611	b2611	>	288	"Hypothetical, unclassified, unknown"	B
	b2612	b2612	>	196	"Hypothetical, unclassified, unknown"	B
	b2613	yfjD	>	227	"Hypothetical, unclassified, unknown"	B
o0498	b2618	b2618	<	102	"Hypothetical, unclassified, unknown"	B Bsu
	b2619	b2619	<	158	"Hypothetical, unclassified, unknown"	B Bsu
o0499	b2627	b2627	<	729	"Hypothetical, unclassified, unknown"	B Bsu
	b2628	b2628	<	538	"Hypothetical, unclassified, unknown"	B Bsu
o0500	b2630	b2630	>	357	"Cell processes (incl. adaptation, protection)"	B
	b2631	b2631	>	106	"Hypothetical, unclassified, unknown"	B
o0501	b2634	b2634	>	233	"Hypothetical, unclassified, unknown"	B
	b2635	b2635	>	130	"Hypothetical, unclassified, unknown"	B
	b2636	b2636	>	230	"Hypothetical, unclassified, unknown"	B
	b2637	b2637	>	155	"Hypothetical, unclassified, unknown"	B
o0501	b2636	b2636	>	230	"Hypothetical, unclassified, unknown"	Eco
	b2637	b2637	>	155	"Hypothetical, unclassified, unknown"	Eco
o0502	b2638	b2638	<	104	"Hypothetical, unclassified, unknown"	B Eco
	b2639	b2639	<	172	"Cell processes (incl. adaptation, protection)"	B Eco
o0503	b2643	b2643	>	152	"Hypothetical, unclassified, unknown"	B
	b2644	b2644	>	160	"DNA replication, recombination, modification and repair"	B
o0504	b2645	b2645	>	105	"Hypothetical, unclassified, unknown"	B Eco
	b2646	b2646	>	109	"Hypothetical, unclassified, unknown"	B Eco
o0505	b2652	ileY	<		tRNA	B
	b2653	b2653	<	57	"Hypothetical, unclassified, unknown"	B
o0506	b2654	b2654	>	110	"Hypothetical, unclassified, unknown"	B
	b2655	b2655	>	164	"Hypothetical, unclassified, unknown"	B
	b2656	b2656	>	62	"Hypothetical, unclassified, unknown"	B
o0507	b2659	b2659	>	360	"Hypothetical, unclassified, unknown"	B
	b2660	ygaF	>	444	"Hypothetical, unclassified, unknown"	B
	b2661	gabD	>	482	Central intermediary metabolism	B
	b2662	gabT	>	426	Central intermediary metabolism	B
	b2663	gabP	>	466	Transport and binding proteins	B
	b2664	ygaE	>	226	Putative regulatory proteins	B
o0507	b2660	ygaF	>	444	"Hypothetical, unclassified, unknown"	Bsu
	b2661	gabD	>	482	Central intermediary metabolism	Bsu
o0507	b2661	gabD	>	482	Central intermediary metabolism	Bsu Eco
	b2662	gabT	>	426	Central intermediary metabolism	Bsu Eco
o0507	b2662	gabT	>	426	Central intermediary metabolism	Bsu
	b2663	gabP	>	466	Transport and binding proteins	Bsu
o0507	b2663	gabP	>	466	Transport and binding proteins	Bsu Eco
	b2664	ygaE	>	226	Putative regulatory proteins	Bsu Eco

o0508	b2667	b2667	>	99	"Hypothetical, unclassified, unknown"	B
	b2668	b2668	>	174	Putative enzymes	B
o0509	b2673	b2673	>	81	"Hypothetical, unclassified, unknown"	B
	b2674	b2674	>	136	"Hypothetical, unclassified, unknown"	B
	b2675	nrdE	>	714	Central intermediary metabolism	B
	b2676	nrdF	>	319	Central intermediary metabolism	B
o0509	b2674	b2674	>	136	"Hypothetical, unclassified, unknown"	Bsu Mge Mpn
	b2675	nrdE	>	714	Central intermediary metabolism	Bsu Mge Mpn
o0509	b2674	b2674	>	136	"Hypothetical, unclassified, unknown"	Bsu
	b2675	nrdE	>	714	Central intermediary metabolism	Bsu
	b2676	nrdF	>	319	Central intermediary metabolism	Bsu
o0509	b2675	nrdE	>	714	Central intermediary metabolism	Bsu Eco Hin Hpy
	b2676	nrdF	>	319	Central intermediary metabolism	Bsu Eco Hin Hpy
o0510	b2677	proV	>	400	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Sce Syn
	b2678	proW	>	354	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Sce Syn
o0510	b2677	proV	>	400	Transport and binding proteins	B Bsu
	b2678	proW	>	354	Transport and binding proteins	B Bsu
	b2679	proX	>	330	"Cell processes (incl. adaptation, protection)"	B Bsu
o0510	b2678	proW	>	354	Transport and binding proteins	Mpn
	b2679	proX	>	330	"Cell processes (incl. adaptation, protection)"	Mpn
o0511	b2680	b2680	>	88	"Hypothetical, unclassified, unknown"	B Bsu Eco
	b2681	b2681	>	305	Putative transport proteins	B Bsu Eco
o0512	b2682	b2682	>	245	"Hypothetical, unclassified, unknown"	B
	b2683	ygaH	>	111	"Hypothetical, unclassified, unknown"	B
o0513	b2685	emrA	>	390	"Cell processes (incl. adaptation, protection)"	B Bsu Eco Hin
	b2686	emrB	>	512	"Cell processes (incl. adaptation, protection)"	B Bsu Eco Hin
o0514	b2689	b2689	<	142	"Hypothetical, unclassified, unknown"	B Hin
	b2690	b2690	<	188	"Hypothetical, unclassified, unknown"	B Hin
o0515	b2691	argQ	<		tRNA	B
	b2692	argZ	<		tRNA	B
	b2693	argY	<		tRNA	B
	b2694	argV	<		tRNA	B
	b2695	serV	<		tRNA	B
o0516	b2702	srlA_1	>	187	Transport and binding proteins	B
	b2703	srlA_2	>	319	Transport and binding proteins	B
	b2704	srlB	>	123	Transport and binding proteins	B
	b2705	srlD	>	259	Carbon compound catabolism	B
	b2706	gutM	>	119	Carbon compound catabolism	B
	b2707	srlR	>	257	Carbon compound catabolism	B
	b2708	gutQ	>	308	Carbon compound catabolism	B
o0517	b2710	b2710	>	479	Putative enzymes	B Mja
	b2711	ygbD	>	377	Putative enzymes	B Mja
o0518	b2715	ascF	>	485	Transport and binding proteins	B Bsu Eco Mja
	b2716	ascB	>	474	Carbon compound catabolism	B Bsu Eco Mja
o0519	b2718	hycH	<	136	Energy metabolism	Eco
	b2719	hycG	<	255	Energy metabolism	Eco
	b2720	hycF	<	180	Energy metabolism	Eco
	b2721	hycE	<	569	Energy metabolism	Eco

o0519	b2718	hycH	<	136	Energy metabolism	B
	b2719	hycG	<	255	Energy metabolism	B
	b2720	hycF	<	180	Energy metabolism	B
	b2721	hycE	<	569	Energy metabolism	B
	b2722	hycD	<	307	Energy metabolism	B
	b2723	hycC	<	608	Energy metabolism	B
	b2724	hycB	<	203	Energy metabolism	B
	b2725	hycA	<	153	Energy metabolism	B
o0519	b2719	hycG	<	255	Energy metabolism	Eco Mja Mth
	b2720	hycF	<	180	Energy metabolism	Eco Mja Mth
o0519	b2720	hycF	<	180	Energy metabolism	Mja Mth
	b2721	hycE	<	569	Energy metabolism	Mja Mth
o0519	b2721	hycE	<	569	Energy metabolism	Mth
	b2722	hycD	<	307	Energy metabolism	Mth
o0519	b2722	hycD	<	307	Energy metabolism	Eco Syn
	b2723	hycC	<	608	Energy metabolism	Eco Syn
o0519	b2722	hycD	<	307	Energy metabolism	Eco
	b2723	hycC	<	608	Energy metabolism	Eco
	b2724	hycB	<	203	Energy metabolism	Eco
o0519	b2723	hycC	<	608	Energy metabolism	Eco Syn
	b2724	hycB	<	203	Energy metabolism	Eco Syn
o0520	b2726	hypA	>	116	Energy metabolism	Mth Syn
	b2727	hypB	>	290	Energy metabolism	Mth Syn
o0520	b2726	hypA	>	116	Energy metabolism	B
	b2727	hypB	>	290	Energy metabolism	B
	b2728	hypC	>	90	Energy metabolism	B
	b2729	hypD	>	373	Energy metabolism	B
	b2730	hypE	>	322	Energy metabolism	B
o0520	b2727	hypB	>	290	Energy metabolism	Hpy
	b2728	hypC	>	90	Energy metabolism	Hpy
	b2729	hypD	>	373	Energy metabolism	Hpy
o0520	b2729	hypD	>	373	Energy metabolism	Bsu
	b2730	hypE	>	322	Energy metabolism	Bsu
o0521	b2736	b2736	>	302	Putative enzymes	B Eco
	b2737	b2737	>	388	"Hypothetical, unclassified, unknown"	B Eco
o0522	b2738	b2738	>	212	Putative enzymes	B
	b2739	b2739	>	258	"Hypothetical, unclassified, unknown"	B
o0523	b2741	rpoS	<	330	"Transcription, RNA processing and degradation"	B Eco Sce
	b2742	nlpD	<	379	Membrane proteins	B Eco Sce
o0524	b2743	pcm	<	208	"Translation, post-translational modification"	B
	b2744	surE	<	253	Other known genes	B
o0525	b2745	b2745	<	349	"Hypothetical, unclassified, unknown"	B
	b2746	ygbB	<	159	"Hypothetical, unclassified, unknown"	B
	b2747	b2747	<	236	"Hypothetical, unclassified, unknown"	B
	b2748	b2748	<	103	"Hypothetical, unclassified, unknown"	B
o0525	b2746	ygbB	<	159	"Hypothetical, unclassified, unknown"	Bsu
	b2747	b2747	<	236	"Hypothetical, unclassified, unknown"	Bsu
o0525	b2746	ygbB	<	159	"Hypothetical, unclassified, unknown"	Hin
	b2747	b2747	<	236	"Hypothetical, unclassified, unknown"	Hin
	b2748	b2748	<	103	"Hypothetical, unclassified, unknown"	Hin

o0526	b2750	cysC	<	201	Central intermediary metabolism	B
	b2751	cysN	<	475	Central intermediary metabolism	B
o0527	b2754	ygbF	<	116	"Hypothetical, unclassified, unknown"	B
	b2755	b2755	<	305	"Hypothetical, unclassified, unknown"	B
	b2756	b2756	<	199	"Hypothetical, unclassified, unknown"	B
	b2757	b2757	<	226	"Hypothetical, unclassified, unknown"	B
	b2758	b2758	<	363	"Hypothetical, unclassified, unknown"	B
	b2759	b2759	<	160	"Hypothetical, unclassified, unknown"	B
	b2760	b2760	<	502	"Hypothetical, unclassified, unknown"	B
o0528	b2762	cysH	<	244	Central intermediary metabolism	B
	b2763	cysI	<	570	Central intermediary metabolism	B
	b2764	cysJ	<	599	Central intermediary metabolism	B
o0528	b2763	cysI	<	570	Central intermediary metabolism	Bsu
	b2764	cysJ	<	599	Central intermediary metabolism	Bsu
o0529	b2765	b2765	>	121	Central intermediary metabolism	Eco
	b2766	b2766	>	433	"Hypothetical, unclassified, unknown"	Eco
o0529	b2765	b2765	>	121	Central intermediary metabolism	B
	b2766	b2766	>	433	"Hypothetical, unclassified, unknown"	B
	b2767	b2767	>	98	"Hypothetical, unclassified, unknown"	B
	b2768	b2768	>	191	Putative regulatory proteins	B
o0529	b2766	b2766	>	433	"Hypothetical, unclassified, unknown"	Eco
	b2767	b2767	>	98	"Hypothetical, unclassified, unknown"	Eco
o0530	b2769	b2769	<	297	Energy metabolism	Bsu Eco
	b2770	b2770	<	261	Energy metabolism	Bsu Eco
o0530	b2769	b2769	<	297	Energy metabolism	B
	b2770	b2770	<	261	Energy metabolism	B
	b2771	b2771	<	469	Putative transport proteins	B
	b2772	b2772	<	264	"Hypothetical, unclassified, unknown"	B
	b2773	b2773	<	218	"Hypothetical, unclassified, unknown"	B
o0530	b2772	b2772	<	264	"Hypothetical, unclassified, unknown"	Eco
	b2773	b2773	<	218	"Hypothetical, unclassified, unknown"	Eco
o0531	b2775	b2775	>	425	Putative transport proteins	B Syn
	b2776	ygcE	>	492	Putative enzymes	B Syn
o0532	b2782	chpA	<	111	Other known genes	B Eco
	b2783	chpR	<	82	Other known genes	B Eco
o0533	b2784	relA	<	744	Regulatory function	B Hin Mja
	b2785	ygcA	<	433	"Translation, post-translational modification"	B Hin Mja
o0534	b2787	b2787	<	446	Carbon compound catabolism	Eco
	b2788	b2788	<	446	Carbon compound catabolism	Eco
o0534	b2787	b2787	<	446	Carbon compound catabolism	B
	b2788	b2788	<	446	Carbon compound catabolism	B
	b2789	b2789	<	450	Carbon compound catabolism	B
o0534	b2788	b2788	<	446	Carbon compound catabolism	Bsu Eco
	b2789	b2789	<	450	Carbon compound catabolism	Bsu Eco
o0535	b2790	b2790	<	149	"Hypothetical, unclassified, unknown"	B
	b2791	b2791	<	260	"Hypothetical, unclassified, unknown"	B
	b2792	b2792	<	109	"Hypothetical, unclassified, unknown"	B
o0535	b2791	b2791	<	260	"Hypothetical, unclassified, unknown"	Hin
	b2792	b2792	<	109	"Hypothetical, unclassified, unknown"	Hin
o0536	b2797	sdaB	>	455	Amino acid biosynthesis and metabolism	B
	b2798	exo	>	281	"Transcription, RNA processing and degradation"	B

operon#	b#	gene	dir	length	function	species
o0537	b2799	fucO	<	383	Carbon compound catabolism	B
	b2800	fucA	<	215	Carbon compound catabolism	B
o0538	b2801	fucP	>	438	Transport and binding proteins	Eco
	b2802	fucI	>	591	Carbon compound catabolism	Eco
o0538	b2801	fucP	>	438	Transport and binding proteins	B
	b2802	fucI	>	591	Carbon compound catabolism	B
	b2803	fucK	>	482	Carbon compound catabolism	B
	b2804	fucU	>	140	Carbon compound catabolism	B
	b2805	fucR	>	243	Carbon compound catabolism	B
o0538	b2802	fucI	>	591	Carbon compound catabolism	Hin
	b2803	fucK	>	482	Carbon compound catabolism	Hin
	b2804	fucU	>	140	Carbon compound catabolism	Hin
o0539	b2806	ygdE	<	366	"Hypothetical, unclassified, unknown"	B
	b2807	ygdD	<	131	"Hypothetical, unclassified, unknown"	B
o0540	b2810	b2810	>	401	"Hypothetical, unclassified, unknown"	B Eco Hin
	b2811	b2811	>	147	"Hypothetical, unclassified, unknown"	B Eco Hin
o0541	b2814	metZ	>		tRNA	B
	b2815	metW	>		tRNA	B
	b2816	metV	>		tRNA	B
o0542	b2819	recD	<	608	"Transcription, RNA processing and degradation"	Hin Mpn Sce
	b2820	recB	<	1180	"Transcription, RNA processing and degradation"	Hin Mpn Sce
o0542	b2819	recD	<	608	"Transcription, RNA processing and degradation"	B
	b2820	recB	<	1180	"Transcription, RNA processing and degradation"	B
	b2821	ptr	<	962	"Translation, post-translational modification"	B
o0543	b2822	recC	<	1122	"Transcription, RNA processing and degradation"	B
	b2823	ppdC	<	107	Other known genes	B
	b2824	ygdB	<	121	"Hypothetical, unclassified, unknown"	B
	b2825	ppdB	<	187	Other known genes	B
	b2826	ppdA	<	156	Other known genes	B
o0543	b2825	ppdB	<	187	Other known genes	Hin
	b2826	ppdA	<	156	Other known genes	Hin
o0544	b2827	thyA	<	264	Nucleotide biosynthesis and metabolism	B Hin
	b2828	lgt	<	291	Fatty acid and phospholipid metabolism	B Hin
o0545	b2835	ygeD	<	397	"Cell processes (incl. adaptation, protection)"	B Bsu Eco Mth Sce
	b2836	aas	<	719	Fatty acid and phospholipid metabolism	B Bsu Eco Mth Sce
o0546	b2842	kduD	<	253	Central intermediary metabolism	B Bsu
	b2843	kduI	<	278	Carbon compound catabolism	B Bsu
o0547	b2847	b2847	>	269	Putative regulatory proteins	B
	b2848	b2848	>	164	"Hypothetical, unclassified, unknown"	B
o0548	b2855	b2855	<	148	Putative regulatory proteins	B
	b2856	b2856	<	51	"Hypothetical, unclassified, unknown"	B
o0549	b2857	b2857	<	143	"Hypothetical, unclassified, unknown"	B
	b2858	b2858	<	73	"Hypothetical, unclassified, unknown"	B
	b2859	b2859	<	141	"Hypothetical, unclassified, unknown"	B
	b2860	yi22_4	<	301	"phage, transposon, or plasmid"	B
	b2861	yi21_4	<	121	"phage, transposon, or plasmid"	B
o0549	b2860	yi22_4	<	301	"phage, transposon, or plasmid"	Eco
	b2861	yi21_4	<	121	"phage, transposon, or plasmid"	Eco

