

Construction of a Contiguous 874-kb Sequence of the *Escherichia coli* -K12 Genome Corresponding to 50.0–68.8 min on the Linkage Map and Analysis of Its Sequence Features

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Abstract

The contiguous 874,423 base pair sequence corresponding to the 50.0–68.8 min region on the genetic map of the *Escherichia coli* K-12 (W3110) was constructed by the determination of DNA sequences in the 50.0–57.9 min region (360 kb) and two large (100 kb in all) and five short gaps in the 57.9–68.8 min region whose sequences had been registered in the DNA databases. We analyzed its sequence features and found that this region contained at least 894 potential open reading frames (ORFs), of which 346 (38.7%) were previously reported, 158 (17.7%) were homologous to other known genes, 232 (26.0%) were identical or similar to hypothetical genes registered in databases, and the remaining 158 (17.7%) showed no significant similarity to any other genes. A homology search of the ORFs also identified several new gene clusters. Those include two clusters of fimbrial genes, a gene cluster of three genes encoding homologues of the human long chain fatty acid degradation enzyme complex in the mitochondrial membrane, a cluster of at least nine genes involved in the utilization of ethanolamine, a cluster of the secondary set of 11 *hyc* genes participating in the formate hydrogenlyase reaction and a cluster of five genes coding for the homologues of degradation enzymes for aromatic hydrocarbons in *Pseudomonas putida*. We also noted a variety of novel genes, including two ORFs, which were homologous to the putative genes encoding xanthine dehydrogenase in the fly and a protein responsible for axonal guidance and outgrowth of the rat, mouse and nematode. An isoleucine tRNA gene, designated *ileY*, was also newly identified at 60.0 min.

Key words: *Escherichia coli* K12; genome sequence; position of 50.0–68.8 min; ORF analysis

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1. Introduction

The complete DNA sequences of the genomes of four prokaryotes, *Haemophilus influenzae*,¹ *Mycoplasma*

genitulum,² *Methanococcus jannaschii*,³ *Synechocystis* sp. strain PCC6803⁴ and *Myc. pneumoniae*,⁵ and one eucaryote, *Saccharomyces cerevisiae*,⁶ has been documented. Since *Escherichia coli* has been thoroughly analyzed genetically and biochemically,⁷ completion of the genomic analysis is important not only for studies on the cellular processes of *E. coli* itself but also as a reference for the structures and functions of genes in other organisms. By the end of 1996, about 80% of the *E. coli* genome had been systematically sequenced.^{8–18}

The *E. coli* genome project in Japan was initiated in 1989 to analyze the sequence of the circular *E. coli* genome from 0 minutes in the clockwise direction and the contiguous DNA sequence from 0 to 50 minutes has been determined and registered in databases.^{8–12} In the present study, we analyzed the nucleotide sequence of the region from 50.0 to 68.8 minutes. When the contiguous sequence of the 0–68.8 min region was combined with that of the 68.8–100 min region reported by Blattner and coworkers,^{13–18} the entire *E. coli* genome can now be expressed as a single nucleotide sequence comprised of 4,636,552 base pairs. Characterization of this sequence showed that the *E. coli* genome contains 4803 possible open reading frames (ORFs). These results will be published elsewhere. At the same time, Blattner and coworkers independently determined the complete nucleotide sequence of the entire *E. coli* genome.

2. Materials and Methods

All materials and methods used in this work were described in previous reports.^{10–12} DNA samples were from miniset clones of Kohara et al.,¹⁹ #376, #377, #379, #380, #401, #403, #404, #405, #406, #407, #409, #410, #411, #412, #414, #416, #417, #418, #419, #420, #421, #422, #423, #424, #425, #427, #428, #429, #430, #431, #432, #436, #437, #438, #442, #443, #445, and #446. Two gaps, one between clone gaps #432 and #436 and the other between gaps #438 and #442, were filled by sequence data: accession nos. ECU36841 and ECOK12RIII for the former and ECU36840 for the latter, those of which had been registered by Blattner and colleagues for ECU number and Nashimoto and coworkers for ECOKRIII. The former and latter gaps were named 432–436 and wiscl, respectively. As the DNA sequence from the right end of clone #446 to the left end of ECU28379, we named this region wisc2, the following sequence data, accession numbers #ECU29579, 29580, 29581, 28375, 28377 and 28379, were used. Five gaps observed between pairs of those sequences were determined by analysis of long or normal polymerase chain reaction (PCR) products which were amplified with *E. coli* genomic DNA as a template, and with a pair of appropriate synthetic primers.

3. Results and Discussions

3.1. Assignment of potential coding frames

We determined the complete nucleotide sequence of 874,423 base pairs (bp) using the sequencing strategy previously described.¹⁰ This sequence corresponded to the 50.0–68.8 min region of the *E. coli* genetic map. First 20,867 bp of this sequence overlapped with those of the terminal part of the 40.1–50.0 min region reported in the previous paper.¹² To predict coding frames, we first selected potential ORFs composed of over 50 consecutive sense codons. All these ORFs were translated into amino acid sequences and subjected to similarity analysis against the SWISSPROT and PIR protein databases using the BLASTP program.²⁰ When the ORFs showed more than 95% identity in sequence and consistency to known gene products, they were referred to as known genes. New ORFs with BLASTP scores of more than 100 were classified as either homologous or hypothetical according to their functions. When the function of the reported ORFs or genes was known, the corresponding ORFs were classified as homologous; when the function of the reported ORFs was not known, the corresponding ORFs were classified as hypothetical. The ORFs that could not be predicted by BLASTP were predicted either using the program GeneMark²¹ or visually. In the latter case, the possible NH₂-terminus of each predicted ORF was estimated by calculating the efficiency of the ribosomal binding site for translation by scoring matrix.²² These ORFs were also classified as new hypothetical. Specific sequences other than ORFs were checked by the FASTA program. The nomenclature of the predicted ORFs was based on the consecutive number of ORFs found in each of the clones of Kohara et al.¹⁹, for example, the ORF designated as o462#1 was ORF number 1 in miniset clone 462. Similarly, owisc2#359 denotes ORF number 359 in a region, termed wisc2, between the left end of clone #446 and the right end of ECOW67.

Computational analysis of the sequence identified at least 894 potential ORFs, as summarized in Table 1 and illustrated in the Supplement. Among them, 346 (38.7%) ORFs were identified as known genes reported previously. One hundred and fifty-eight (17.7%) and 232 (26.0%) ORFs were identified as homologues of known genes and hypothetical genes, respectively. The remaining 158 (17.7%) ORFs showed no significant similarity to any other gene registered in the databases.

3.2. Unique new ORFs

Homology analysis of all ORFs against the SWISSPROT and PIR databases revealed the presence of two fibrin(ogen) (fibr) gene clusters. One cluster located at 52.9 min contained four ORFs, o409#7, o409#8, o409#9 and o409#10. The products of o409#7 were a homo-

logue of *Proteus mirabilis* periplasmic chaperon protein PmFD, while the products of o409#8 and o409#9 were homologues of an *E. coli* outer membrane usher protein, PapC. o409#10 showed significant similarity to the *Serratia marcescens* fimbria A protein, a major fimbriae subunit. The other located at 68.6 min, contained three ORFs: owisc2#359, owisc2#360 and owisc2#361. The products of the first two ORFs were homologous to usher and the product of the last ORFs to a chaperon.

At the 5' region of the first fimbrial gene cluster, there are three ORFs, o409#12, o409#13, and o409#14 which encode proteins showing a significant similarity (40% and more) to a human mitochondrial trifunctional enzyme complex. The first and the latter two ORFs are homologues to α and β subunits, respectively. The human enzymes are involved in the β -oxidation pathway of fatty acid degradation and correspond to *E. coli fadA* and *fadB* products which are cytoplasmic proteins. Pawar and Schulz reported that in addition to *fadA* and *fadB* products, *E. coli* also contains a separate long-chain enoyl CoA hydratase that may be membrane bound.²³ Thus, our identified ORFs may encode membrane-bound type FadA- and FadB-like proteins. It should be noted that the *fadL* (o410#1) gene encoding a long-chain fatty acid transport protein is located at the 5' region of this gene cluster, although the orientation is opposite that of the gene cluster.

The attachment site of a lysogenic phage PA-2 is mapped at 53.2 min, close to where an arginine t-RNA gene, *argW*,²⁴ is placed. In this site, there is an ORF (o410#4) encoding a putative prophage SF6-like integrase. In addition, several ORFs (o410#7-o410#10), whose products are homologous (40–83%) to proteins encoded by the genes within the e14 element, a cryptic prophage located at 25.8 min,¹⁰ and one ORF (o411#4), which is homologous (31.2%) to the lambda phage O gene, though the size is smaller than that of the original O protein, are also found in this region. Thus, the region between the o410#4 and the O homologous gene may be a cryptic prophage.

Salmonella has a *cut* gene cluster which consists of more than seven genes encoding ethanolaniline utilization proteins, at 53.3 minutes on the linkage map. We identified an *E. coli* corresponding to the gene cluster at 55.2 minutes. The *E. coli cut*-like gene cluster is composed of more than nine genes, among which each product of the seven ORFs (o421#2, o421#3, o421#4, o421#5, o421#6, o421#7 and o421#8) shows a high similarity (more than 80% except *chA*) to each of the *Salmonella* corresponding genes, *cutH*, *cutG*, *cutJ*, *cutE*, *cutB*, *cutA*, and *cutI*.²⁵ The order of their genes matches perfectly. Thus, these *E. coli cut*-like genes may form an operon with a function similar to that of the *cut* operon in *Salmonella*. The *Salmonella cutR* gene is located at the distal end of the gene cluster and encodes

a transcriptional positive regulator protein for the *cut* operon. Because an ORF (o420#5, *yjcG*) is placed at the corresponding site of the *E. coli cut*-like gene cluster and its product belongs to a family of *araC/xylS* type transcriptional regulator, it may be a counterpart of the *cutR* gene.

At 56.1 minutes, a large gene cluster is present and consists of more than 12 genes which are apparently involved in the formate hydrogelyase reaction. This reaction is known to be carried out by proteins which are encoded in the *hyc* operon at 61.3 minutes.²⁶ Thus, the cluster we found is probably a secondary set of *hyc* genes. The cluster contains six ORFs (o423#10, o423#11, o424#4, o424#5, o424#6 and o424#7), the products of which showed close similarity (more than 45%) to the corresponding products of the *hycC*, *hycD*, *hycE*, *hycF*, *hycG* and *hycH* genes and they were in the same order. In addition, at the distal end of the gene cluster, we noted two ORFs; one (o425#1) encodes protein similar (51.2%) to FhlA, a positive regulator for the *hyc* operon, and other (o425#3) codes for a protein homologous (50.5%) to a probable formate transporter which is encoded in the *focA* gene. In this cluster, three additional genes (o424#1, o424#2 and o424#3), all of which seem to function in the dehydrogenase reaction, are inserted among *hycD*- and *hycE*-like genes.