o0550	b2862	b2862	<	99	"Hypothetical, unclassified, unknown"	B
	b2863	b2863	<	278	"Hypothetical, unclassified, unknown"	B
o0551	b2864	glyU	<		tRNA	B
	b2865	b2865	<	259	Cell structure	B
o0552	b2866	b2866	>	752	"Hypothetical, unclassified, unknown"	Bsu Eco
	b2867	b2867	>	292	Putative enzymes	Bsu Eco
o0552	b2866	b2866	>	752	"Hypothetical, unclassified, unknown"	B Eco
	b2867	b2867	>	292	Putative enzymes	B Eco
	b2868	b2868	>	159	Putative enzymes	B Eco
o0552	b2867	b2867	>	292	Putative enzymes	Eco
	b2868	b2868	>	159	Putative enzymes	Eco
o0553	b2872	b2872	>	403	Putative enzymes	B
	b2873	b2873	>	465	"Hypothetical, unclassified, unknown"	B
	b2874	b2874	>	310	Putative enzymes	B
o0554	b2875	b2875	<	541	Putative enzymes	B
	b2876	b2876	<	235	"Hypothetical, unclassified, unknown"	B
o0555	b2878	b2878	>	1032	Putative enzymes	B
	b2879	b2879	>	464	Structural proteins	B
o0556	b2880	b2880	>	259	"Hypothetical, unclassified, unknown"	B Bsu Eco
	b2881	b2881	>	956	Putative enzymes	B Bsu Eco
o0557	b2882	b2882	>	485	Putative transport proteins	Eco
	b2883	b2883	>	439	"Hypothetical, unclassified, unknown"	Eco
o0557	b2882	b2882	>	485	Putative transport proteins	B
	b2883	b2883	>	439	"Hypothetical, unclassified, unknown"	B
	b2884	b2884	>	189	"Hypothetical, unclassified, unknown"	B
	b2885	b2885	>	276	Putative enzymes	B
o0557	b2883	b2883	>	439	"Hypothetical, unclassified, unknown"	Eco
	b2884	b2884	>	189	"Hypothetical, unclassified, unknown"	Eco
o0557	b2884	b2884	>	189	"Hypothetical, unclassified, unknown"	Bsu Eco
	b2885	b2885	>	276	Putative enzymes	Bsu Eco
o0558	b2886	b2886	<	163	Energy metabolism	B Eco Hin Mja Mth
	b2887	b2887	<	644	Putative enzymes	B Eco Hin Mja Mth
o0559	b2890	lysS	<	505	"Translation, post-translational modification"	B
	b2891	prfB	<	365	"Translation, post-translational modification"	B
o0560	b2892	recJ	<	577	"Transcription, RNA processing and degradation"	Hin
	b2893	dsbC	<	236	Cell structure	Hin
o0560	b2892	recJ	<	577	"Transcription, RNA processing and degradation"	B
	b2893	dsbC	<	236	Cell structure	B
	b2894	xerD	<	298	"DNA replication, recombination, modification and repair"	B
o0561	b2896	b2896	<	135	"Hypothetical, unclassified, unknown"	B
	b2897	b2897	<	88	"Hypothetical, unclassified, unknown"	B
o0562	b2903	gcvP	<	957	Central intermediary metabolism	B
	b2904	gcvH	<	129	Central intermediary metabolism	B
	b2905	gcvT	<	364	Central intermediary metabolism	B
o0563	b2906	visC	<	400	"Hypothetical, unclassified, unknown"	Eco
	b2907	ubiH	<	392	"Biosynthesis of cofactors, prosthetic groups and carriers"	Eco
o0563	b2906	visC	<	400	"Hypothetical, unclassified, unknown"	B
	b2907	ubiH	<	392	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2908	pepP	<	441	"Translation, post-translational modification"	B
	b2909	ygfB	<	194	"Hypothetical, unclassified, unknown"	B

o0563	b2908	pepP	<	441	"Translation, post-translational modification"	Hin
	b2909	ygfB	<	194	"Hypothetical, unclassified, unknown"	Hin
o0564	b2917	sbm	>	714	Fatty acid and phospholipid metabolism	Bsu Mth
	b2918	ygfD	>	331	Putative transport proteins	Bsu Mth
o0564	b2917	sbm	>	714	Fatty acid and phospholipid metabolism	B
	b2918	ygfD	>	331	Putative transport proteins	B
	b2919	b2919	>	275	Putative enzymes	B
	b2920	b2920	>	492	Putative enzymes	B
o0564	b2918	ygfD	>	331	Putative transport proteins	Bsu Sce
	b2919	b2919	>	275	Putative enzymes	Bsu Sce
o0565	b2925	fba	<	359	Energy metabolism	Bsu Hin
	b2926	pgk	<	387	Energy metabolism	Bsu Hin
o0565	b2925	fba	<	359	Energy metabolism	B
	b2926	pgk	<	387	Energy metabolism	B
	b2927	epd	<	339	Central intermediary metabolism	B
o0565	b2926	pgk	<	387	Energy metabolism	Bsu Hpy Mge Mpn
	b2927	epd	<	339	Central intermediary metabolism	Bsu Hpy Mge Mpn
o0566	b2928	yggC	<	237	"Hypothetical, unclassified, unknown"	B
	b2929	yggD	<	169	Putative regulatory proteins	B
	b2930	yggF	<	321	"Hypothetical, unclassified, unknown"	B
	b2931	b2931	<	329	Putative enzymes	B
	b2932	b2932	<	118	"Hypothetical, unclassified, unknown"	B
	b2933	cmtA	<	462	Transport and binding proteins	B
	b2934	cmtB	<	147	Transport and binding proteins	B
o0566	b2930	yggF	<	321	"Hypothetical, unclassified, unknown"	Eco Mge
	b2931	b2931	<	329	Putative enzymes	Eco Mge
o0566	b2931	b2931	<	329	Putative enzymes	Eco Sce
	b2932	b2932	<	118	"Hypothetical, unclassified, unknown"	Eco Sce
o0566	b2933	cmtA	<	462	Transport and binding proteins	Eco
	b2934	cmtB	<	147	Transport and binding proteins	Eco
o0567	b2946	yggJ	>	252	"Hypothetical, unclassified, unknown"	B
	b2947	gshB	>	316	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b2948	b2948	>	211	"Hypothetical, unclassified, unknown"	B
	b2949	b2949	>	138	"Hypothetical, unclassified, unknown"	B
o0567	b2948	b2948	>	211	"Hypothetical, unclassified, unknown"	Hin
	b2949	b2949	>	138	"Hypothetical, unclassified, unknown"	Hin
o0568	b2951	b2951	>	234	"Hypothetical, unclassified, unknown"	B
	b2952	b2952	>	188	Putative transport proteins	B
	b2953	b2953	>	100	"Hypothetical, unclassified, unknown"	B
	b2954	b2954	>	197	Structural proteins	B
	b2955	b2955	>	378	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0569	b2959	yggL	<	118	"Hypothetical, unclassified, unknown"	B Hin
	b2960	yggH	<	239	"Hypothetical, unclassified, unknown"	B Hin
o0570	b2961	mutY	>	350	"DNA replication, recombination, modification and repair"	B
	b2962	b2962	>	91	"Hypothetical, unclassified, unknown"	B
o0571	b2968	b2968	<	178	Transport and binding proteins	B
	b2969	b2969	<	286	"Hypothetical, unclassified, unknown"	B
o0572	b2973	b2973	<	848	"Hypothetical, unclassified, unknown"	B
	b2974	b2974	<	675	Putative enzymes	B

o0573	b2976	glcB	<	723	Central intermediary metabolism	B
	b2977	glcG	<	134	Carbon compound catabolism	B
	b2978	b2978	<	761	Putative enzymes	B
	b2979	glcD	<	499	Carbon compound catabolism	B
o0573	b2978	b2978	<	761	Putative enzymes	Bsu Eco Mth
	b2979	glcD	<	499	Carbon compound catabolism	Bsu Eco Mth
o0574	b2984	b2984	<	252	"Hypothetical, unclassified, unknown"	B Eco
	b2985	b2985	<	237	"Hypothetical, unclassified, unknown"	B Eco
o0575	b2990	hybG	<	82	Energy metabolism	B
	b2991	hybF	<	113	Energy metabolism	B
	b2992	hybE	<	162	Energy metabolism	B
	b2993	hybD	<	164	Energy metabolism	B
	b2994	hybC	<	567	Energy metabolism	B
	b2995	hybB	<	392	Energy metabolism	B
	b2996	hybA	<	328	Energy metabolism	B
o0575	b2993	hybD	<	164	Energy metabolism	Mja Mth
	b2994	hybC	<	567	Energy metabolism	Mja Mth
o0575	b2995	hybB	<	392	Energy metabolism	Hin Mth
	b2996	hybA	<	328	Energy metabolism	Hin Mth
o0576	b2999	b2999	<	136	"Hypothetical, unclassified, unknown"	B
	b3000	b3000	<	141	"Hypothetical, unclassified, unknown"	B
o0577	b3005	exbD	<	141	Transport and binding proteins	B Eco Hin Hpy Syn
	b3006	exbB	<	244	Transport and binding proteins	B Eco Hin Hpy Syn
o0578	b3015	b3015	<	413	"Hypothetical, unclassified, unknown"	B
	b3016	b3016	<	325	"Hypothetical, unclassified, unknown"	B
o0579	b3021	b3021	<	131	"Hypothetical, unclassified, unknown"	B
	b3022	b3022	<	98	"Hypothetical, unclassified, unknown"	B
o0580	b3025	b3025	>	219	Putative regulatory proteins	B Bsu Eco Hin Hpy Mth Syn
	b3026	b3026	>	449	Putative regulatory proteins	B Bsu Eco Hin Hpy Mth Syn
o0581	b3028	mdaB	>	193	Other known genes	B
	b3029	ygiN	>	104	"Hypothetical, unclassified, unknown"	B
o0582	b3030	parE	<	630	"DNA replication, recombination, modification and repair"	B
	b3031	yqiA	<	193	"Hypothetical, unclassified, unknown"	B
	b3032	icc	<	275	Carbon compound catabolism	B
	b3033	yqiB	<	140	Putative enzymes	B
	b3034	b3034	<	209	"Hypothetical, unclassified, unknown"	B
o0583	b3035	tolC	>	495	"Cell processes (incl. adaptation, protection)"	B
	b3036	ygiA	>	86	"Hypothetical, unclassified, unknown"	B
	b3037	ygiB	>	234	"Hypothetical, unclassified, unknown"	B
	b3038	ygiC	>	386	Putative enzymes	B
o0583	b3037	ygiB	>	234	"Hypothetical, unclassified, unknown"	Eco Hin Syn
	b3038	ygiC	>	386	Putative enzymes	Eco Hin Syn
o0584	b3044	yi21_5	>	121	"phage, transposon, or plasmid"	Eco
	b3045	yi22_5	>	301	"phage, transposon, or plasmid"	Eco
o0584	b3044	yi21_5	>	121	"phage, transposon, or plasmid"	B
	b3045	yi22_5	>	301	"phage, transposon, or plasmid"	B
	b3046	b3046	>	821	Cell structure	B
	b3047	b3047	>	252	Cell structure	B
	b3048	b3048	>	354	"Hypothetical, unclassified, unknown"	B
o0584	b3046	b3046	>	821	Cell structure	Eco Mpn
	b3047	b3047	>	252	Cell structure	Eco Mpn

o0584	b3046	b3046	>	821	Cell structure	Eco
	b3047	b3047	>	252	Cell structure	Eco
	b3048	b3048	>	354	"Hypothetical, unclassified, unknown"	Eco
o0584	b3047	b3047	>	252	Cell structure	Sce
	b3048	b3048	>	354	"Hypothetical, unclassified, unknown"	Sce
o0585	b3050	b3050	>	209	Putative enzymes	B Mge
	b3051	b3051	>	553	Structural proteins	B Mge
o0586	b3052	b3052	<	477	Putative enzymes	B
	b3053	glnE	<	946	"Translation, post-translational modification"	B
	b3054	ygiF	<	433	"Hypothetical, unclassified, unknown"	B
o0586	b3053	glnE	<	946	"Translation, post-translational modification"	Eco Syn
	b3054	ygiF	<	433	"Hypothetical, unclassified, unknown"	Eco Syn
o0587	b3061	ttdA	>	303	Energy metabolism	B
	b3062	ttdB	>	201	Energy metabolism	B
o0588	b3065	rpsU	>	71	"Translation, post-translational modification"	B
	b3066	dnaG	>	581	"DNA replication, recombination, modification and repair"	B
	b3067	rpoD	>	613	"Transcription, RNA processing and degradation"	B
o0588	b3066	dnaG	>	581	"DNA replication, recombination, modification and repair"	Bsu Mge Mpn Sce
	b3067	rpoD	>	613	"Transcription, RNA processing and degradation"	Bsu Mge Mpn Sce
o0589	b3076	ebgA	>	1042	Carbon compound catabolism	B
	b3077	ebgC	>	149	Carbon compound catabolism	B
o0590	b3079	ygjJ	>	356	"Hypothetical, unclassified, unknown"	B
	b3080	ygjK	>	783	"Hypothetical, unclassified, unknown"	B
o0591	b3082	ygjM	<	138	"Hypothetical, unclassified, unknown"	B
	b3083	ygjN	<	104	"Hypothetical, unclassified, unknown"	B
o0592	b3091	uxaA	<	495	Carbon compound catabolism	B
	b3092	uxaC	<	470	Carbon compound catabolism	B
o0593	b3095	b3095	>	220	"Hypothetical, unclassified, unknown"	B
	b3096	yqjB	>	127	"Hypothetical, unclassified, unknown"	B
o0594	b3097	yqjC	>	127	"Hypothetical, unclassified, unknown"	B
	b3098	yqjD	>	101	"Hypothetical, unclassified, unknown"	B
	b3099	yqjE	>	134	"Hypothetical, unclassified, unknown"	B
	b3100	b3100	>	99	"Hypothetical, unclassified, unknown"	B
o0595	b3106	yhaK	>	233	"Hypothetical, unclassified, unknown"	B
	b3107	yhaL	>	56	"Hypothetical, unclassified, unknown"	B
o0596	b3109	yhaN	<	187	"Hypothetical, unclassified, unknown"	B
	b3110	yhaO	<	425	Putative regulatory proteins	B
o0597	b3111	yhaP	<	275	"Hypothetical, unclassified, unknown"	B Bsu
	b3112	yhaQ	<	140	"Hypothetical, unclassified, unknown"	B Bsu
o0598	b3113	yhaR	<	150	"Hypothetical, unclassified, unknown"	B
	b3114	yhaS	<	746	"Hypothetical, unclassified, unknown"	B
	b3115	yhaA	<	406	Energy metabolism	B
o0599	b3116	tdcC	<	443	Transport and binding proteins	B
	b3117	tdcB	<	329	Amino acid biosynthesis and metabolism	B
	b3118	tdcA	<	312	Amino acid biosynthesis and metabolism	B
o0599	b3117	tdcB	<	329	Amino acid biosynthesis and metabolism	Eco
	b3118	tdcA	<	312	Amino acid biosynthesis and metabolism	Eco
o0600	b3120	yhaB	>	186	"Hypothetical, unclassified, unknown"	B
	b3121	yhaC	>	395	"Hypothetical, unclassified, unknown"	B
o0601	b3124	yhaD	<	408	"Hypothetical, unclassified, unknown"	Bsu
	b3125	yhaE	<	299	Putative enzymes	Bsu

o0601	b3124	yhaD	<	408	"Hypothetical, unclassified, unknown"	B
	b3125	yhaE	<	299	Putative enzymes	B
	b3126	yhaF	<	256	"Hypothetical, unclassified, unknown"	B
	b3127	yhaU	<	444	Carbon compound catabolism	B
o0601	b3126	yhaF	<	256	"Hypothetical, unclassified, unknown"	Eco
	b3127	yhaU	<	444	Carbon compound catabolism	Eco
o0602	b3129	sohA	>	111	"Translation, post-translational modification"	B Syn
	b3130	yhaV	>	154	"Hypothetical, unclassified, unknown"	B Syn
o0603	b3132	agaZ	>	426	Carbon compound catabolism	B
	b3133	agaV	>	169	Central intermediary metabolism	B
	b3134	agaW	>	133	Central intermediary metabolism	B
	b3135	agaA	>	167	Central intermediary metabolism	B
	b3136	agaS	>	384	Central intermediary metabolism	B
	b3137	agaY	>	286	Central intermediary metabolism	B
o0603	b3133	agaV	>	169	Central intermediary metabolism	Bsu Eco
	b3134	agaW	>	133	Central intermediary metabolism	Bsu Eco
o0604	b3138	agaB	>	158	Central intermediary metabolism	Eco
	b3139	agaC	>	267	Central intermediary metabolism	Eco
o0604	b3138	agaB	>	158	Central intermediary metabolism	Bsu Eco
	b3139	agaC	>	267	Central intermediary metabolism	Bsu Eco
	b3140	agaD	>	263	Central intermediary metabolism	Bsu Eco
o0604	b3138	agaB	>	158	Central intermediary metabolism	B
	b3139	agaC	>	267	Central intermediary metabolism	B
	b3140	agaD	>	263	Central intermediary metabolism	B
	b3141	agaI	>	251	Central intermediary metabolism	B
o0604	b3139	agaC	>	267	Central intermediary metabolism	Eco
	b3140	agaD	>	263	Central intermediary metabolism	Eco
o0605	b3143	yraI	>	231	Putative chaperones	Eco
	b3144	yraJ	>	838	Cell structure	Eco
o0605	b3143	yraI	>	231	Putative chaperones	B Eco
	b3144	yraJ	>	838	Cell structure	B Eco
	b3145	yraK	>	363	Cell structure	B Eco
o0606	b3147	yraM	>	678	Energy metabolism	B
	b3148	yraN	>	131	"Hypothetical, unclassified, unknown"	B
	b3149	yraO	>	196	"Hypothetical, unclassified, unknown"	B
	b3150	yraP	>	191	"Cell processes (incl. adaptation, protection)"	B

operon#	b#	gene	dir	length	function	species
o0607	b3156	b3156	<	167	"Hypothetical, unclassified, unknown"	B
	b3157	yhbT	<	174	"Hypothetical, unclassified, unknown"	B
o0608	b3158	yhbU	>	331	"Translation, post-translational modification"	B Bsu
	b3159	yhbV	>	298	"Hypothetical, unclassified, unknown"	B Bsu
o0609	b3164	pnp	<	734	"Transcription, RNA processing and degradation"	B Bsu
	b3165	rpsO	<	89	"Translation, post-translational modification"	B Bsu
o0610	b3166	truB	<	314	"Translation, post-translational modification"	B Bsu Hin
	b3167	rbfA	<	133	"Translation, post-translational modification"	B Bsu Hin
o0611	b3168	infB	<	890	"Translation, post-translational modification"	B Bsu Mpn Mth
	b3169	nusA	<	495	"Transcription, RNA processing and degradation"	B Bsu Mpn Mth
o0612	b3176	mrsA	<	445	Central intermediary metabolism	B
	b3177	folP	<	297	"Biosynthesis of cofactors, prosthetic groups and carriers"	B

o0613	b3178	hflB	<	644	"Cell processes (incl. adaptation, protection)"	B
	b3179	ftsJ	<	209	"Cell processes (incl. adaptation, protection)"	B
o0614	b3183	yhbZ	<	390	Other known genes	B
	b3184	yhbE	<	321	"Hypothetical, unclassified, unknown"	B
o0615	b3185	rpmA	<	85	"Translation, post-translational modification"	B Hpy Syn
	b3186	rplU	<	103	"Translation, post-translational modification"	B Hpy Syn
o0616	b3191	yrbB	<	129	"Hypothetical, unclassified, unknown"	B
	b3192	yrbC	<	211	"Hypothetical, unclassified, unknown"	B
	b3193	b3193	<	183	"Hypothetical, unclassified, unknown"	B
	b3194	yrbE	<	260	"Hypothetical, unclassified, unknown"	B
	b3195	b3195	<	269	Putative transport proteins	B
o0616	b3194	yrbE	<	260	"Hypothetical, unclassified, unknown"	Bsu Eco Hpy Mja Mth Syn
	b3195	b3195	<	269	Putative transport proteins	Bsu Eco Hpy Mja Mth Syn
o0617	b3196	yrbG	>	325	"Hypothetical, unclassified, unknown"	B
	b3197	yrbH	>	328	Putative enzymes	B
	b3198	yrbI	>	188	"Hypothetical, unclassified, unknown"	B
	b3199	yrbK	>	191	"Hypothetical, unclassified, unknown"	B
	b3200	yhbN	>	185	"Hypothetical, unclassified, unknown"	B
	b3201	yhbG	>	241	Putative transport proteins	B
	b3202	rpoN	>	477	Regulatory function	B
	b3203	yhbH	>	95	"Hypothetical, unclassified, unknown"	B
o0617	b3197	yrbH	>	328	Putative enzymes	Hin
	b3198	yrbI	>	188	"Hypothetical, unclassified, unknown"	Hin
o0617	b3199	yrbK	>	191	"Hypothetical, unclassified, unknown"	Hin
	b3200	yhbN	>	185	"Hypothetical, unclassified, unknown"	Hin
	b3201	yhbG	>	241	Putative transport proteins	Hin
o0617	b3200	yhbN	>	185	"Hypothetical, unclassified, unknown"	Syn
	b3201	yhbG	>	241	Putative transport proteins	Syn
o0617	b3201	yhbG	>	241	Putative transport proteins	Hpy Sce
	b3202	rpoN	>	477	Regulatory function	Hpy Sce
o0618	b3204	ptsN	>	163	Transport and binding proteins	Hin
	b3205	b3205	>	284	"Hypothetical, unclassified, unknown"	Hin
o0618	b3204	ptsN	>	163	Transport and binding proteins	B
	b3205	b3205	>	284	"Hypothetical, unclassified, unknown"	B
	b3206	ptsO	>	90	Transport and binding proteins	B
o0619	b3208	yrbM	<	242	Cell structure	B
	b3209	yhbL	<	220	"Hypothetical, unclassified, unknown"	B
o0620	b3212	gltB	>	1517	Central intermediary metabolism	Bsu
	b3213	gltD	>	472	Central intermediary metabolism	Bsu
o0620	b3212	gltB	>	1517	Central intermediary metabolism	B
	b3213	gltD	>	472	Central intermediary metabolism	B
	b3214	gltF	>	254	Central intermediary metabolism	B
o0620	b3213	gltD	>	472	Central intermediary metabolism	Bsu
	b3214	gltF	>	254	Central intermediary metabolism	Bsu
o0621	b3215	yhcA	>	224	Putative chaperones	Eco Sce
	b3216	yhcD	>	793	"Hypothetical, unclassified, unknown"	Eco Sce
o0621	b3215	yhcA	>	224	Putative chaperones	B
	b3216	yhcD	>	793	"Hypothetical, unclassified, unknown"	B
	b3217	yhcE	>	159	"Hypothetical, unclassified, unknown"	B

o0622	b3221	b3221	<	154	"Hypothetical, unclassified, unknown"	B
	b3222	yhcI	<	302	Putative enzymes	B
	b3223	b3223	<	229	Putative enzymes	B
	b3224	nanT	<	506	Cell structure	B
o0622	b3222	yhcI	<	302	Putative enzymes	Hin
	b3223	b3223	<	229	Putative enzymes	Hin
o0622	b3223	b3223	<	229	Putative enzymes	Eco Mth
	b3224	nanT	<	506	Cell structure	Eco Mth
o0623	b3228	sspB	<	165	Regulatory function	B
	b3229	sspA	<	212	Regulatory function	B
o0624	b3230	rpsI	<	130	"Translation, post-translational modification"	B Bsu Hpy Mge Mja Mpn Syn
	b3231	rplM	<	142	"Translation, post-translational modification"	B Bsu Hpy Mge Mja Mpn Syn
o0625	b3234	hhoA	>	455	"Translation, post-translational modification"	B Eco
	b3235	hhoB	>	355	"Translation, post-translational modification"	B Eco
o0626	b3240	yhcP	<	655	"Hypothetical, unclassified, unknown"	B Eco
	b3241	yhcQ	<	310	Putative enzymes	B Eco
	b3242	b3242	<	90	"Hypothetical, unclassified, unknown"	B Eco
o0627	b3245	b3245	<	986	"Hypothetical, unclassified, unknown"	B
	b3246	yhdR	<	282	"Hypothetical, unclassified, unknown"	B
o0628	b3247	cafA	<	495	"Cell processes (incl. adaptation, protection)"	B
	b3248	yhdE	<	197	"Hypothetical, unclassified, unknown"	B
o0629	b3249	mreD	<	162	Cell structure	B Bsu Hin
	b3250	mreC	<	367	Cell structure	B Bsu Hin
	b3251	mreB	<	367	Cell structure	B Bsu Hin
o0629	b3250	mreC	<	367	Cell structure	Hpy
	b3251	mreB	<	367	Cell structure	Hpy
o0630	b3255	accB	>	156	Fatty acid and phospholipid metabolism	B Bsu Hin Hpy
	b3256	accC	>	449	Fatty acid and phospholipid metabolism	B Bsu Hin Hpy
o0631	b3258	panF	>	485	Transport and binding proteins	B Hin
	b3259	prmA	>	293	"Translation, post-translational modification"	B Hin
o0632	b3265	acrE	>	385	Cell structure	B Eco Syn
	b3266	acrF	>	1034	"Cell processes (incl. adaptation, protection)"	B Eco Syn
o0633	b3268	yhdW	>	305	Putative transport proteins	B Bsu Eco Hin Hpy
	b3269	yhdX	>	368	Putative transport proteins	B Bsu Eco Hin Hpy
o0634	b3270	yhdY	>	368	Putative transport proteins	B Bsu Eco Hin Hpy Mja Mpn Syn
	b3271	yhdZ	>	252	Putative transport proteins	B Bsu Eco Hin Hpy Mja Mpn Syn
o0635	b3275	rrlD	<		rRNA	B
	b3276	alaU	<		tRNA	B
	b3277	ileU	<		tRNA	B
	b3278	rrsD	<		rRNA	B
o0636	b3280	yrdB	<	85	"Hypothetical, unclassified, unknown"	B
	b3281	aroE	<	272	Amino acid biosynthesis and metabolism	B
	b3282	yrdC	<	190	"Hypothetical, unclassified, unknown"	B
	b3283	yrdD	<	169	"DNA replication, recombination, modification and repair"	B
o0636	b3281	aroE	<	272	Amino acid biosynthesis and metabolism	Hin
	b3282	yrdC	<	190	"Hypothetical, unclassified, unknown"	Hin
	b3283	yrdD	<	169	"DNA replication, recombination, modification and repair"	Hin
o0637	b3284	smg	<	157	"Hypothetical, unclassified, unknown"	B
	b3285	smf	<	102	"Hypothetical, unclassified, unknown"	B
o0638	b3287	def	>	169	"Translation, post-translational modification"	B
	b3288	fmt	>	315	"Translation, post-translational modification"	B

o0639	b3289	fmu	>	429	"Hypothetical, unclassified, unknown"	B Eco
	b3290	trkA	>	458	Transport and binding proteins	B Eco
o0640	b3292	yhdM	<	141	Putative regulatory proteins	B
	b3293	yhdN	<	122	"Hypothetical, unclassified, unknown"	B
o0641	b3294	rplQ	<	127	"Translation, post-translational modification"	Bsu Mge Mpn Syn
	b3295	rpoA	<	329	"Transcription, RNA processing and degradation"	Bsu Mge Mpn Syn
o0641	b3294	rplQ	<	127	"Translation, post-translational modification"	B
	b3295	rpoA	<	329	"Transcription, RNA processing and degradation"	B
	b3296	rpsD	<	206	"Translation, post-translational modification"	B
	b3297	rpsK	<	129	"Translation, post-translational modification"	B
	b3298	rpsM	<	118	"Translation, post-translational modification"	B
o0641	b3295	rpoA	<	329	"Transcription, RNA processing and degradation"	Hin
	b3296	rpsD	<	206	"Translation, post-translational modification"	Hin
o0641	b3296	rpsD	<	206	"Translation, post-translational modification"	Mja Mth
	b3297	rpsK	<	129	"Translation, post-translational modification"	Mja Mth
o0642	b3299	rpmJ	<	38	"Translation, post-translational modification"	B
	b3300	prlA	<	443	Putative transport proteins	B
	b3301	rplO	<	144	"Translation, post-translational modification"	B
	b3302	rpmD	<	59	"Translation, post-translational modification"	B
	b3303	rpsE	<	167	"Translation, post-translational modification"	B
	b3304	rplR	<	117	"Translation, post-translational modification"	B
	b3305	rplF	<	177	"Translation, post-translational modification"	B
	b3306	rpsH	<	130	"Translation, post-translational modification"	B
	b3307	rpsN	<	101	"Translation, post-translational modification"	B
	b3308	rplE	<	179	"Translation, post-translational modification"	B
	b3309	rplX	<	104	"Translation, post-translational modification"	B
	b3310	rplN	<	123	"Translation, post-translational modification"	B
o0642	b3300	prlA	<	443	Putative transport proteins	Hpy Mge Mja Mpn Mth Syn
	b3301	rplO	<	144	"Translation, post-translational modification"	Hpy Mge Mja Mpn Mth Syn
o0642	b3303	rpsE	<	167	"Translation, post-translational modification"	Mja Mth
	b3304	rplR	<	117	"Translation, post-translational modification"	Mja Mth
o0642	b3303	rpsE	<	167	"Translation, post-translational modification"	Syn
	b3304	rplR	<	117	"Translation, post-translational modification"	Syn
	b3305	rplF	<	177	"Translation, post-translational modification"	Syn
	b3306	rpsH	<	130	"Translation, post-translational modification"	Syn
o0642	b3305	rplF	<	177	"Translation, post-translational modification"	Mja Mth
	b3306	rpsH	<	130	"Translation, post-translational modification"	Mja Mth
o0643	b3311	rpsQ	<	84	"Translation, post-translational modification"	B Hin
	b3312	rpmC	<	63	"Translation, post-translational modification"	B Hin
	b3313	rplP	<	136	"Translation, post-translational modification"	B Hin
	b3314	rpsC	<	233	"Translation, post-translational modification"	B Hin
	b3315	rplV	<	110	"Translation, post-translational modification"	B Hin
	b3316	rpsS	<	92	"Translation, post-translational modification"	B Hin
	b3317	rplB	<	273	"Translation, post-translational modification"	B Hin
	b3318	rplW	<	100	"Translation, post-translational modification"	B Hin
	b3319	rplD	<	201	"Translation, post-translational modification"	B Hin
	b3320	rplC	<	209	"Translation, post-translational modification"	B Hin
	b3321	rpsJ	<	103	"Translation, post-translational modification"	B Hin
o0643	b3314	rpsC	<	233	"Translation, post-translational modification"	Mja Sce
	b3315	rplV	<	110	"Translation, post-translational modification"	Mja Sce