In *E. coli*, the presence of a serine/threonine protein kinase homologue has not been described. An ORF (o427#9) at 56.6 min shows 32.8% homology with serine/threonine protein kinase in a prokaryote, *Streptomyces coelicolor*.²⁷ The *Streptomyces* enzyme has protein kinase activity, which is located at the first half of the protein. However, similarity of product of the o427#9 to the *Streptomyces* kinase is restricted to the latter half of the enzyme, hence the o427#9 product may not have kinase activity. On the other hand, serine/threonine protein phosphatase may be present in *E. coli*, because the owisc#33 noted in the present study is a homologue of serine/threonine protein phosphatase of phage lambda as well as o336#5 at 41.3 min, as mentioned in the previous report.¹²

We identified a gene cluster at 57.5 min, in which all five ORFs (o431#1, o431#3, o431#4, o431#5, o431#6) showed significant similarity (30–49%) to *Pseudomonas* genes participating in the metabolic pathway for degradation of aromatic hydrocarbon, such as benzene or biphenyl. They encode five proteins; α and β subunits of benzene dioxygenase, ferredoxin, and biphenyl derivative dehydrogenase and ferredoxin-NAD(+) reductase in biphenyl dioxygenase system, respectively. This suggests that *E. coli* cells may have the potential for partial degradation of such carbon sources.

At a site neighboring the cluster, there is a sugar transport gene cluster consisting of four ORFs (o432#1, o431#11, o431#10 and o431#9). The product of the first

one is similar (26.3%) to D-galactose-binding protein, the second is a galactoside transport ATP-binding protein (37.2%), the third is L-arabinose permease (33.0%) and the fourth is sorbitol dehydrogenase (31.6%). Thus, while the sugar substrate for this system is unknown it is a typical ABC type transport system.²⁸

There is a cluster of four genes at 64.4 min, all of which are related to invasion into host cells, with virulence. The product of *owisc2#150* (correspond to ORF_o163 in accession #ECU28375; the all following ORFs are in the same accession no.) is a homologue related to virulence, the structural gene of which is on a plasmid in *Shigella*. Products of *owisc2#151* (=ORF_o458) and *owisc2#152* (=ORF_o138) are homologues of an activator for expression of the invasive gene in *Salmonella*. An ORF_owisc2#153 (=ORF_f148), encodes protein, the *Bordetella* homologue of which is a putative transcriptional regulator of a two-component system for virulence factors.

At about 64.6 min, there is a 20-kb region flanked by two ORFs (*owisc2#161*=ORF_o752 and *owisc2#178*=ORF_o956), both encoding xanthine dehydrogenase homologues of two kinds of fly (*Drosophila* and *Calliphora*). In this region, three ORFs, *owisc2#166* (=ORF_o363), *owisc2#168* (=ORF_o403) and *owisc2#170* (=ORF_o310), were homologous to genes related to the final two steps in the reactions in the biosynthesis of arginine. In addition, *owisc2#164* (=ORF_o159) encodes a protein which shows a significant similarity (45.6%) to a small subunit of carbon monoxide dehydrogenase in *Pseudomonas carboxydovorans*. The product of *owisc2#169* (=ORF_o465) showed significant similarity to a rat and mouse 64-kd protein, called TOAD-64 and Ullip, respectively and a protein in *Caenorhabditis elegans*, named *unc-33*, and all are thought to be involved in axon guidance and outgrowth. The Ullip is reported to have high similarity (about 40%) to D-hydroantoinase of *P. putida*.²⁹ Indeed, the product of the *owisc2#169* showed a significant similarity to the *P. hydroantoinase*. Thus, the *owisc2#169* product may have hydroantoinase or its related activity.

3.3. Other features

In the 50.0–68.8 min region, there are four open spaces at about 53.2 min, 53.3 min, 60.0 min and 64.2 min with few or no ORF. The striking example is a region between two ORFs, o442#14 (*gpiA*) and o443#1, at about 60.0 min. Within this region of about 8 kb, there are only two protein-encoding genes; the first (o442#17) is *pin*-like (DNA invertase) and the second (o442#18) is an amylase homologue, and the both genes are short. Between these two genes, we identified a new ile-tRNA gene, which will be described later. Though this region may contain a cryptic prophage, it is curious why so large an

open space exists.