o0643	b3314	rpsC	<	233	"Translation, post-translational modification"	Mth
	b3315	rplV	<	110	"Translation, post-translational modification"	Mth
	b3316	rpsS	<	92	"Translation, post-translational modification"	Mth
	b3317	rplB	<	273	"Translation, post-translational modification"	Mth
	b3318	rplW	<	100	"Translation, post-translational modification"	Mth
o0643	b3316	rpsS	<	92	"Translation, post-translational modification"	Mja
	b3317	rplB	<	273	"Translation, post-translational modification"	Mja
	b3318	rplW	<	100	"Translation, post-translational modification"	Mja
	b3319	rplD	<	201	"Translation, post-translational modification"	Mja
	b3320	rplC	<	209	"Translation, post-translational modification"	Mja
o0643	b3319	rplD	<	201	"Translation, post-translational modification"	Mpn
	b3320	rplC	<	209	"Translation, post-translational modification"	Mpn
	b3321	rpsJ	<	103	"Translation, post-translational modification"	Mpn
o0643	b3320	rplC	<	209	"Translation, post-translational modification"	Syn
	b3321	rpsJ	<	103	"Translation, post-translational modification"	Syn
o0644	b3322	pinO	<	139	"DNA replication, recombination, modification and repair"	B
	b3323	yheD	<	489	"Hypothetical, unclassified, unknown"	B
o0645	b3324	yheE	>	271	"Hypothetical, unclassified, unknown"	B
	b3325	yheF	>	654	"Hypothetical, unclassified, unknown"	B
	b3326	yheG	>	493	"Hypothetical, unclassified, unknown"	B
	b3327	hofF	>	398	Transport and binding proteins	B
	b3328	hofG	>	145	Transport and binding proteins	B
	b3329	hofH	>	169	Transport and binding proteins	B
	b3330	yheH	>	138	"Hypothetical, unclassified, unknown"	B
	b3331	yheI	>	195	"Hypothetical, unclassified, unknown"	B
	b3332	yheJ	>	327	"Hypothetical, unclassified, unknown"	B
	b3333	yheK	>	388	"Hypothetical, unclassified, unknown"	B
	b3334	pshM	>	161	Transport and binding proteins	B
	b3335	hofD	>	225	"Translation, post-translational modification"	B
o0645	b3325	yheF	>	654	"Hypothetical, unclassified, unknown"	Hin Hpy Mth Syn
	b3326	yheG	>	493	"Hypothetical, unclassified, unknown"	Hin Hpy Mth Syn
o0645	b3326	yheG	>	493	"Hypothetical, unclassified, unknown"	Eco Hin Mth Syn
	b3327	hofF	>	398	Transport and binding proteins	Eco Hin Mth Syn
o0645	b3326	yheG	>	493	"Hypothetical, unclassified, unknown"	Bsu
	b3327	hofF	>	398	Transport and binding proteins	Bsu
	b3328	hofG	>	145	Transport and binding proteins	Bsu
	b3329	hofH	>	169	Transport and binding proteins	Bsu
o0645	b3328	hofG	>	145	Transport and binding proteins	Eco Syn
	b3329	hofH	>	169	Transport and binding proteins	Eco Syn
o0645	b3328	hofG	>	145	Transport and binding proteins	Eco
	b3329	hofH	>	169	Transport and binding proteins	Eco
	b3330	yheH	>	138	"Hypothetical, unclassified, unknown"	Eco
o0645	b3328	hofG	>	145	Transport and binding proteins	Eco
	b3329	hofH	>	169	Transport and binding proteins	Eco
	b3330	yheH	>	138	"Hypothetical, unclassified, unknown"	Eco
	b3331	yheI	>	195	"Hypothetical, unclassified, unknown"	Eco
o0645	b3329	hofH	>	169	Transport and binding proteins	Eco
	b3330	yheH	>	138	"Hypothetical, unclassified, unknown"	Eco
	b3331	yheI	>	195	"Hypothetical, unclassified, unknown"	Eco
o0645	b3330	yheH	>	138	"Hypothetical, unclassified, unknown"	Eco
	b3331	yheI	>	195	"Hypothetical, unclassified, unknown"	Eco

o0646	b3339	tufA	<	394	"Translation, post-translational modification"	Bsu Eco Hin Mge Mja Mth Syn
	b3340	fusA	<	704	"Translation, post-translational modification"	Bsu Eco Hin Mge Mja Mth Syn
o0646	b3339	tufA	<	394	"Translation, post-translational modification"	B Bsu Hin Mth Syn
	b3340	fusA	<	704	"Translation, post-translational modification"	B Bsu Hin Mth Syn
	b3341	rpsG	<	179	"Translation, post-translational modification"	B Bsu Hin Mth Syn
	b3342	rpsL	<	124	"Translation, post-translational modification"	B Bsu Hin Mth Syn
o0646	b3340	fusA	<	704	"Translation, post-translational modification"	Hpy Mge Mja Mpn
	b3341	rpsG	<	179	"Translation, post-translational modification"	Hpy Mge Mja Mpn
	b3342	rpsL	<	124	"Translation, post-translational modification"	Hpy Mge Mja Mpn
o0647	b3343	yheL	<	95	"Hypothetical, unclassified, unknown"	B
	b3344	b3344	<	119	"Hypothetical, unclassified, unknown"	B
	b3345	yheN	<	128	"Hypothetical, unclassified, unknown"	B
	b3346	b3346	<	244	"Hypothetical, unclassified, unknown"	B
o0647	b3344	b3344	<	119	"Hypothetical, unclassified, unknown"	Mth
	b3345	yheN	<	128	"Hypothetical, unclassified, unknown"	Mth
o0648	b3350	kefB	<	601	Transport and binding proteins	B Eco
	b3351	yheR	<	184	"Hypothetical, unclassified, unknown"	B Eco
o0649	b3352	yheS	>	637	"Hypothetical, unclassified, unknown"	Sce Syn
	b3353	yheT	>	340	"Hypothetical, unclassified, unknown"	Sce Syn
o0649	b3352	yheS	>	637	"Hypothetical, unclassified, unknown"	B
	b3353	yheT	>	340	"Hypothetical, unclassified, unknown"	B
	b3354	yheU	>	72	"Hypothetical, unclassified, unknown"	B
o0650	b3360	pabA	<	187	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3361	fic	<	200	"Cell processes (incl. adaptation, protection)"	B
	b3362	yhfG	<	55	"Hypothetical, unclassified, unknown"	B
o0651	b3365	nirB	>	847	Energy metabolism	Bsu
	b3366	nirD	>	108	Energy metabolism	Bsu
o0651	b3365	nirB	>	847	Energy metabolism	B
	b3366	nirD	>	108	Energy metabolism	B
	b3367	nirC	>	184	Energy metabolism	B
	b3368	cysG	>	457	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0652	b3370	yhfM	>	462	Putative transport proteins	Eco Mja Mth
	b3371	yhfN	>	347	Putative transport proteins	Eco Mja Mth
o0652	b3370	yhfM	>	462	Putative transport proteins	B
	b3371	yhfN	>	347	Putative transport proteins	B
	b3372	yhfO	>	149	"Hypothetical, unclassified, unknown"	B
o0653	b3373	yhfP	>	134	"Hypothetical, unclassified, unknown"	B
	b3374	yhfQ	>	261	Putative enzymes	B
	b3375	yhfR	>	265	Putative regulatory proteins	B
o0653	b3374	yhfQ	>	261	Putative enzymes	Bsu Eco
	b3375	yhfR	>	265	Putative regulatory proteins	Bsu Eco
o0654	b3376	yhfS	<	361	"Hypothetical, unclassified, unknown"	Bsu Eco
	b3377	yhfT	<	434	"Hypothetical, unclassified, unknown"	Bsu Eco
o0654	b3376	yhfS	<	361	"Hypothetical, unclassified, unknown"	B
	b3377	yhfT	<	434	"Hypothetical, unclassified, unknown"	B
	b3378	yhfU	<	130	"Hypothetical, unclassified, unknown"	B
	b3379	yhfV	<	292	Putative enzymes	B
	b3380	yhfW	<	408	Putative enzymes	B
	b3381	yhfX	<	387	"Hypothetical, unclassified, unknown"	B
o0654	b3380	yhfW	<	408	Putative enzymes	Hin
	b3381	yhfX	<	387	"Hypothetical, unclassified, unknown"	Hin

o0655	b3382	yhfY	<	134	"Hypothetical, unclassified, unknown"	B
	b3383	yhfZ	<	228	"Hypothetical, unclassified, unknown"	B
o0656	b3384	trpS	<	334	"Translation, post-translational modification"	B
	b3385	gph	<	252	Carbon compound catabolism	B
	b3386	rpe	<	225	Energy metabolism	B
	b3387	dam	<	278	"DNA replication, recombination, modification and repair"	B
	b3388	damX	<	428	Central intermediary metabolism	B
	b3389	aroB	<	362	Amino acid biosynthesis and metabolism	B
	b3390	aroK	<	240	Amino acid biosynthesis and metabolism	B
o0656	b3385	gph	<	252	Carbon compound catabolism	Eco Hin
	b3386	rpe	<	225	Energy metabolism	Eco Hin
o0656	b3387	dam	<	278	"DNA replication, recombination, modification and repair"	Sce
	b3388	damX	<	428	Central intermediary metabolism	Sce
o0656	b3388	damX	<	428	Central intermediary metabolism	Eco
	b3389	aroB	<	362	Amino acid biosynthesis and metabolism	Eco
o0656	b3389	aroB	<	362	Amino acid biosynthesis and metabolism	Hin Syn
	b3390	aroK	<	240	Amino acid biosynthesis and metabolism	Hin Syn
o0657	b3391	hofQ	<	412	Transport and binding proteins	B
	b3392	yrfA	<	147	"Hypothetical, unclassified, unknown"	B
	b3393	yrfB	<	146	"Hypothetical, unclassified, unknown"	B
	b3394	yrfC	<	179	"Hypothetical, unclassified, unknown"	B
	b3395	yrfD	<	268	"Hypothetical, unclassified, unknown"	B
o0658	b3398	yrfF	>	711	Putative enzymes	B
	b3399	yrfG	>	237	Putative enzymes	B
	b3400	yrfH	>	133	"Hypothetical, unclassified, unknown"	B
	b3401	yrfI	>	294	"Hypothetical, unclassified, unknown"	B
o0659	b3404	envZ	<	450	Regulatory function	B Bsu Eco Hin Mth Syn
	b3405	ompR	<	239	Regulatory function	B Bsu Eco Hin Mth Syn
o0660	b3408	feoA	>	75	Transport and binding proteins	B Mth
	b3409	feoB	>	773	Transport and binding proteins	B Mth

operon#	b#	gene	dir	length	function	species
o0661	b3416	malQ	<	694	Carbon compound catabolism	B Mge
	b3417	malP	<	797	Carbon compound catabolism	B Mge
o0662	b3419	yhgJ	<	201	"Hypothetical, unclassified, unknown"	B
	b3420	yhgK	<	146	"Hypothetical, unclassified, unknown"	B
	b3421	yhgL	<	408	"Hypothetical, unclassified, unknown"	B
o0663	b3423	glpR	<	252	Energy metabolism	Bsu Hin
	b3424	glpG	<	276	Energy metabolism	Bsu Hin
o0663	b3423	glpR	<	252	Energy metabolism	B
	b3424	glpG	<	276	Energy metabolism	B
	b3425	glpE	<	108	Energy metabolism	B
o0664	b3428	glgP	<	815	Cell structure	Bsu
	b3429	glgA	<	477	Cell structure	Bsu
	b3430	glgC	<	431	Cell structure	Bsu
o0664	b3428	glgP	<	815	Cell structure	B Hin
	b3429	glgA	<	477	Cell structure	B Hin
	b3430	glgC	<	431	Cell structure	B Hin
	b3431	glgX	<	657	Cell structure	B Hin
	b3432	glgB	<	728	Cell structure	B Hin

o0664	b3430	glgC	<	431	Cell structure	Bsu
	b3431	glgX	<	657	Cell structure	Bsu
o0664	b3431	glgX	<	657	Cell structure	Eco Hin Syn
	b3432	glgB	<	728	Cell structure	Eco Hin Syn
o0665	b3435	gntU_2	<	111	Transport and binding proteins	Hin
	b3436	gntU_1	<	332	Transport and binding proteins	Hin
o0665	b3435	gntU_2	<	111	Transport and binding proteins	B
	b3436	gntU_1	<	332	Transport and binding proteins	B
	b3437	gntK	<	162	Central intermediary metabolism	B
o0666	b3442	yhhZ	>	392	"Hypothetical, unclassified, unknown"	B
	b3443	b3443	>	138	"Hypothetical, unclassified, unknown"	B
	b3444	insA_6	>	91	"phage, transposon, or plasmid"	B
	b3445	insB_6	>	167	"phage, transposon, or plasmid"	B
o0666	b3444	insA_6	>	91	"phage, transposon, or plasmid"	Eco Syn
	b3445	insB_6	>	167	"phage, transposon, or plasmid"	Eco Syn
o0667	b3449	ugpQ	<	247	Central intermediary metabolism	B
	b3450	ugpC	<	369	Transport and binding proteins	B
	b3451	ugpE	<	281	Transport and binding proteins	B
	b3452	ugpA	<	295	Transport and binding proteins	B
	b3453	ugpB	<	438	Transport and binding proteins	B
o0667	b3450	ugpC	<	369	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Syn
	b3451	ugpE	<	281	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Syn
o0667	b3450	ugpC	<	369	Transport and binding proteins	Eco Hin Mge Mpn
	b3451	ugpE	<	281	Transport and binding proteins	Eco Hin Mge Mpn
	b3452	ugpA	<	295	Transport and binding proteins	Eco Hin Mge Mpn
o0667	b3451	ugpE	<	281	Transport and binding proteins	Bsu Eco Hin Mge Mpn Syn
	b3452	ugpA	<	295	Transport and binding proteins	Bsu Eco Hin Mge Mpn Syn
o0667	b3451	ugpE	<	281	Transport and binding proteins	Bsu Eco
	b3452	ugpA	<	295	Transport and binding proteins	Bsu Eco
	b3453	ugpB	<	438	Transport and binding proteins	Bsu Eco
o0668	b3454	livF	<	241	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b3455	livG	<	255	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0668	b3454	livF	<	241	Transport and binding proteins	Eco
	b3455	livG	<	255	Transport and binding proteins	Eco
	b3456	livM	<	425	Transport and binding proteins	Eco
o0668	b3454	livF	<	241	Transport and binding proteins	B
	b3455	livG	<	255	Transport and binding proteins	B
	b3456	livM	<	425	Transport and binding proteins	B
	b3457	livH	<	308	Transport and binding proteins	B
	b3458	livK	<	369	Transport and binding proteins	B
o0668	b3455	livG	<	255	Transport and binding proteins	Bsu Eco Hin Mth Syn
	b3456	livM	<	425	Transport and binding proteins	Bsu Eco Hin Mth Syn
o0668	b3455	livG	<	255	Transport and binding proteins	Eco
	b3456	livM	<	425	Transport and binding proteins	Eco
	b3457	livH	<	308	Transport and binding proteins	Eco
o0668	b3456	livM	<	425	Transport and binding proteins	Eco Mja Syn
	b3457	livH	<	308	Transport and binding proteins	Eco Mja Syn
o0669	b3462	ftsX	<	352	"Cell processes (incl. adaptation, protection)"	Bsu Eco Mja Mth
	b3463	ftsE	<	222	"Cell processes (incl. adaptation, protection)"	Bsu Eco Mja Mth

o0669	b3462	ftsX	<	352	"Cell processes (incl. adaptation, protection)"	B
	b3463	ftsE	<	222	"Cell processes (incl. adaptation, protection)"	B
	b3464	ftsY	<	497	"Cell processes (incl. adaptation, protection)"	B
o0669	b3463	ftsE	<	222	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hin Mpn
	b3464	ftsY	<	497	"Cell processes (incl. adaptation, protection)"	Bsu Eco Hin Mpn
o0670	b3465	yhhF	>	198	"Hypothetical, unclassified, unknown"	B
	b3466	b3466	>	89	"Hypothetical, unclassified, unknown"	B
o0671	b3471	yhhQ	>	221	"Hypothetical, unclassified, unknown"	B
	b3472	b3472	>	203	"Hypothetical, unclassified, unknown"	B
o0672	b3476	nikA	>	524	Transport and binding proteins	Hpy
	b3477	nikB	>	314	Transport and binding proteins	Hpy
o0672	b3476	nikA	>	524	Transport and binding proteins	Bsu Eco
	b3477	nikB	>	314	Transport and binding proteins	Bsu Eco
	b3478	nikC	>	277	Transport and binding proteins	Bsu Eco
o0672	b3476	nikA	>	524	Transport and binding proteins	Eco
	b3477	nikB	>	314	Transport and binding proteins	Eco
	b3478	nikC	>	277	Transport and binding proteins	Eco
	b3479	nikD	>	254	Transport and binding proteins	Eco
o0672	b3476	nikA	>	524	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3477	nikB	>	314	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3478	nikC	>	277	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3479	nikD	>	254	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3480	nikE	>	268	Transport and binding proteins	B Bsu Eco Hin Hpy
o0672	b3477	nikB	>	314	Transport and binding proteins	Bsu Eco Hin
	b3478	nikC	>	277	Transport and binding proteins	Bsu Eco Hin
o0672	b3477	nikB	>	314	Transport and binding proteins	Bsu Syn
	b3478	nikC	>	277	Transport and binding proteins	Bsu Syn
	b3479	nikD	>	254	Transport and binding proteins	Bsu Syn
o0672	b3477	nikB	>	314	Transport and binding proteins	Hin Mge Mpn
	b3478	nikC	>	277	Transport and binding proteins	Hin Mge Mpn
	b3479	nikD	>	254	Transport and binding proteins	Hin Mge Mpn
	b3480	nikE	>	268	Transport and binding proteins	Hin Mge Mpn
o0672	b3478	nikC	>	277	Transport and binding proteins	Eco Hpy Mpn Syn
	b3479	nikD	>	254	Transport and binding proteins	Eco Hpy Mpn Syn
o0672	b3479	nikD	>	254	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b3480	nikE	>	268	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0673	b3482	rhsB	>	1411	"Hypothetical, unclassified, unknown"	B Eco
	b3483	yhhH	>	122	"Hypothetical, unclassified, unknown"	B Eco
o0674	b3485	yhhJ	<	375	"Hypothetical, unclassified, unknown"	Bsu Eco Mja Mpn Mth Syn
	b3486	b3486	<	894	Putative transport proteins	Bsu Eco Mja Mpn Mth Syn
o0674	b3485	yhhJ	<	375	"Hypothetical, unclassified, unknown"	B Eco
	b3486	b3486	<	894	Putative transport proteins	B Eco
	b3487	yhiI	<	355	Putative regulatory proteins	B Eco
o0674	b3486	b3486	<	894	Putative transport proteins	Bsu Eco Syn
	b3487	yhiI	<	355	Putative regulatory proteins	Bsu Eco Syn
o0675	b3489	yhiK	<	123	"Hypothetical, unclassified, unknown"	B Eco
	b3490	yhiL	<	412	"Hypothetical, unclassified, unknown"	B Eco
o0676	b3497	yhiQ	<	250	"Hypothetical, unclassified, unknown"	B
	b3498	prlC	<	680	"Translation, post-translational modification"	B
o0677	b3501	arsR	>	117	"Cell processes (incl. adaptation, protection)"	Bsu Syn
	b3502	arsB	>	436	"Cell processes (incl. adaptation, protection)"	Bsu Syn

o0677	b3501	arsR	>	117	"Cell processes (incl. adaptation, protection)"	B
	b3502	arsB	>	436	"Cell processes (incl. adaptation, protection)"	B
	b3503	arsC	>	141	"Cell processes (incl. adaptation, protection)"	B
o0677	b3502	arsB	>	436	"Cell processes (incl. adaptation, protection)"	Eco
	b3503	arsC	>	141	"Cell processes (incl. adaptation, protection)"	Eco
o0678	b3509	hdeB	<	112	"Hypothetical, unclassified, unknown"	B Eco
	b3510	hdeA	<	110	"Hypothetical, unclassified, unknown"	B Eco
o0679	b3513	yhiU	>	385	"Cell processes (incl. adaptation, protection)"	B Eco Hin Hpy Sce Syn
	b3514	yhiV	>	1037	"Cell processes (incl. adaptation, protection)"	B Eco Hin Hpy Sce Syn
o0680	b3521	yhjC	>	323	Putative regulatory proteins	B Bsu
	b3522	yhjD	>	337	"Hypothetical, unclassified, unknown"	B Bsu
o0681	b3530	yhjL	<	1166	Putative enzymes	B
	b3531	yhjM	<	368	Putative enzymes	B
	b3532	yhjN	<	779	"Hypothetical, unclassified, unknown"	B
	b3533	b3533	<	888	"Hypothetical, unclassified, unknown"	B
	b3534	b3534	<	242	"Hypothetical, unclassified, unknown"	B
	b3535	b3535	<	62	"Hypothetical, unclassified, unknown"	B
o0681	b3532	yhjN	<	779	"Hypothetical, unclassified, unknown"	Syn
	b3533	b3533	<	888	"Hypothetical, unclassified, unknown"	Syn
o0682	b3536	yhjS	>	523	"Translation, post-translational modification"	B
	b3537	b3537	>	62	"Hypothetical, unclassified, unknown"	B
	b3538	yhjU	>	559	"Hypothetical, unclassified, unknown"	B
o0683	b3540	dppF	<	334	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b3541	dppD	<	327	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0683	b3540	dppF	<	334	Transport and binding proteins	Bsu Syn
	b3541	dppD	<	327	Transport and binding proteins	Bsu Syn
	b3542	dppC	<	300	Transport and binding proteins	Bsu Syn
o0683	b3540	dppF	<	334	Transport and binding proteins	Hin Mge Mpn
	b3541	dppD	<	327	Transport and binding proteins	Hin Mge Mpn
	b3542	dppC	<	300	Transport and binding proteins	Hin Mge Mpn
	b3543	dppB	<	339	Transport and binding proteins	Hin Mge Mpn
o0683	b3540	dppF	<	334	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3541	dppD	<	327	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3542	dppC	<	300	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3543	dppB	<	339	Transport and binding proteins	B Bsu Eco Hin Hpy
	b3544	dppA	<	535	Transport and binding proteins	B Bsu Eco Hin Hpy
o0683	b3541	dppD	<	327	Transport and binding proteins	Bsu Eco Hin Hpy Mth Syn
	b3542	dppC	<	300	Transport and binding proteins	Bsu Eco Hin Hpy Mth Syn
o0683	b3541	dppD	<	327	Transport and binding proteins	Bsu
	b3542	dppC	<	300	Transport and binding proteins	Bsu
	b3543	dppB	<	339	Transport and binding proteins	Bsu
o0683	b3541	dppD	<	327	Transport and binding proteins	Eco
	b3542	dppC	<	300	Transport and binding proteins	Eco
	b3543	dppB	<	339	Transport and binding proteins	Eco
	b3544	dppA	<	535	Transport and binding proteins	Eco
o0683	b3542	dppC	<	300	Transport and binding proteins	Bsu Eco Hin Mpn
	b3543	dppB	<	339	Transport and binding proteins	Bsu Eco Hin Mpn
o0683	b3542	dppC	<	300	Transport and binding proteins	Bsu Eco
	b3543	dppB	<	339	Transport and binding proteins	Bsu Eco
	b3544	dppA	<	535	Transport and binding proteins	Bsu Eco

o0683	b3543	dppB	<	339	Transport and binding proteins	Hpy
	b3544	dppA	<	535	Transport and binding proteins	Hpy
o0684	b3549	tag	>	187	"DNA replication, recombination, modification and repair"	B
	b3550	yiaC	>	146	"Hypothetical, unclassified, unknown"	B
o0685	b3557	yi5A	>	173	"Hypothetical, unclassified, unknown"	B Hin
	b3558	yi5B	>	283	"phage, transposon, or plasmid"	B Hin
o0686	b3559	glyS	<	689	"Translation, post-translational modification"	B Bsu
	b3560	glyQ	<	303	"Translation, post-translational modification"	B Bsu
o0687	b3562	yiaA	<	146	"Hypothetical, unclassified, unknown"	B Eco
	b3563	yiaB	<	117	"Hypothetical, unclassified, unknown"	B Eco
o0688	b3564	xylB	<	484	Carbon compound catabolism	B Bsu
	b3565	xylA	<	440	Carbon compound catabolism	B Bsu
o0689	b3566	xylF	>	330	Transport and binding proteins	Eco Sce
	b3567	xylG	>	513	Transport and binding proteins	Eco Sce
o0689	b3566	xylF	>	330	Transport and binding proteins	Eco
	b3567	xylG	>	513	Transport and binding proteins	Eco
	b3568	xylH	>	393	Transport and binding proteins	Eco
o0689	b3566	xylF	>	330	Transport and binding proteins	B
	b3567	xylG	>	513	Transport and binding proteins	B
	b3568	xylH	>	393	Transport and binding proteins	B
	b3569	xylR	>	392	Carbon compound catabolism	B
o0689	b3567	xylG	>	513	Transport and binding proteins	Bsu Eco Hin Mge Mja Mpn Syn
	b3568	xylH	>	393	Transport and binding proteins	Bsu Eco Hin Mge Mja Mpn Syn
o0689	b3567	xylG	>	513	Transport and binding proteins	Eco
	b3568	xylH	>	393	Transport and binding proteins	Eco
	b3569	xylR	>	392	Carbon compound catabolism	Eco
o0689	b3568	xylH	>	393	Transport and binding proteins	Eco
	b3569	xylR	>	392	Carbon compound catabolism	Eco
o0690	b3575	b3575	>	332	Putative enzymes	B
	b3576	yiaL	>	155	Putative enzymes	B
o0691	b3577	yiaM	>	157	"Hypothetical, unclassified, unknown"	Bsu Hin Syn
	b3578	yiaN	>	424	Cell structure	Bsu Hin Syn
o0691	b3577	yiaM	>	157	"Hypothetical, unclassified, unknown"	Hin
	b3578	yiaN	>	424	Cell structure	Hin
	b3579	yiaO	>	328	Putative transport proteins	Hin
	b3580	lyxK	>	498	Carbon compound catabolism	Hin
o0691	b3577	yiaM	>	157	"Hypothetical, unclassified, unknown"	B
	b3578	yiaN	>	424	Cell structure	B
	b3579	yiaO	>	328	Putative transport proteins	B
	b3580	lyxK	>	498	Carbon compound catabolism	B
	b3581	yiaQ	>	220	"Hypothetical, unclassified, unknown"	B
	b3582	yiaR	>	297	"Hypothetical, unclassified, unknown"	B
	b3583	yiaS	>	231	Energy metabolism	B
o0691	b3578	yiaN	>	424	Cell structure	Hin
	b3579	yiaO	>	328	Putative transport proteins	Hin
o0691	b3581	yiaQ	>	220	"Hypothetical, unclassified, unknown"	Mpn
	b3582	yiaR	>	297	"Hypothetical, unclassified, unknown"	Mpn
o0691	b3581	yiaQ	>	220	"Hypothetical, unclassified, unknown"	Eco
	b3582	yiaR	>	297	"Hypothetical, unclassified, unknown"	Eco
	b3583	yiaS	>	231	Energy metabolism	Eco

o0691	b3582	yiaR	>	297	"Hypothetical, unclassified, unknown"	Hin
	b3583	yiaS	>	231	Energy metabolism	Hin
o0692	b3586	yiaV	<	378	Putative transport proteins	B Eco
	b3587	yiaW	<	107	"Hypothetical, unclassified, unknown"	B Eco
o0693	b3590	selB	<	614	"Translation, post-translational modification"	B Hin
	b3591	selA	<	463	"Translation, post-translational modification"	B Hin
o0694	b3593	rhsA	>	1377	"Hypothetical, unclassified, unknown"	B
	b3594	yibA	>	280	"Hypothetical, unclassified, unknown"	B
	b3595	yibJ	>	233	"Hypothetical, unclassified, unknown"	B
o0694	b3594	yibA	>	280	"Hypothetical, unclassified, unknown"	Eco
	b3595	yibJ	>	233	"Hypothetical, unclassified, unknown"	Eco
o0695	b3597	yibH	<	378	Structural proteins	B Eco
	b3598	yibI	<	120	"Hypothetical, unclassified, unknown"	B Eco
o0696	b3599	mtlA	>	637	Transport and binding proteins	Bsu Mpn
	b3600	mtlD	>	382	Carbon compound catabolism	Bsu Mpn
o0696	b3599	mtlA	>	637	Transport and binding proteins	B
	b3600	mtlD	>	382	Carbon compound catabolism	B
	b3601	mtlR	>	195	Carbon compound catabolism	B
o0697	b3604	lctR	>	258	Energy metabolism	B
	b3605	lctD	>	396	Energy metabolism	B
o0698	b3608	gpsA	<	339	Energy metabolism	B
	b3609	secB	<	155	Transport and binding proteins	B
o0699	b3612	yibO	>	514	"Hypothetical, unclassified, unknown"	B Bsu
	b3613	yibP	>	427	Cell structure	B Bsu
o0700	b3616	tdh	<	341	Amino acid biosynthesis and metabolism	B Bsu Eco
	b3617	kbl	<	398	Central intermediary metabolism	B Bsu Eco
o0701	b3619	rfaD	>	310	Cell structure	Syn
	b3620	rfaF	>	348	Cell structure	Syn
o0701	b3619	rfaD	>	310	Cell structure	B
	b3620	rfaF	>	348	Cell structure	B
	b3621	rfaC	>	319	Cell structure	B
	b3622	rfaL	>	419	Cell structure	B
o0701	b3620	rfaF	>	348	Cell structure	Eco
	b3621	rfaC	>	319	Cell structure	Eco
o0702	b3623	rfaK	<	357	Cell structure	B
	b3624	rfaZ	<	283	Cell structure	B
	b3625	rfaY	<	232	Cell structure	B
	b3626	rfaJ	<	338	Cell structure	B
	b3627	rfaI	<	339	Cell structure	B
	b3628	rfaB	<	369	Cell structure	B
	b3629	rfaS	<	311	Cell structure	B
	b3630	rfaP	<	265	Cell structure	B
	b3631	rfaG	<	374	Cell structure	B
	b3632	rfaQ	<	344	Cell structure	B
o0702	b3626	rfaJ	<	338	Cell structure	Eco
	b3627	rfaI	<	339	Cell structure	Eco
o0702	b3627	rfaI	<	339	Cell structure	Syn
	b3628	rfaB	<	369	Cell structure	Syn
o0702	b3631	rfaG	<	374	Cell structure	Mth
	b3632	rfaQ	<	344	Cell structure	Mth

o0703	b3633	kdtA	>	425	Cell structure	B Hin
	b3634	kdtB	>	159	Cell structure	B Hin

operon#	b#	gene	dir	length	function	species
o0704	b3636	rpmG	<	55	"Translation, post-translational modification"	B
	b3637	rpmB	<	78	"Translation, post-translational modification"	B
o0705	b3639	dfp	>	430	"DNA replication, recombination, modification and repair"	B
	b3640	dut	>	151	Nucleotide biosynthesis and metabolism	B
o0706	b3642	pyrE	<	213	Nucleotide biosynthesis and metabolism	B Hin
	b3643	rph	<	228	"DNA replication, recombination, modification and repair"	B Hin
o0707	b3649	rpoZ	>	91	"Transcription, RNA processing and degradation"	Hpy
	b3650	spoT	>	702	Regulatory function	Hpy
o0707	b3649	rpoZ	>	91	"Transcription, RNA processing and degradation"	B
	b3650	spoT	>	702	Regulatory function	B
	b3651	spoU	>	229	"Transcription, RNA processing and degradation"	B
	b3652	recG	>	693	"DNA replication, recombination, modification and repair"	B
o0707	b3650	spoT	>	702	Regulatory function	Syn
	b3651	spoU	>	229	"Transcription, RNA processing and degradation"	Syn
o0708	b3656	yicI	<	772	"Hypothetical, unclassified, unknown"	B Eco
	b3657	yicJ	<	479	Putative transport proteins	B Eco
o0709	b3662	yicM	<	451	Putative regulatory proteins	Eco
	b3663	yicN	<	159	"Hypothetical, unclassified, unknown"	Eco
o0709	b3662	yicM	<	451	Putative regulatory proteins	B
	b3663	yicN	<	159	"Hypothetical, unclassified, unknown"	B
	b3664	yicO	<	470	"Hypothetical, unclassified, unknown"	B
o0710	b3667	uhpC	<	440	Transport and binding proteins	Eco Sce
	b3668	uhpB	<	501	Transport and binding proteins	Eco Sce
o0710	b3667	uhpC	<	440	Transport and binding proteins	B
	b3668	uhpB	<	501	Transport and binding proteins	B
	b3669	uhpA	<	196	Transport and binding proteins	B
o0710	b3668	uhpB	<	501	Transport and binding proteins	Bsu Eco Mth Syn
	b3669	uhpA	<	196	Transport and binding proteins	Bsu Eco Mth Syn
o0711	b3670	ilvN	<	96	Amino acid biosynthesis and metabolism	Bsu Eco Hin Mth
	b3671	ilvB	<	562	Amino acid biosynthesis and metabolism	Bsu Eco Hin Mth
o0711	b3670	ilvN	<	96	Amino acid biosynthesis and metabolism	B
	b3671	ilvB	<	562	Amino acid biosynthesis and metabolism	B
	b3672	b3672	<	32	"Hypothetical, unclassified, unknown"	B
o0712	b3674	yidF	<	165	Putative regulatory proteins	B
	b3675	yidG	<	120	"Hypothetical, unclassified, unknown"	B
	b3676	yidH	<	115	"Hypothetical, unclassified, unknown"	B
o0713	b3678	yidJ	<	497	Putative enzymes	B Hin
	b3679	yidK	<	571	Putative transport proteins	B Hin
o0714	b3681	glvG	<	212	Transport and binding proteins	B
	b3682	glvB	<	161	Transport and binding proteins	B
	b3683	glvC	<	455	Transport and binding proteins	B
o0715	b3692	yidU	<	587	Putative regulatory proteins	Syn
	b3693	yidV	<	292	"Hypothetical, unclassified, unknown"	Syn