The *seeA* and *sseB* genes, whose mutants enhance sensitivity for serine, were reported to locate at 54.8 minutes on the genetical and physical map.²⁴ However, we found their location to be at 57.1 min, about 100 kb from the reported site. The case of the *uraB* gene is similar; the gene is involved in the utilization of hexuronate and is reported to be at 56.1 minutes on the genetical and physical maps. Here, too, we noted the location to be at 34.6 min,¹¹ close to one of DNA replication termination sites, *TerC*.

tRNA genes and IS elements are located at the sites reported (see Fig. 1 in the Supplement). Of the 19 tRNA genes identified, one is located between the two ORFs (o442#17 and o442#18) at 60.0 min, the large open space mentioned above. This gene seems to code for a newly identified ile-tRNA, tentatively named *iley*. The nucleotide sequence predicted from the mature tRNA molecule of *iley* gene was the same as that of *ileX*, except for two separate nucleotides. This *ileX* tRNA gene located at 69.2 min is unique because although three other *ile*-tRNA genes are in a spacer region between 16S and 23S rRNA genes in three different rRNA (*rnn*) operons, the *ileX* tRNA gene exists in a isolated form.³⁰ Thus, *iley* is another *ileX*-type tRNA gene. In the 50–68.8 min region, there is one *rnn* operon, *rnnG*, and two stable RNA genes, *ssrA* at 59.2 min and *ssrS* at 65.8 min, as indicated in the figure in the Supplement. The exact location of repeated sequences (BIME, RSA, IRU, iap and BoxC) and *cis*-elements (DNA replication terminus: *Ter*, recombination hotspot sequence: *Chi*) are also indicated.