o0715	b3692	yidU	<	587	Putative regulatory proteins	B
	b3693	yidV	<	292	"Hypothetical, unclassified, unknown"	B
	b3694	b3694	<	98	Putative regulatory proteins	B
	b3695	yidW	<	128	"Hypothetical, unclassified, unknown"	B
o0716	b3700	recF	<	357	"DNA replication, recombination, modification and repair"	B Hin
	b3701	dnaN	<	366	"DNA replication, recombination, modification and repair"	B Hin
	b3702	dnaA	<	467	"DNA replication, recombination, modification and repair"	B Hin
o0717	b3703	rpmH	>	46	"Translation, post-translational modification"	B Hin Syn
	b3704	rnpA	>	119	"DNA replication, recombination, modification and repair"	B Hin Syn
o0718	b3708	tnaA	>	476	Amino acid biosynthesis and metabolism	B Mja
	b3709	tnaB	>	415	Transport and binding proteins	B Mja
o0719	b3710	yidY	>	391	Putative regulatory proteins	B Bsu Eco
	b3711	yidZ	>	319	Putative regulatory proteins	B Bsu Eco
o0720	b3712	yieE	>	253	"Hypothetical, unclassified, unknown"	B
	b3713	b3713	>	188	"Hypothetical, unclassified, unknown"	B
o0721	b3716	yieI	>	155	"Hypothetical, unclassified, unknown"	B
	b3717	yieJ	>	195	"Hypothetical, unclassified, unknown"	B
o0722	b3719	yieL	<	400	Putative enzymes	B
	b3720	yieC	<	538	"Hypothetical, unclassified, unknown"	B
o0723	b3721	bglB	<	470	Carbon compound catabolism	Bsu Eco Sce
	b3722	bglF	<	625	Transport and binding proteins	Bsu Eco Sce
o0723	b3721	bglB	<	470	Carbon compound catabolism	B
	b3722	bglF	<	625	Transport and binding proteins	B
	b3723	bglG	<	278	Carbon compound catabolism	B
o0723	b3722	bglF	<	625	Transport and binding proteins	Bsu Eco
	b3723	bglG	<	278	Carbon compound catabolism	Bsu Eco
o0724	b3724	phoU	<	241	Regulatory function	Bsu
	b3725	pstB	<	257	Transport and binding proteins	Bsu
o0724	b3724	phoU	<	241	Regulatory function	Mge Mpn
	b3725	pstB	<	257	Transport and binding proteins	Mge Mpn
	b3726	pstA	<	296	Transport and binding proteins	Mge Mpn
o0724	b3724	phoU	<	241	Regulatory function	B Mja Mth
	b3725	pstB	<	257	Transport and binding proteins	B Mja Mth
	b3726	pstA	<	296	Transport and binding proteins	B Mja Mth
	b3727	pstC	<	319	Transport and binding proteins	B Mja Mth
	b3728	pstS	<	346	Transport and binding proteins	B Mja Mth
o0724	b3725	pstB	<	257	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b3726	pstA	<	296	Transport and binding proteins	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0724	b3725	pstB	<	257	Transport and binding proteins	Bsu Eco Hin Mpn Syn
	b3726	pstA	<	296	Transport and binding proteins	Bsu Eco Hin Mpn Syn
	b3727	pstC	<	319	Transport and binding proteins	Bsu Eco Hin Mpn Syn
o0724	b3725	pstB	<	257	Transport and binding proteins	Syn
	b3726	pstA	<	296	Transport and binding proteins	Syn
	b3727	pstC	<	319	Transport and binding proteins	Syn
	b3728	pstS	<	346	Transport and binding proteins	Syn
o0724	b3726	pstA	<	296	Transport and binding proteins	Bsu Eco Hin Mja Mth Syn
	b3727	pstC	<	319	Transport and binding proteins	Bsu Eco Hin Mja Mth Syn
o0724	b3726	pstA	<	296	Transport and binding proteins	Hin Hpy
	b3727	pstC	<	319	Transport and binding proteins	Hin Hpy
	b3728	pstS	<	346	Transport and binding proteins	Hin Hpy

o0724	b3727	pstC	<	319	Transport and binding proteins	Mpn
	b3728	pstS	<	346	Transport and binding proteins	Mpn
o0725	b3729	glmS	<	609	Central intermediary metabolism	B Mja
	b3730	glmU	<	456	Central intermediary metabolism	B Mja
o0726	b3731	atpC	<	139	Energy metabolism	Syn
	b3732	atpD	<	460	Energy metabolism	Syn
o0726	b3731	atpC	<	139	Energy metabolism	Hpy
	b3732	atpD	<	460	Energy metabolism	Hpy
	b3733	atpG	<	287	Energy metabolism	Hpy
	b3734	atpA	<	513	Energy metabolism	Hpy
o0726	b3731	atpC	<	139	Energy metabolism	Mpn
	b3732	atpD	<	460	Energy metabolism	Mpn
	b3733	atpG	<	287	Energy metabolism	Mpn
	b3734	atpA	<	513	Energy metabolism	Mpn
	b3735	atpH	<	177	Energy metabolism	Mpn
	b3736	atpF	<	156	Energy metabolism	Mpn
	b3737	atpE	<	79	Energy metabolism	Mpn
o0726	b3731	atpC	<	139	Energy metabolism	Bsu Hin Mge
	b3732	atpD	<	460	Energy metabolism	Bsu Hin Mge
	b3733	atpG	<	287	Energy metabolism	Bsu Hin Mge
	b3734	atpA	<	513	Energy metabolism	Bsu Hin Mge
	b3735	atpH	<	177	Energy metabolism	Bsu Hin Mge
	b3736	atpF	<	156	Energy metabolism	Bsu Hin Mge
	b3737	atpE	<	79	Energy metabolism	Bsu Hin Mge
	b3738	atpB	<	271	Energy metabolism	Bsu Hin Mge
o0726	b3731	atpC	<	139	Energy metabolism	B
	b3732	atpD	<	460	Energy metabolism	B
	b3733	atpG	<	287	Energy metabolism	B
	b3734	atpA	<	513	Energy metabolism	B
	b3735	atpH	<	177	Energy metabolism	B
	b3736	atpF	<	156	Energy metabolism	B
	b3737	atpE	<	79	Energy metabolism	B
	b3738	atpB	<	271	Energy metabolism	B
	b3739	atpI	<	130	Energy metabolism	B
o0726	b3732	atpD	<	460	Energy metabolism	Syn
	b3733	atpG	<	287	Energy metabolism	Syn
o0726	b3732	atpD	<	460	Energy metabolism	Bsu Hin Hpy Mge Mpn
	b3733	atpG	<	287	Energy metabolism	Bsu Hin Hpy Mge Mpn
	b3734	atpA	<	513	Energy metabolism	Bsu Hin Hpy Mge Mpn
o0726	b3733	atpG	<	287	Energy metabolism	Eco Syn
	b3734	atpA	<	513	Energy metabolism	Eco Syn
o0726	b3736	atpF	<	156	Energy metabolism	Syn
	b3737	atpE	<	79	Energy metabolism	Syn
	b3738	atpB	<	271	Energy metabolism	Syn
o0726	b3737	atpE	<	79	Energy metabolism	Hin
	b3738	atpB	<	271	Energy metabolism	Hin
o0727	b3740	gidB	<	207	"DNA replication, recombination, modification and repair"	Bsu Mge Mpn
	b3741	gidA	<	629	"DNA replication, recombination, modification and repair"	Bsu Mge Mpn
o0727	b3740	gidB	<	207	"DNA replication, recombination, modification and repair"	B
	b3741	gidA	<	629	"DNA replication, recombination, modification and repair"	B
	b3742	mioC	<	147	"DNA replication, recombination, modification and repair"	B

o0727	b3741	gidA	<	629	"DNA replication, recombination, modification and repair"	Bsu
	b3742	mioC	<	147	"DNA replication, recombination, modification and repair"	Bsu
o0728	b3748	rbsD	>	151	Transport and binding proteins	Bsu
	b3749	rbsA	>	501	Transport and binding proteins	Bsu
	b3750	rbsC	>	321	Transport and binding proteins	Bsu
	b3751	rbsB	>	296	Transport and binding proteins	Bsu
o0728	b3748	rbsD	>	151	Transport and binding proteins	B
	b3749	rbsA	>	501	Transport and binding proteins	B
	b3750	rbsC	>	321	Transport and binding proteins	B
	b3751	rbsB	>	296	Transport and binding proteins	B
	b3752	rbsK	>	309	Carbon compound catabolism	B
o0728	b3749	rbsA	>	501	Transport and binding proteins	Bsu Eco Hin Hpy Mja Syn
	b3750	rbsC	>	321	Transport and binding proteins	Bsu Eco Hin Hpy Mja Syn
o0728	b3749	rbsA	>	501	Transport and binding proteins	Eco
	b3750	rbsC	>	321	Transport and binding proteins	Eco
	b3751	rbsB	>	296	Transport and binding proteins	Eco
o0728	b3750	rbsC	>	321	Transport and binding proteins	Eco
	b3751	rbsB	>	296	Transport and binding proteins	Eco
o0728	b3751	rbsB	>	296	Transport and binding proteins	Bsu
	b3752	rbsK	>	309	Carbon compound catabolism	Bsu
o0729	b3754	yieO	<	475	Putative transport proteins	B Eco
	b3755	yieP	<	181	"Hypothetical, unclassified, unknown"	B Eco
o0730	b3756	rrsC	>		rRNA	B
	b3757	gltU	>		tRNA	B
	b3758	rrlC	>		rRNA	B
	b3759	rrfC	>		rRNA	B
	b3760	aspT	>		tRNA	B
	b3761	trpT	>		tRNA	B
o0731	b3762	yifA	<	198	"Hypothetical, unclassified, unknown"	B
	b3763	pssR	<	133	Fatty acid and phospholipid metabolism	B
o0732	b3766	ilvL	>	32	Amino acid biosynthesis and metabolism	B
	b3767	ilvG_1	>	327	Amino acid biosynthesis and metabolism	B
	b3768	ilvG_2	>	221	Amino acid biosynthesis and metabolism	B
	b3769	ilvM	>	87	Amino acid biosynthesis and metabolism	B
	b3770	ilvE	>	309	Amino acid biosynthesis and metabolism	B
	b3771	ilvD	>	605	Amino acid biosynthesis and metabolism	B
o0733	b3776	b3776	<	91	"Hypothetical, unclassified, unknown"	B
	b3777	b3777	<	86	"Hypothetical, unclassified, unknown"	B
o0734	b3782	rhoL	>	33	"Transcription, RNA processing and degradation"	B
	b3783	rho	>	419	"Transcription, RNA processing and degradation"	B
o0735	b3784	rfe	>	367	Cell structure	B
	b3785	b3785	>	349	Cell structure	B
	b3786	rffE	>	389	Central intermediary metabolism	B
	b3787	rffD	>	420	Central intermediary metabolism	B
	b3788	rffG	>	355	Central intermediary metabolism	B
	b3789	rffH	>	293	Central intermediary metabolism	B
o0735	b3786	rffE	>	389	Central intermediary metabolism	Mth
	b3787	rffD	>	420	Central intermediary metabolism	Mth
o0735	b3787	rffD	>	420	Central intermediary metabolism	Bsu Mja
	b3788	rffG	>	355	Central intermediary metabolism	Bsu Mja

o0735	b3788	rffG	>	355	Central intermediary metabolism	Bsu Eco Hpy Mth Syn
	b3789	rffH	>	293	Central intermediary metabolism	Bsu Eco Hpy Mth Syn
o0736	b3790	yifH	>	181	"Hypothetical, unclassified, unknown"	Bsu
	b3791	yifI	>	376	Putative regulatory proteins	Bsu
-	b3790	yifH	>	181	"Hypothetical, unclassified, unknown"	B
	b3791	yifI	>	376	Putative regulatory proteins	B
	b3792	yifJ	>	416	Putative enzymes	B
	b4404	b4404	>	74	"Hypothetical, unclassified, unknown"	B
	b4405	b4405	>	204	"Hypothetical, unclassified, unknown"	B
	b3793	rffT	>	450	Cell structure	B
	b3794	rffM	>	246	Cell structure	B
o0737	b3796	argX	>		tRNA	B
	b3797	hisR	>		tRNA	B
	b3798	leuT	>		tRNA	B
	b3799	proM	>		tRNA	B
o0738	b3802	hemY	<	398	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin Sce
	b3803	hemX	<	393	"Biosynthesis of cofactors, prosthetic groups and carriers"	Hin Sce
o0738	b3802	hemY	<	398	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3803	hemX	<	393	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3804	hemD	<	246	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3805	hemC	<	320	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0738	b3803	hemX	<	393	"Biosynthesis of cofactors, prosthetic groups and carriers"	Syn
	b3804	hemD	<	246	"Biosynthesis of cofactors, prosthetic groups and carriers"	Syn
o0738	b3804	hemD	<	246	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b3805	hemC	<	320	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0739	b3809	dapF	>	275	Amino acid biosynthesis and metabolism	B
	b3810	yigA	>	235	"Hypothetical, unclassified, unknown"	B
	b3811	xerC	>	298	"DNA replication, recombination, modification and repair"	B
	b3812	yigB	>	238	Putative enzymes	B
o0740	b3814	b3814	<	99	"Hypothetical, unclassified, unknown"	B
	b3815	yigE	<	161	"Hypothetical, unclassified, unknown"	B
o0741	b3817	yigF	<	126	"Hypothetical, unclassified, unknown"	B
	b3818	yigG	<	138	"Hypothetical, unclassified, unknown"	B
o0742	b3819	rarD	<	300	"Hypothetical, unclassified, unknown"	B
	b3820	yigI	<	161	"Hypothetical, unclassified, unknown"	B
o0743	b3833	yigO	>	251	"Hypothetical, unclassified, unknown"	Syn
	b3834	yigP	>	201	"Hypothetical, unclassified, unknown"	Syn
o0743	b3833	yigO	>	251	"Hypothetical, unclassified, unknown"	B
	b3834	yigP	>	201	"Hypothetical, unclassified, unknown"	B
	b3835	b3835	>	546	"Hypothetical, unclassified, unknown"	B
	b3836	b3836	>	103	"Hypothetical, unclassified, unknown"	B
	b3837	b3837	>	113	"Hypothetical, unclassified, unknown"	B
	b3838	b3838	>	145	"Hypothetical, unclassified, unknown"	B
	b3839	yigU	>	258	"Hypothetical, unclassified, unknown"	B
	b3840	yigW	>	206	"Hypothetical, unclassified, unknown"	B
	b3841	yigW	>	113	"Hypothetical, unclassified, unknown"	B
o0743	b3838	b3838	>	145	"Hypothetical, unclassified, unknown"	Bsu Eco
	b3839	yigU	>	258	"Hypothetical, unclassified, unknown"	Bsu Eco
o0744	b3843	yigC	>	497	"Hypothetical, unclassified, unknown"	B
	b3844	ubiB	>	233	Energy metabolism	B

operon#	b#	gene	dir	length	function	species
o0745	b3845	fadA	<	387	Fatty acid and phospholipid metabolism	B Bsu Eco
	b3846	fadB	<	729	Fatty acid and phospholipid metabolism	B Bsu Eco
o0746	b3847	pepQ	>	443	"Translation, post-translational modification"	B
	b3848	yigZ	>	205	Putative enzymes	B
	b3849	trkH	>	432	Transport and binding proteins	B
o0746	b3848	yigZ	>	205	Putative enzymes	Hin
	b3849	trkH	>	432	Transport and binding proteins	Hin
o0747	b3851	rrsA	>		rRNA	B
	b3852	ileT	>		tRNA	B
	b3853	alaT	>		tRNA	B
	b3854	rrlA	>		rRNA	B
	b3855	rrfA	>		rRNA	B
o0748	b3856	b3856	<	170	"Hypothetical, unclassified, unknown"	B Hin
	b3857	mobA	<	194	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Hin
o0749	b3859	yihE	>	328	"Hypothetical, unclassified, unknown"	B
	b3860	dsbA	>	208	"Translation, post-translational modification"	B
o0750	b3868	glnG	<	469	Amino acid biosynthesis and metabolism	Bsu Eco Hin Mth Syn
	b3869	glnL	<	349	Amino acid biosynthesis and metabolism	Bsu Eco Hin Mth Syn
o0750	b3868	glnG	<	469	Amino acid biosynthesis and metabolism	B Syn
	b3869	glnL	<	349	Amino acid biosynthesis and metabolism	B Syn
	b3870	glnA	<	469	Amino acid biosynthesis and metabolism	B Syn
o0751	b3872	b3872	>	236	"Hypothetical, unclassified, unknown"	B
	b3873	yihM	>	326	"Hypothetical, unclassified, unknown"	B
o0752	b3875	b3875	<	230	"Hypothetical, unclassified, unknown"	B
	b3876	b3876	<	487	Putative transport proteins	B
	b3877	yihP	<	468	Putative transport proteins	B
	b3878	yihQ	<	678	Putative enzymes	B
o0752	b3876	b3876	<	487	Putative transport proteins	Bsu Eco
	b3877	yihP	<	468	Putative transport proteins	Bsu Eco
o0752	b3877	yihP	<	468	Putative transport proteins	Bsu Eco
	b3878	yihQ	<	678	Putative enzymes	Bsu Eco
o0753	b3880	yihS	<	418	"Hypothetical, unclassified, unknown"	B
	b3881	yihT	<	292	Putative enzymes	B
	b3882	yihU	<	298	Putative enzymes	B
o0754	b3883	yihV	>	300	Putative enzymes	B Bsu Eco Mth
	b3884	yihW	>	269	Putative regulatory proteins	B Bsu Eco Mth
o0755	b3885	yihX	>	206	Putative enzymes	B
	b3886	yihY	>	290	"Hypothetical, unclassified, unknown"	B
	b3887	yihZ	>	145	"Hypothetical, unclassified, unknown"	B
	b3888	yiiD	>	329	Putative enzymes	B
o0756	b3891	fdhE	<	309	Energy metabolism	Hin
	b3892	fdoI	<	211	Energy metabolism	Hin
	b3893	fdoH	<	300	Energy metabolism	Hin
o0756	b3891	fdhE	<	309	Energy metabolism	B
	b3892	fdoI	<	211	Energy metabolism	B
	b3893	fdoH	<	300	Energy metabolism	B
	b3894	fdoG	<	1016	Energy metabolism	B

o0756	b3892	fdoI	<	211	Energy metabolism	Eco
	b3893	fdoH	<	300	Energy metabolism	Eco
	b3894	fdoG	<	1016	Energy metabolism	Eco
o0756	b3893	fdoH	<	300	Energy metabolism	Bsu Eco Hin Mja Mth
	b3894	fdoG	<	1016	Energy metabolism	Bsu Eco Hin Mja Mth
o0757	b3897	frvR	<	582	Transport and binding proteins	B
	b3898	frvX	<	356	"Hypothetical, unclassified, unknown"	B
	b3899	frvB	<	485	Transport and binding proteins	B
	b3900	frvA	<	148	Transport and binding proteins	B
o0757	b3899	frvB	<	485	Transport and binding proteins	Bsu
	b3900	frvA	<	148	Transport and binding proteins	Bsu
o0758	b3902	rhaD	<	274	Carbon compound catabolism	Bsu
	b3903	rhaA	<	419	Carbon compound catabolism	Bsu
o0758	b3902	rhaD	<	274	Carbon compound catabolism	B
	b3903	rhaA	<	419	Carbon compound catabolism	B
	b3904	rhaB	<	489	Carbon compound catabolism	B
o0758	b3903	rhaA	<	419	Carbon compound catabolism	Hin
	b3904	rhaB	<	489	Carbon compound catabolism	Hin
o0759	b3905	rhaS	>	278	Carbon compound catabolism	B Eco
	b3906	rhaR	>	312	Carbon compound catabolism	B Eco
o0760	b3911	cpxA	<	457	Regulatory function	B Bsu Eco Hin Hpy Mth Syn
	b3912	cpxR	<	232	Putative regulatory proteins	B Bsu Eco Hin Hpy Mth Syn
o0761	b3913	b3913	>	49	"Hypothetical, unclassified, unknown"	B
	b3914	b3914	>	122	"Hypothetical, unclassified, unknown"	B
o0762	b3922	yiiS	>	99	"Hypothetical, unclassified, unknown"	B
	b3923	yiiT	>	142	Putative regulatory proteins	B
o0763	b3926	glpK	<	502	Central intermediary metabolism	B Bsu Hin
	b3927	glpF	<	281	Transport and binding proteins	B Bsu Hin
o0764	b3929	menG	<	161	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Hin
	b3930	menA	<	308	"Biosynthesis of cofactors, prosthetic groups and carriers"	B Hin
o0765	b3931	hslU	<	443	"Cell processes (incl. adaptation, protection)"	B Bsu Hin Hpy
	b3932	hslV	<	176	"Translation, post-translational modification"	B Bsu Hin Hpy
o0766	b3939	metB	>	386	Amino acid biosynthesis and metabolism	B Mth
	b3940	metL	>	810	Amino acid biosynthesis and metabolism	B Mth
o0767	b3945	gldA	<	380	Central intermediary metabolism	B
	b3946	talC	<	220	Energy metabolism	B
	b3947	ptsA	<	711	Transport and binding proteins	B
o0767	b3946	talC	<	220	Energy metabolism	Bsu
	b3947	ptsA	<	711	Transport and binding proteins	Bsu
o0768	b3949	frwC	>	359	Carbon compound catabolism	B Eco
	b3950	frwB	>	106	Carbon compound catabolism	B Eco
o0769	b3951	pflD	>	765	Energy metabolism	B Eco Hin Mth
	b3952	pflC	>	292	Energy metabolism	B Eco Hin Mth
o0770	b3958	argC	>	334	Amino acid biosynthesis and metabolism	B
	b3959	argB	>	258	Amino acid biosynthesis and metabolism	B
	b3960	argH	>	457	Amino acid biosynthesis and metabolism	B
o0771	b3963	yijC	>	234	"Hypothetical, unclassified, unknown"	B
	b3964	yijD	>	119	"Hypothetical, unclassified, unknown"	B
o0772	b3966	btuB	>	614	Transport and binding proteins	Syn
	b3967	murI	>	289	Cell structure	Syn

o0772	b3966	btuB	>	614	Transport and binding proteins	B
	b3967	murI	>	289	Cell structure	B
	b3968	rrsB	>		rRNA	B
	b3969	gltT	>		tRNA	B
	b3970	rrlB	>		rRNA	B
	b3971	rrfB	>		rRNA	B
o0773	b3972	murB	>	342	Cell structure	B
	b3973	birA	>	321	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0774	b3976	thrU	>		tRNA	B
	b3977	tyrU	>		tRNA	B
	b3978	glyT	>		tRNA	B
	b3979	thrT	>		tRNA	B
o0775	b3983	rplK	>	142	"Translation, post-translational modification"	B Hin Mge Mpn Mth
	b3984	rplA	>	234	"Translation, post-translational modification"	B Hin Mge Mpn Mth
o0776	b3985	rplJ	>	165	"Translation, post-translational modification"	B Hin Mge Mpn
	b3986	rplL	>	121	"Translation, post-translational modification"	B Hin Mge Mpn
o0777	b3987	rpoB	>	1342	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Mge Mja Mpn Mth Syn
	b3988	rpoC	>	1407	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Mge Mja Mpn Mth Syn
o0778	b3990	thiH	<	377	"Biosynthesis of cofactors, prosthetic groups and carriers"	Eco
	b3991	thiG	<	281	"Biosynthesis of cofactors, prosthetic groups and carriers"	Eco
o0778	b3990	thiH	<	377	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3991	thiG	<	281	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3992	thiF	<	245	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3993	thiE	<	211	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3994	thiC	<	631	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0778	b3991	thiG	<	281	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b3992	thiF	<	245	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0778	b3993	thiE	<	211	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
	b3994	thiC	<	631	"Biosynthesis of cofactors, prosthetic groups and carriers"	Bsu
o0779	b3996	yjaD	>	257	"Hypothetical, unclassified, unknown"	B
	b3997	hemE	>	354	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b3998	yjaF	>	225	"Hypothetical, unclassified, unknown"	B
	b3999	yjaG	>	196	"Hypothetical, unclassified, unknown"	B
o0780	b4000	hupA	>	90	"DNA replication, recombination, modification and repair"	B
	b4001	yjaH	>	231	"Hypothetical, unclassified, unknown"	B
o0781	b4005	purD	<	429	Nucleotide biosynthesis and metabolism	B Bsu Hin
	b4006	purH	<	529	Nucleotide biosynthesis and metabolism	B Bsu Hin
o0782	b4007	rrsE	>		rRNA	B
	b4008	gltV	>		tRNA	B
	b4009	rrlE	>		rRNA	B
	b4010	rrfE	>		rRNA	B
o0783	b4014	aceB	>	533	Central intermediary metabolism	B
	b4015	aceA	>	434	Central intermediary metabolism	B
	b4016	aceK	>	578	Central intermediary metabolism	B
o0784	b4027	yjbF	>	222	"Hypothetical, unclassified, unknown"	B
	b4028	yjbG	>	245	"Hypothetical, unclassified, unknown"	B
	b4029	yjbH	>	698	"Hypothetical, unclassified, unknown"	B
o0785	b4032	malG	<	296	Transport and binding proteins	Bsu Eco Hin Mge Mpn Syn
	b4033	malF	<	514	Transport and binding proteins	Bsu Eco Hin Mge Mpn Syn

o0785	b4032	malG	<	296	Transport and binding proteins	B Bsu Syn
	b4033	malF	<	514	Transport and binding proteins	B Bsu Syn
	b4034	malE	<	396	Transport and binding proteins	B Bsu Syn
o0785	b4033	malF	<	514	Transport and binding proteins	Hin
	b4034	malE	<	396	Transport and binding proteins	Hin
o0786	b4035	malK	>	371	Transport and binding proteins	Syn
	b4036	lamB	>	446	Transport and binding proteins	Syn
o0786	b4035	malK	>	371	Transport and binding proteins	B
	b4036	lamB	>	446	Transport and binding proteins	B
	b4037	malM	>	306	Carbon compound catabolism	B
o0786	b4036	lamB	>	446	Transport and binding proteins	Sce
	b4037	malM	>	306	Carbon compound catabolism	Sce
o0787	b4039	ubiC	>	202	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
	b4040	ubiA	>	290	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0788	b4043	lexA	>	202	Regulatory function	B
	b4044	dinF	>	459	"Hypothetical, unclassified, unknown"	B
o0789	b4047	yjbL	>	84	"Hypothetical, unclassified, unknown"	B
	b4048	yjbM	>	235	"Hypothetical, unclassified, unknown"	B
o0790	b4049	yjbN	>	345	"Hypothetical, unclassified, unknown"	B
	b4050	yjbO	>	150	"Hypothetical, unclassified, unknown"	B
o0791	b4056	yjbQ	>	138	"Hypothetical, unclassified, unknown"	B
	b4057	yjbR	>	118	"Hypothetical, unclassified, unknown"	B
o0792	b4067	yjcG	<	549	"Hypothetical, unclassified, unknown"	B
	b4068	yjcH	<	104	"Hypothetical, unclassified, unknown"	B
o0793	b4070	nrfA	>	478	Energy metabolism	Eco
	b4071	nrfB	>	190	Energy metabolism	Eco
o0793	b4070	nrfA	>	478	Energy metabolism	Hin
	b4071	nrfB	>	190	Energy metabolism	Hin
	b4072	nrfC	>	223	Energy metabolism	Hin
	b4073	nrfD	>	318	Energy metabolism	Hin
o0793	b4070	nrfA	>	478	Energy metabolism	B
	b4071	nrfB	>	190	Energy metabolism	B
	b4072	nrfC	>	223	Energy metabolism	B
	b4073	nrfD	>	318	Energy metabolism	B
	b4074	nrfE	>	552	Energy metabolism	B
	b4075	nrfF	>	127	Energy metabolism	B
	b4076	nrfG	>	198	Energy metabolism	B
o0793	b4071	nrfB	>	190	Energy metabolism	Hin
	b4072	nrfC	>	223	Energy metabolism	Hin
o0793	b4072	nrfC	>	223	Energy metabolism	Eco
	b4073	nrfD	>	318	Energy metabolism	Eco
o0793	b4073	nrfD	>	318	Energy metabolism	Bsu
	b4074	nrfE	>	552	Energy metabolism	Bsu
o0794	b4080	yjcP	<	488	Putative enzymes	B Sce
	b4081	yjcQ	<	636	Putative enzymes	B Sce
o0795	b4084	yjcT	<	309	"Cell processes (incl. adaptation, protection)"	B
	b4085	yjcU	<	231	Energy metabolism	B
	b4086	yjcV	<	326	Putative transport proteins	B
	b4087	yjcW	<	510	Putative transport proteins	B
o0795	b4086	yjcV	<	326	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn
	b4087	yjcW	<	510	Putative transport proteins	Bsu Eco Hin Hpy Mge Mja Mpn Mth Syn

o0796	b4091	phnQ	<	135	"Hypothetical, unclassified, unknown"	B
	b4092	phnP	<	252	Central intermediary metabolism	B
	b4093	phnO	<	144	Central intermediary metabolism	B
	b4094	phnN	<	185	Central intermediary metabolism	B
	b4095	phnM	<	378	Central intermediary metabolism	B
	b4096	phnL	<	226	Central intermediary metabolism	B
	b4097	phnK	<	252	Central intermediary metabolism	B
	b4098	phnJ	<	281	Central intermediary metabolism	B
	b4099	phnI	<	354	Central intermediary metabolism	B
	b4100	phnH	<	194	Central intermediary metabolism	B
	b4101	phnG	<	150	Central intermediary metabolism	B
	b4102	phnF	<	241	Central intermediary metabolism	B
	b4103	b4103	<	73	"Hypothetical, unclassified, unknown"	B
	b4104	phnE	<	206	Transport and binding proteins	B
	b4105	phnD	<	338	Transport and binding proteins	B
	b4106	phnC	<	262	Transport and binding proteins	B
o0796	b4096	phnL	<	226	Central intermediary metabolism	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
	b4097	phnK	<	252	Central intermediary metabolism	Bsu Eco Hin Hpy Mge Mja Mpn Sce Syn
o0796	b4097	phnK	<	252	Central intermediary metabolism	Bsu
	b4098	phnJ	<	281	Central intermediary metabolism	Bsu
o0796	b4105	phnD	<	338	Transport and binding proteins	Mpn
	b4106	phnC	<	262	Transport and binding proteins	Mpn
o0797	b4109	yjdA	>	742	Structural proteins	B Eco Syn
	b4110	yjcZ	>	281	"Hypothetical, unclassified, unknown"	B Eco Syn
o0798	b4112	basS	<	363	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Hpy Mth Syn
	b4113	basR	<	222	"Transcription, RNA processing and degradation"	B Bsu Eco Hin Hpy Mth Syn
o0799	b4116	adiY	<	253	Putative regulatory proteins	B
	b4117	adi	<	756	Amino acid biosynthesis and metabolism	B
o0800	b4119	melA	>	451	Carbon compound catabolism	B Eco
	b4120	melB	>	469	Transport and binding proteins	B Eco
o0801	b4124	yjdG	<	239	Putative regulatory proteins	B Bsu Eco Hin Hpy Syn
	b4125	yjdH	<	543	Putative regulatory proteins	B Bsu Eco Hin Hpy Syn
o0802	b4126	yjdI	>	76	"Hypothetical, unclassified, unknown"	B
	b4127	yjdJ	>	90	"Hypothetical, unclassified, unknown"	B
o0803	b4131	cadA	<	715	Amino acid biosynthesis and metabolism	Eco Hin
	b4132	cadB	<	444	Transport and binding proteins	Eco Hin
o0803	b4131	cadA	<	715	Amino acid biosynthesis and metabolism	B
	b4132	cadB	<	444	Transport and binding proteins	B
	b4133	cadC	<	512	Amino acid biosynthesis and metabolism	B
o0803	b4132	cadB	<	444	Transport and binding proteins	Syn
	b4133	cadC	<	512	Amino acid biosynthesis and metabolism	Syn
o0804	b4135	yjdC	<	199	"Hypothetical, unclassified, unknown"	B
	b4136	dsbD	<	565	Central intermediary metabolism	B
	b4137	cutA	<	112	"Cell processes (incl. adaptation, protection)"	B
o0805	b4142	mopB	>	97	"Cell processes (incl. adaptation, protection)"	B Bsu Hin Hpy Mge Syn
	b4143	mopA	>	548	"Cell processes (incl. adaptation, protection)"	B Bsu Hin Hpy Mge Syn
o0806	b4151	frdD	<	119	Energy metabolism	B
	b4152	frdC	<	131	Energy metabolism	B
	b4153	frdB	<	244	Energy metabolism	B
	b4154	frdA	<	602	Energy metabolism	B