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Table 1. List of open reading frames of known, suggested or hypothetical genes.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o376#1	127	531	50.2	135	+	840	72.2	176	(<i>THL, THI, HI0771</i>)		P44873	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	<i>Haemophilus influenzae</i>
o376#2	1384	611	50.2	258	-	no_similarity							
o376#3	3038	1392	50.3	549	-	no_similarity							
o376#4	3524	3042	50.3	161	-	no_similarity							
o376#5	7643	3543	50.4	1367	-	no_similarity							
o376#6	8200	7580	50.4	207	-	no_similarity							
o376#7	9885	8200	50.4	562	-	1585	100.0	243			S03759	Hypothetical protein (<i>gyrA</i> 3' region)	<i>Escherichia coli</i>
o376#8	12661	10037	50.5	875	-	5589	100.0	875	<i>gyrA, parD, nalA, hisW</i>		P09097	DNA gyrase subunit A (EC 5.99.1.3).	<i>Escherichia coli</i>
o376#9	12808	13527	50.5	240	+	1623	100.0	240	<i>ubiG</i>		A47682	2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone methyltransferase, UbiG	<i>Escherichia coli</i>
o376#10	17416	13661	50.6	1252	-	2053	93.4	348		<i>yfaL</i>	P45508	Hypothetical 36.4 Kd protein in <i>ubiG-nrdA</i> intergenic region.	<i>Escherichia coli</i>
o377#1	18106	20388	50.6	761	+	5021	99.7	761	<i>nrdA, dnaF</i>		P00452	Ribonucleoside-diphosphate reductase 1 α chain (EC 1.17.4.1)	<i>Escherichia coli</i>
o377#2	20625	21752	50.6	376	+	2488	100.0	376	<i>nrdB</i>		A00527	Ribonucleoside-diphosphate reductase (EC 1.17.4.1) β chain	<i>Escherichia coli</i>
o377#3	21755	22006	50.7	84	+	577	98.8	84		<i>yfaE</i>	P37910	Hypothetical 9.3 Kd protein in <i>nrdB</i> 5' region.	<i>Escherichia coli</i>
o377#4	22713	22066	50.7	216	-	1452	98.1	216	<i>inaA</i>		P27294	InaA protein.	<i>Escherichia coli</i>
o377#5	22928	23131	50.7	68	+	440	100.0	68		<i>yfaH</i>	P45505	Hypothetical 7.5 Kd protein in <i>inaA-glpQ</i> intergenic region.	<i>Escherichia coli</i>
o377#6	24252	23179	50.7	358	-	2406	100.0	358	<i>glpQ</i>		S15945	Glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor, periplasmic	<i>Escherichia coli</i>
o377#7	25615	24260	50.8	452	-	3123	100.0	452	<i>glpT</i>		S00868	Glycerol-3-phosphate transport protein	<i>Escherichia coli</i>
o377#8	25888	27513	50.8	542	+	3574	100.0	542	<i>glpA</i>		A32006	Glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) chain A, anaerobic	<i>Escherichia coli</i>
o377#9	27506	28762	50.8	419	+	2839	100.0	419	<i>glpB</i>		B32006	Glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) (anaerobic) chain	<i>Escherichia coli</i>
o377#10	28762	29949	50.8	396	+	2686	99.5	396	<i>glpC</i>		C32006	Glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) (anaerobic) chain	<i>Escherichia coli</i>
o377#11	30145	31041	50.8	299	+	1187	59.0	295		(<i>yhgA</i>)	P31667	Hypothetical 33.3 Kd protein in <i>feoB-bioH</i> intergenic region (O292).	<i>Escherichia coli</i>
o377#12	31057	31239	50.9	61	+	no_similarity							
o379#2	32085	31300	50.9	262	-	327	44.8	116		(<i>yhaF</i>)	P23522	Hypothetical 27.4 Kd protein in <i>rnpB-sohA</i> intergenic region (ORF 1) (F256).	<i>Escherichia coli</i>
o379#3	33392	32106	50.9	429	-	726	31.0	436	(<i>phl1</i>)		Q05181	Phthalate transporter.	<i>Pseudomonas putida</i>
o379#4	34666	33452	50.9	405	-	178	28.2	344		(<i>gidU</i>)	P31458	Hypothetical 64.0 Kd protein in <i>ibpA-gyrB</i> intergenic region.	<i>Escherichia coli</i>
o379#5	35451	34672	51.0	260	-	391	31.7	246		(<i>yjhI</i>)	P39360	Hypothetical transcriptional regulator in <i>fecI-fimB</i> intergenic region (F262A).	<i>Escherichia coli</i>
o379#6	36873	35674	51.0	400	-	436	30.4	303	(<i>cinA</i>)		P46323	Putative competence-damage protein.	<i>Bacillus subtilis</i>
o379#7	37482	36976	51.0	169	-	no_similarity							
o379#8	37793	38215	51.0	141	+	534	100.0	81		<i>yfaO</i>	P52006	Hypothetical protein in <i>ais</i> 3' region.	<i>Escherichia coli</i>
o379#9	38859	38260	51.0	200	-	1304	99.0	200	<i>ais</i>		P45565	Ais protein.	<i>Escherichia coli</i>
o379#10	39134	40303	51.0	390	+	1088	44.6	379	(<i>spsC, IPA-65D</i>)		P39623	Spore coat polysaccharide biosynthesis protein SpsC.	<i>Bacillus subtilis</i>
o379#11	40310	41275	51.1	322	+	220	26.6	229	(<i>DPM1, SED3, YPR183W, P9705.3</i>)		P14020	Dolichol-phosphate mannosyltransferase (EC 2.4.1.83)	<i>Saccharomyces cerevisiae (baker's yeast)</i>
o379#12	41278	43257	51.1	660	+	478	29.8	309	(<i>fnt</i>)		P23882	Methionyl-tRNA formyltransferase (EC 2.1.2.9).	<i>Escherichia coli</i>
o379#13	43257	44144	51.1	296	+	no_similarity							
o379#14	44147	45796	51.2	550	+	no_similarity							
o379#15	45796	46128	51.2	111	+	no_similarity							
o379#16	46047	46514	51.2	156	+	no_similarity							