o0806	b4153	frdB	<	244	Energy metabolism	Bsu Eco Hpy
	b4154	frdA	<	602	Energy metabolism	Bsu Eco Hpy
o0807	b4157	yjeN	>	104	"Hypothetical, unclassified, unknown"	B
	b4158	yjeO	>	104	"Hypothetical, unclassified, unknown"	B
o0808	b4159	yjeP	<	1107	Structural proteins	B
	b4160	psd	<	322	Fatty acid and phospholipid metabolism	B
o0809	b4167	yjeF	>	515	"Hypothetical, unclassified, unknown"	B
	b4168	yjeE	>	153	"Hypothetical, unclassified, unknown"	B
o0810	b4169	amiB	>	445	Cell structure	B
	b4170	mutL	>	615	"DNA replication, recombination, modification and repair"	B
	b4171	miaA	>	316	"Translation, post-translational modification"	B
	b4172	hfq	>	102	"phage, transposon, or plasmid"	B
	b4173	hflX	>	426	"Translation, post-translational modification"	B
	b4174	hflK	>	419	"Translation, post-translational modification"	B
	b4175	hflC	>	334	"Translation, post-translational modification"	B
o0810	b4170	mutL	>	615	"DNA replication, recombination, modification and repair"	Bsu
	b4171	miaA	>	316	"Translation, post-translational modification"	Bsu
o0810	b4171	miaA	>	316	"Translation, post-translational modification"	Bsu
	b4172	hfq	>	102	"phage, transposon, or plasmid"	Bsu
o0810	b4174	hflK	>	419	"Translation, post-translational modification"	Eco Hin
	b4175	hflC	>	334	"Translation, post-translational modification"	Eco Hin
o0811	b4178	yjeB	>	141	"Hypothetical, unclassified, unknown"	B
	b4179	vacB	>	827	"Hypothetical, unclassified, unknown"	B
o0812	b4181	yjfI	>	133	"Hypothetical, unclassified, unknown"	B
	b4182	yjfJ	>	232	Structural proteins	B
o0813	b4183	yjfK	>	219	"Hypothetical, unclassified, unknown"	B
	b4184	yjfL	>	132	"Hypothetical, unclassified, unknown"	B
	b4185	yjfM	>	212	"Hypothetical, unclassified, unknown"	B
	b4186	yjfC	>	387	Putative enzymes	B
o0813	b4185	yjfM	>	212	"Hypothetical, unclassified, unknown"	Eco
	b4186	yjfC	>	387	Putative enzymes	Eco
o0814	b4193	yjfS	>	484	"Hypothetical, unclassified, unknown"	B
	b4194	yjfT	>	101	"Hypothetical, unclassified, unknown"	B
	b4195	ptxA	>	154	Putative transport proteins	B
	b4196	yjfV	>	216	"Hypothetical, unclassified, unknown"	B
	b4197	yjfW	>	284	"Hypothetical, unclassified, unknown"	B
	b4198	b4198	>	228	Carbon compound catabolism	B
o0814	b4194	yjfT	>	101	"Hypothetical, unclassified, unknown"	Eco
	b4195	ptxA	>	154	Putative transport proteins	Eco
o0814	b4195	ptxA	>	154	Putative transport proteins	Mpn
	b4196	yjfV	>	216	"Hypothetical, unclassified, unknown"	Mpn
	b4197	yjfW	>	284	"Hypothetical, unclassified, unknown"	Mpn
o0814	b4196	yjfV	>	216	"Hypothetical, unclassified, unknown"	Eco
	b4197	yjfW	>	284	"Hypothetical, unclassified, unknown"	Eco
	b4198	b4198	>	228	Carbon compound catabolism	Eco
o0814	b4197	yjfW	>	284	"Hypothetical, unclassified, unknown"	Hin
	b4198	b4198	>	228	Carbon compound catabolism	Hin
o0815	b4200	rpsF	>	131	"Translation, post-translational modification"	Bsu
	b4201	priB	>	104	"DNA replication, recombination, modification and repair"	Bsu
	b4202	rpsR	>	75	"Translation, post-translational modification"	Bsu

o0815	b4200	rpsF	>	131	"Translation, post-translational modification"	B Hin
	b4201	priB	>	104	"DNA replication, recombination, modification and repair"	B Hin
	b4202	rpsR	>	75	"Translation, post-translational modification"	B Hin
	b4203	rplI	>	149	"Translation, post-translational modification"	B Hin
o0815	b4202	rpsR	>	75	"Translation, post-translational modification"	Mge Mpn
	b4203	rplI	>	149	"Translation, post-translational modification"	Mge Mpn
o0816	b4220	ytfM	>	577	"Hypothetical, unclassified, unknown"	Eco Hin Sce
	b4221	ytfN	>	1259	"Hypothetical, unclassified, unknown"	Eco Hin Sce
o0816	b4220	ytfM	>	577	"Hypothetical, unclassified, unknown"	B
	b4221	ytfN	>	1259	"Hypothetical, unclassified, unknown"	B
	b4222	ytfP	>	113	"Hypothetical, unclassified, unknown"	B
o0817	b4224	chpS	>	85	Other known genes	B Eco
	b4225	chpB	>	116	Other known genes	B Eco
o0818	b4228	ytfR	>	417	Putative transport proteins	Bsu Eco Hin Hpy Mge Mpn Sce Syn
	b4229	ytfS	>	90	Putative transport proteins	Bsu Eco Hin Hpy Mge Mpn Sce Syn
o0818	b4228	ytfR	>	417	Putative transport proteins	Bsu Eco
	b4229	ytfS	>	90	Putative transport proteins	Bsu Eco
	b4230	ytfT	>	341	Putative transport proteins	Bsu Eco

operon#	b#	gene	dir	length	function	species
o0818	b4228	ytfR	>	417	Putative transport proteins	B
	b4229	ytfS	>	90	Putative transport proteins	B
	b4230	ytfT	>	341	Putative transport proteins	B
	b4231	yjfF	>	323	Putative transport proteins	B
o0818	b4229	ytfS	>	90	Putative transport proteins	Bsu Eco Hin Mth Syn
	b4230	ytfT	>	341	Putative transport proteins	Bsu Eco Hin Mth Syn
o0818	b4229	ytfS	>	90	Putative transport proteins	Bsu Eco
	b4230	ytfT	>	341	Putative transport proteins	Bsu Eco
	b4231	yjfF	>	323	Putative transport proteins	Bsu Eco
o0818	b4230	ytfT	>	341	Putative transport proteins	Bsu Eco Mge Mja Syn
	b4231	yjfF	>	323	Putative transport proteins	Bsu Eco Mge Mja Syn
o0819	b4239	treC	<	551	Carbon compound catabolism	B Bsu
	b4240	treB	<	473	Transport and binding proteins	B Bsu
o0820	b4244	pyrI	<	153	Nucleotide biosynthesis and metabolism	B
	b4245	pyrB	<	311	Nucleotide biosynthesis and metabolism	B
o0821	b4258	valS	<	951	"Translation, post-translational modification"	B
	b4259	holC	<	147	"DNA replication, recombination, modification and repair"	B
o0822	b4261	yjgP	>	366	"Hypothetical, unclassified, unknown"	B Eco Hin
	b4262	yjgQ	>	361	"Hypothetical, unclassified, unknown"	B Eco Hin
o0823	b4266	yjgU	<	254	Putative enzymes	B
	b4267	yjgV	<	343	Putative enzymes	B
o0824	b4272	b4272	>	136	"Hypothetical, unclassified, unknown"	B Eco
	b4273	b4273	>	301	"phage, transposon, or plasmid"	B Eco
o0825	b4275	yjgX	<	148	"Hypothetical, unclassified, unknown"	B
	b4276	yjgY	<	149	"Hypothetical, unclassified, unknown"	B
o0826	b4279	yjhB	>	425	"Hypothetical, unclassified, unknown"	B Bsu
	b4280	yjhC	>	377	Putative enzymes	B Bsu
o0827	b4287	fecE	<	255	Transport and binding proteins	Bsu Hin Hpy
	b4288	fecD	<	318	Transport and binding proteins	Bsu Hin Hpy

o0827	b4287	fecE	<	255	Transport and binding proteins	Bsu Eco Syn
	b4288	fecD	<	318	Transport and binding proteins	Bsu Eco Syn
	b4289	fecC	<	332	Transport and binding proteins	Bsu Eco Syn
o0827	b4287	fecE	<	255	Transport and binding proteins	Bsu
	b4288	fecD	<	318	Transport and binding proteins	Bsu
	b4289	fecC	<	332	Transport and binding proteins	Bsu
	b4290	fecB	<	302	Transport and binding proteins	Bsu
o0827	b4287	fecE	<	255	Transport and binding proteins	B
	b4288	fecD	<	318	Transport and binding proteins	B
	b4289	fecC	<	332	Transport and binding proteins	B
	b4290	fecB	<	302	Transport and binding proteins	B
	b4291	fecA	<	774	Transport and binding proteins	B
	b4292	fecR	<	317	Transport and binding proteins	B
	b4293	fecI	<	173	Transport and binding proteins	B
o0827	b4288	fecD	<	318	Transport and binding proteins	Bsu Eco Mja Syn
	b4289	fecC	<	332	Transport and binding proteins	Bsu Eco Mja Syn
o0827	b4288	fecD	<	318	Transport and binding proteins	Bsu
	b4289	fecC	<	332	Transport and binding proteins	Bsu
	b4290	fecB	<	302	Transport and binding proteins	Bsu
o0827	b4289	fecC	<	332	Transport and binding proteins	Eco Hin
	b4290	fecB	<	302	Transport and binding proteins	Eco Hin
o0827	b4290	fecB	<	302	Transport and binding proteins	Eco Syn
	b4291	fecA	<	774	Transport and binding proteins	Eco Syn
o0828	b4297	yjhG	<	655	Putative enzymes	Eco
	b4298	yjhH	<	319	"Hypothetical, unclassified, unknown"	Eco
o0828	b4297	yjhG	<	655	Putative enzymes	B
	b4298	yjhH	<	319	"Hypothetical, unclassified, unknown"	B
	b4299	yjhI	<	262	Putative regulatory proteins	B
o0829	b4300	yjhJ	<	260	Putative regulatory proteins	B
	b4301	yjhK	<	210	"Hypothetical, unclassified, unknown"	B
	b4302	yjhL	<	143	"Hypothetical, unclassified, unknown"	B
o0830	b4303	yjhM	<	268	Putative enzymes	B
	b4304	yjhN	<	437	Transport and binding proteins	B
o0831	b4310	yjhT	<	404	"Hypothetical, unclassified, unknown"	B
	b4311	yjhA	<	241	"Hypothetical, unclassified, unknown"	B
o0832	b4312	fimB	>	200	Cell structure	Eco
	b4313	fimE	>	198	Cell structure	Eco
o0832	b4312	fimB	>	200	Cell structure	B
	b4313	fimE	>	198	Cell structure	B
	b4314	fimA	>	182	Cell structure	B
	b4315	fimI	>	215	Cell structure	B
	b4316	fimC	>	241	Cell structure	B
	b4317	fimD	>	878	Cell structure	B
	b4318	fimF	>	176	Cell structure	B
	b4319	fimG	>	167	Cell structure	B
	b4320	fimH	>	300	Cell structure	B
o0832	b4314	fimA	>	182	Cell structure	Eco
	b4315	fimI	>	215	Cell structure	Eco
o0832	b4314	fimA	>	182	Cell structure	Eco
	b4315	fimI	>	215	Cell structure	Eco
	b4316	fimC	>	241	Cell structure	Eco

o0832	b4315	fimI	>	215	Cell structure	Eco
	b4316	fimC	>	241	Cell structure	Eco
	b4317	fimD	>	878	Cell structure	Eco
o0832	b4315	fimI	>	215	Cell structure	Eco
	b4316	fimC	>	241	Cell structure	Eco
	b4317	fimD	>	878	Cell structure	Eco
	b4318	fimF	>	176	Cell structure	Eco
	b4319	fimG	>	167	Cell structure	Eco
o0832	b4316	fimC	>	241	Cell structure	Eco
	b4317	fimD	>	878	Cell structure	Eco
o0832	b4316	fimC	>	241	Cell structure	Eco
	b4317	fimD	>	878	Cell structure	Eco
	b4318	fimF	>	176	Cell structure	Eco
o0832	b4317	fimD	>	878	Cell structure	Eco
	b4318	fimF	>	176	Cell structure	Eco
o0832	b4317	fimD	>	878	Cell structure	Eco
	b4318	fimF	>	176	Cell structure	Eco
	b4319	fimG	>	167	Cell structure	Eco
	b4320	fimH	>	300	Cell structure	Eco
o0832	b4318	fimF	>	176	Cell structure	Eco
	b4319	fimG	>	167	Cell structure	Eco
o0832	b4319	fimG	>	167	Cell structure	Eco
	b4320	fimH	>	300	Cell structure	Eco
o0833	b4322	uxuA	>	394	Carbon compound catabolism	B
	b4323	uxuB	>	486	Carbon compound catabolism	B
o0834	b4328	iadA	<	390	"Translation, post-translational modification"	B
	b4329	yjiG	<	153	"Hypothetical, unclassified, unknown"	B
	b4330	yjiH	<	231	"Hypothetical, unclassified, unknown"	B
o0834	b4329	yjiG	<	153	"Hypothetical, unclassified, unknown"	Eco
	b4330	yjiH	<	231	"Hypothetical, unclassified, unknown"	Eco
o0835	b4334	yjiL	<	257	Putative enzymes	B
	b4335	yjiM	<	390	"Hypothetical, unclassified, unknown"	B
o0836	b4336	yjiN	<	426	"Hypothetical, unclassified, unknown"	B Eco
	b4337	yjiO	<	410	Putative transport proteins	B Eco
o0837	b4338	yjiP	>	103	"Hypothetical, unclassified, unknown"	B
	b4339	yjiQ	>	186	"Hypothetical, unclassified, unknown"	B
o0838	b4343	b4343	>	513	"Hypothetical, unclassified, unknown"	B
	b4344	mcrD	>	420	"Transcription, RNA processing and degradation"	B
o0839	b4345	mcrC	<	348	"Transcription, RNA processing and degradation"	B Bsu Sce
	b4346	mcrB	<	465	"Transcription, RNA processing and degradation"	B Bsu Sce
o0840	b4348	hsdS	<	464	"DNA replication, recombination, modification and repair"	B Mth
	b4349	hsdM	<	529	"DNA replication, recombination, modification and repair"	B Mth
o0841	b4353	yjiX	<	67	"Hypothetical, unclassified, unknown"	B
	b4354	yjiY	<	721	"Cell processes (incl. adaptation, protection)"	B
o0842	b4361	dnaC	<	245	"DNA replication, recombination, modification and repair"	B Bsu Eco
	b4362	dnaT	<	179	"DNA replication, recombination, modification and repair"	B Bsu Eco
o0843	b4365	yjjQ	>	241	Putative regulatory proteins	B Eco
	b4366	yjjR	>	225	Putative regulatory proteins	B Eco
o0844	b4368	leuV	<		tRNA	B
	b4369	leuP	<		tRNA	B
	b4370	leuQ	<		tRNA	B

o0845	b4372	holD	>	137	"DNA replication, recombination, modification and repair"	B
	b4373	rimI	>	148	"Translation, post-translational modification"	B
	b4374	yjjG	>	225	Putative enzymes	B
	b4375	prfC	>	529	"Translation, post-translational modification"	B
	b4376	osmY	>	201	"Cell processes (incl. adaptation, protection)"	B
o0845	b4375	prfC	>	529	"Translation, post-translational modification"	Hin Mja
	b4376	osmY	>	201	"Cell processes (incl. adaptation, protection)"	Hin Mja
o0846	b4379	yjjW	<	287	Energy metabolism	B Eco Hin
	b4380	yjjI	<	516	"Hypothetical, unclassified, unknown"	B Eco Hin
o0847	b4381	deoC	>	259	Nucleotide biosynthesis and metabolism	Mge Mpn Mth Syn
	b4382	deoA	>	440	Nucleotide biosynthesis and metabolism	Mge Mpn Mth Syn
o0847	b4381	deoC	>	259	Nucleotide biosynthesis and metabolism	B
	b4382	deoA	>	440	Nucleotide biosynthesis and metabolism	B
	b4383	deoB	>	407	Nucleotide biosynthesis and metabolism	B
	b4384	deoD	>	239	Nucleotide biosynthesis and metabolism	B
o0847	b4382	deoA	>	440	Nucleotide biosynthesis and metabolism	Syn
	b4383	deoB	>	407	Nucleotide biosynthesis and metabolism	Syn
o0847	b4383	deoB	>	407	Nucleotide biosynthesis and metabolism	Hpy
	b4384	deoD	>	239	Nucleotide biosynthesis and metabolism	Hpy
o0848	b4386	lplA	<	338	"Translation, post-translational modification"	B
	b4387	smp	<	214	"Hypothetical, unclassified, unknown"	B
o0849	b4388	serB	>	322	Amino acid biosynthesis and metabolism	B
	b4389	sms	>	460	"Translation, post-translational modification"	B
	b4390	nadR	>	417	"Biosynthesis of cofactors, prosthetic groups and carriers"	B
o0850	b4397	creA	>	157	"Hypothetical, unclassified, unknown"	B
	b4398	creB	>	229	Regulatory function	B
	b4399	creC	>	474	Regulatory function	B
	b4400	creD	>	450	"phage, transposon, or plasmid"	B
o0850	b4398	creB	>	229	Regulatory function	Bsu Eco Hin Hpy Mth Syn
	b4399	creC	>	474	Regulatory function	Bsu Eco Hin Hpy Mth Syn
o0850	b4399	creC	>	474	Regulatory function	Hin
	b4400	creD	>	450	"phage, transposon, or plasmid"	Hin