o379#17	46813	46514	51.2	100	-	599	100.0	88	<i>pmrD</i>		P37590	Polymyxin b resistance protein PmrD.	<i>Escherichia coli</i>
o380#1	48242	46890	51.2	451	-	3072	99.8	451	<i>menE</i>		P37353	O-succinylbenzoic acid-CoA ligase (EC 6.2.1.26)	<i>Escherichia coli</i>
o380#2	49228	48242	51.3	329	-	2108	99.4	320	<i>menC</i>		P29208	O-succinylbenzoate-CoA synthase	<i>Escherichia coli</i>
o380#3	50058	49204	51.3	285	-	1964	100.0	285	<i>menB</i>		A42714	Cmaphthoate synthase, DhnA synthase, MenB=menaquinone biosynthesis enzyme/mitochondrial enoyl-CoA hydratase homolog	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o380#5	50885	50076	51.3	270	-	1243	99.4	181		<i>yfbB</i>	P37355	Hypothetical 26.7 Kd protein in <i>menD-menB</i> intergenic region.	<i>Escherichia coli</i>
o380#6	50410	50108	51.3	101	-	392	100.0	60		<i>yfbB</i>	P37355	Hypothetical 26.7 Kd protein in <i>menD-menB</i> intergenic region.	<i>Escherichia coli</i>
o380#7	52702	50831	51.3	624	-	3493	96.1	542	<i>menD</i>		P17109	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (ShcHC synthase) (EC 4.1.1.71)	<i>Escherichia coli</i>
o380#10	53882	52590	51.4	431	-	2861	98.8	431	<i>menF</i>		P38051	Menaquinone-specific isochorismate synthase (EC 5.4.99.6).	<i>Escherichia coli</i>
o380#11	54266	53964	51.4	101	-	642	99.0	101		<i>yfbD</i>	P52084	Hypothetical 11.3 Kd protein in <i>menF</i> 3' region.	<i>Escherichia coli</i>
o380#12	54782	54324	51.4	153	-	986	99.3	146		<i>yfbC</i>	P52077	Hypothetical protein in <i>menF</i> 5' region.	<i>Escherichia coli</i>
o380#13	54829	55761	51.4	311	+	982	48.2	305	<i>(yqjK)</i>		P54548	Hypothetical 34.0 Kd protein in <i>glnQ-ansR</i> intergenic region.	<i>Bacillus subtilis</i>
o380-401#1	58961	57237	51.5	575	-	no_similarity							
o380-401#2	59099	60067	51.5	323	+	no_similarity							
o380-401#3	60173	60673	51.5	167	+	no_similarity							
o401#4	62354	63202	51.5	283	+	no_similarity							
o401#6	64566	63292	51.6	425	-	2619	96.5	425	<i>nuoN</i>		P33608	NADH dehydrogenase I chain N (EC 1.6.5.3)	<i>Escherichia coli</i>
o403#1	66281	64755	51.6	509	-	3387	99.6	509	<i>nuoM</i>		A48643	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4	<i>Escherichia coli</i>
o403#2	68286	66448	51.7	613	-	3869	97.6	613	<i>nuoL</i>		S38321	NADH dehydrogenase I chain <i>nuoL</i>	<i>Escherichia coli</i>
o403#3	68621	68286	51.7	112	-	476	83.2	101	<i>nuoK</i>		P33606	NADH dehydrogenase I chain K (EC 1.6.5.3)	<i>Escherichia coli</i>
o403#4	69136	68585	51.7	184	-	1139	98.9	184	<i>nuoJ</i>		S38319	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain J	<i>Escherichia coli</i>
o403#5	69798	69151	51.7	216	-	1139	90.6	180	<i>nuoI</i>		P33604	NADH dehydrogenase I chain I (EC 1.6.5.3)	<i>Escherichia coli</i>
o403#6	70682	69708	51.7	325	-	2151	99.1	325	<i>nuoH</i>		P33603	NADH dehydrogenase I chain H (EC 1.6.5.3)	<i>Escherichia coli</i>
o403#7	73471	70682	51.8	930	-	3994	97.2	611	<i>nuoG</i>		P33900	NADH dehydrogenase I chain G (EC 1.6.5.3)	<i>Salmonella typhimurium</i>
o403#9	74795	73461	51.8	445	-	3038	99.8	445	<i>nuoF</i>		P31979	NADH dehydrogenase I chain F (EC 1.6.5.3)	<i>Escherichia coli</i>
o403#10	75292	74795	51.8	166	-	1140	99.4	166	<i>nuoE</i>		S38314	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain E	<i>Escherichia coli</i>
o403#11	76518	75298	51.8	407	-	2734	99.0	407	<i>nuoD</i>		P33600	NADH dehydrogenase I chain D (EC 1.6.5.3)	<i>Escherichia coli</i>
o404#1	76517	77098	51.9	183	-	976	100.0	183	<i>nuoC</i>		P33599	NADH dehydrogenase I chain C (EC 1.6.5.3)	<i>Escherichia coli</i>
o404#2	77854	77195	51.9	220	-	1510	100.0	220	<i>nuoB</i>		S38311	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain B	<i>Escherichia coli</i>
o404#3	78313	77873	51.9	147	-	881	92.5	147	<i>nuoA</i>		P33597	NADH dehydrogenase I chain A (EC 1.6.5.3)	<i>Escherichia coli</i>
o404#4	79885	78947	51.9	313	-	1879	100.0	290	<i>lrhA, genR</i>		P36771	Probable transcriptional regulator LrhA.	<i>Escherichia coli</i>
o404#5	80547	80047	51.9	167	-	1147	100.0	167	<i>IS1</i>		JN0135	Hypothetical protein InsB' (insertion sequence IS1A/is1E)	<i>Escherichia coli</i>
o404#6	80741	80469	51.9	91	-	617	98.9	91	<i>IS1</i>		JN0134	Hypothetical protein InsA (insertion sequence IS1A/is1E)	<i>Escherichia coli</i>
o404#7	81578	82792	52.0	405	+	551	28.4	388	<i>(aspC)</i>		P23034	Aspartate aminotransferase (EC 2.6.1.1)	<i>Bacillus sp. (Strain YM-2)</i>
o404#8	82879	83475	52.0	199	+	no_similarity							
o404#9	85369	83540	52.0	610	-	240	26.4	208	<i>(AG45)</i>		P46838	46 Kd membrane protein.	<i>Mycobacterium leprae</i>
o404#10	86124	85459	52.1	222	-	195	32.3	229	<i>(DOGI, YHR044C)</i>		P38774	2-deoxyglucose-6-phosphate phosphatase 1 (EC 3.1.3.-)	<i>Saccharomyces cerevisiae (baker's yeast)</i>
o404#11	86611	86120	52.1	164	-	no_similarity							
o404#12	87149	86697	52.1	151	-	421	44.8	145	<i>(HI1205)</i>		P44127	Hypothetical protein HI1205.	<i>Haemophilus influenzae</i>
o404-405#1	87487	88686	52.1	400	+	2590	100.0	400	<i>ackA</i>		JT0498	Acetate kinase (EC 2.7.2.1)	<i>Escherichia coli</i>
o404-405#2	88767	90905	52.1	713	+	4510	99.7	713	<i>pta</i>		P39184	Phosphate acetyltransferase (EC 2.3.1.8)	<i>Escherichia coli</i>
o405#3	91098	92615	52.2	506	+	784	30.0	513	<i>(HI0594)</i>		P44023	Hypothetical protein HI0594.	<i>Haemophilus influenzae</i>
o405#4	93193	92654	52.2	180	-	no_similarity							
o405#5	93802	93254	52.2	183	-	no_similarity							
o405#6	94502	93861	52.2	214	-	193	29.7	195	<i>(GST1, CARSR8)</i>		P28342	Glutathione S-transferase 1 (EC 2.5.1.18)	<i>Dianthus caryophyllus (carnation) (clove pink)</i>
o405#7	94638	95282	52.2	215	+	328	34.3	233	<i>(URE2, YNL229C, N1165)</i>		P23202	URE2 protein.	<i>Saccharomyces cerevisiae (baker's yeast)</i>
o405#8	95342	95701	52.3	120	+	175	25.5	110		<i>(ygiG)</i>	P31055	Hypothetical 13.6 Kd protein in <i>bacA-tdA</i> intergenic region (F123).	<i>Escherichia coli</i>
o405#9	95725	96615	52.3	297	+	640	39.8	294	<i>(MTCY190.27)</i>		Q10403	Hypothetical 31.7 Kd protein CY190.27.	<i>Mycobacterium tuberculosis</i>
o405#10	97556	96669	52.3	296	-	1333	66.2	296		<i>(yhgA)</i>	P31667	Hypothetical 33.3 Kd protein in <i>feoB-bioH</i> intergenic region	<i>Escherichia coli</i>
o405#11	98526	97756	52.3	257	-	1650	99.6	257	<i>hisP</i>		A27835	histidine transport protein HisP	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o406#1	99250	98537	52.3	238	-	1534	99.6	238	<i>hisM</i>		P20091	Histidine transport system permease protein HisM.	<i>Escherichia coli</i>
o406#2	99933	99250	52.4	228	-	1385	96.5	228	<i>hisQ</i>		P52094	Histidine transport system permease protein HisQ.	<i>Escherichia coli</i>
o406#3	100805	100026	52.4	260	-	1657	99.2	260	<i>hisJ</i>		P39182	Histidine-binding periplasmic protein precursor (HBP).	<i>Escherichia coli</i>
o406#4	101808	101029	52.4	260	-	1597	96.2	260	<i>argT</i>		P09551	Lysine-arginine-ornithine-binding periplasmic protein precursor	<i>Escherichia coli</i>
o406#5	102643	102077	52.4	189	-	1120	94.2	189	<i>ubiX, dedF</i>		P09550	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.1-)	<i>Escherichia coli</i>
o406#6	104252	102741	52.4	504	-	3305	99.8	504	<i>purF</i>		P00496	Amidophosphoribosyltransferase (EC 2.4.2.14)	<i>Escherichia coli</i>
o406#7	104780	104295	52.5	162	-	1045	100.0	162	<i>dedE, cvpA</i>		A29803	DedE protein	<i>Escherichia coli</i>
o406#10	105674	105042	52.5	211	-	1397	100.0	211	<i>dedD</i>		E29803	DedD protein	<i>Escherichia coli</i>
o406#12	106959	105694	52.5	422	-	2749	99.8	422	<i>folC, dedC</i>		P08192	Folypolyglutamate synthase (EC 6.3.2.17) / Dihydrofolate synthase (EC 6.3.2.12).	<i>Escherichia coli</i>
o407#1	107943	107032	52.5	304	-	1912	96.1	304	<i>accD, dedB, usg</i>		C29803	Acetyl-CoA carboxylase (EC 6.4.1.2)	<i>Escherichia coli</i>
o407#2	108758	108102	52.5	219	-	1416	100.0	219	<i>dedA</i>		B29803	DedA protein	<i>Escherichia coli</i>
o407#3	109653	108844	52.6	270	-	1832	100.0	270	<i>truA, hisT, asuC, leuK</i>		P07649	Pseudouridylylase synthase I (EC 4.2.1.70)	<i>Escherichia coli</i>
o407#4	110666	109656	52.6	337	-	2168	100.0	337	<i>usgI</i>		A23792	UsgI protein	<i>Escherichia coli</i>
o407#5	111868	110735	52.6	378	-	2483	99.7	378	<i>pdxB</i>		JV0051	Probable erythronate-4-phosphate dehydrogenase (EC 1.1.1.1-)	<i>Escherichia coli</i>
o407#6	111967	112959	52.6	331	+	277	100.0	39	<i>div</i>		P15286	DIV protein.	<i>Escherichia coli</i>
o407#7	114137	112962	52.7	392	-	975	41.6	373		(<i>yhhS</i>)	P37621	Hypothetical 43.8 Kd protein in <i>fsY-nikA</i> intergenic region	<i>Escherichia coli</i>
o407#8	115622	114405	52.7	406	-	2641	100.0	406	<i>fabB, fabC</i>		P14926	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)	<i>Escherichia coli</i>
o407#9	115721	117784	52.7	688	+	990	44.3	343	(<i>HI1535</i>)		P44246	Hypothetical protein HI1535.	<i>Haemophilus influenzae</i>
o407#10	118186	117911	52.7	92	-	no_similarity							
o407#11	118954	118223	52.8	244	-	627	54.5	165	(<i>HI1563</i>)		P44255	Hypothetical protein HI1563.	<i>Haemophilus influenzae</i>
o407#12	119577	118771	52.8	269	-	1735	100.0	269			S08346	hypothetical protein (<i>mepA</i> 3' region)	<i>Escherichia coli</i>
o407#13	120401	119580	52.8	274	-	1900	100.0	274	<i>mepA</i>		P14007	D-alanyl-D-alanine-endopeptidase (EC 3.4.99.-)	<i>Escherichia coli</i>
o407#15	121487	120408	52.8	360	-	2389	100.0	360	<i>aroC</i>		P12008	Chorismate synthase (EC 4.6.1.4)	<i>Escherichia coli</i>
o409#1	122790	121528	52.8	421	-	1020	100.0	152		(<i>yfcB</i>)	P39199	Hypothetical adenine-specific methylase in <i>aroC</i> 3' region (EC 2.1.1.72).	<i>Escherichia coli</i>
o409#2	122623	123171	52.8	183	+	568	53.1	162	(<i>HI1202</i>)		P44126	Hypothetical protein HI1202.	<i>Haemophilus influenzae</i>
o409#3	124066	123248	52.9	273	-	no_similarity							
o409#4	124607	124071	52.9	179	-	no_similarity							
o409#5	125092	124607	52.9	162	-	no_similarity							
o409#6	125601	125092	52.9	170	-	no_similarity							
o409#7	126353	125604	52.9	250	-	671	42.8	250	(<i>pmfD</i>)		P53520	Chaperone protein PmfD precursor.	<i>Proteus mirabilis</i>
o409#8	127269	126376	52.9	298	-	744	45.2	272	(<i>papC</i>)		P07110	Outer membrane USHER protein PapC precursor.	<i>Escherichia coli</i>
o409#9	129018	127285	53.0	578	-	1468	45.5	506	(<i>papC</i>)		P07110	Outer membrane USHER protein PapC precursor.	<i>Escherichia coli</i>
o409#10	129663	129103	53.0	187	-	254	32.8	186	(<i>smfA</i>)		P13421	Fimbria A protein precursor.	<i>Serratia marcescens</i>
o409#11	130829	130347	53.0	161	-	340	39.4	160	(<i>HI1338</i>)		P44164	Hypothetical protein HI1338.	<i>Haemophilus influenzae</i>
o409#12	133176	131035	53.1	714	-	1233	40.5	730	(<i>HADHA, HADH</i>)		P40939	Mitochondrial trifunctional enzyme α subunit precursor (contains: Long-chain enoyl-CoA hydratase (EC 4.2.1.17) / Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)).	<i>Homo sapiens (human)</i>
o409#13	133544	133179	53.1	122	-	417	46.2	132	(<i>HADHB</i>)		P55084	Mitochondrial trifunctional enzyme β subunit precursor (contains: 3-ketoacyl-CoA thiolase (EC 2.3.1.16)).	<i>Homo sapiens (human)</i>
o409#14	134542	133493	53.1	350	-	709	39.4	297	(<i>HADHB</i>)		P55084	Mitochondrial trifunctional enzyme β subunit precursor (contains: 3-ketoacyl-CoA thiolase (EC 2.3.1.16)).	<i>Homo sapiens (human)</i>
o409#15	134949	134668	53.1	94	-	299	44.6	92	(<i>HI0400</i>)		P44686	Hypothetical protein HI0400.	<i>Haemophilus influenzae</i>
o410#1	135315	136658	53.1	448	+	2990	99.6	448	<i>fadL, trr</i>		P10384	Long-chain fatty acid transport protein precursor	<i>Escherichia coli</i>
o410#2	139046	138270	53.2	259	-	1692	99.2	247	<i>vacJ</i>		P43262	VacJ lipoprotein precursor.	<i>Shigella flexneri</i>
o410#3	139315	140244	53.2	310	+	2025	100.0	310		(<i>yfdC</i>)	P37327	Hypothetical 34.5 Kd protein in <i>argW</i> 5' region.	<i>Escherichia coli</i>
o410#4	140559	141713	53.2	385	+	2552	100.0	385		(<i>yfdB</i>)	P37326	Putative prophage SF6-like integrase in <i>argW</i> 3' region.	<i>Escherichia coli</i>
o410#5	141869	142228	53.3	120	+	332	45.1	113	(<i>RFBI</i>)		P37785	RfbI protein.	<i>Shigella flexneri</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o410#6	142228	143145	53.3	306	+	47	27.8	108	(DPM1, SED3, YPR183W, P9705.3)		P14020	Dolichol-phosphate mannosyltransferase (EC 2.4.1.83)	<i>Saccharomyces cerevisiae</i> (baker's yeast)
o410#7	144775	145116	53.3	114	+	580	83.5	109		ycfA	P09153	Hypothetical 32.8 Kd protein in <i>pin</i> 5' region.	<i>Escherichia coli</i>
o410#8	145212	144988	53.3	75	-	250	83.3	42			P09154	Very Hypothetical 16.7 Kd protein in invertible-p region of excisable element E14.	<i>Escherichia coli</i>
o410#9	145061	145396	53.3	112	+	221	41.3	92		ycfA	P09153	Hypothetical 32.8 Kd protein in <i>pin</i> 5' region.	<i>Escherichia coli</i>
o410#10	145531	145094	53.3	146	-	352	69.0	71			P09154	Very hypothetical 16.7 Kd protein in invertible-p region of excisable element E14.	<i>Escherichia coli</i>
o410#11	146250	145561	53.4	230	-	no_similarity							
o411#1	146401	146129	53.4	91	-	no_similarity							
o411#2	146889	146404	53.4	162	-	no_similarity							
o411#3	146445	146627	53.4	61	+	454	100.0	61	<i>xytU</i>		A24334	D-xylose uptake protein	<i>Escherichia coli</i>
o411#4	147128	146895	53.4	78	-	236	31.2	202	(<i>O</i>)		P03688	Replication protein O.	<i>Bacteriophage lambda</i>
o411#5	147534	147977	53.4	148	+	no_similarity							
o411#6	148046	148867	53.4	274	+	no_similarity							
o411#7	148998	149531	53.4	178	+	no_similarity							
o411#8	149525	149884	53.4	120	+	no_similarity							
o411#9	149887	150189	53.4	101	+	no_similarity							
o411#10	151643	150711	53.5	311	-	2080	99.7	311	<i>dsdC</i>		P46068	D-serine deaminase activator.	<i>Escherichia coli</i>
o411#11	151861	153195	53.5	445	+	2803	100.0	445	<i>dsdX</i>		P08555	DsdX permease.	<i>Escherichia coli</i>
o411#15	153216	154541	53.5	442	+	2920	99.8	442	<i>dsdX</i>		A31784	D-serine dehydratase (EC 4.2.1.14)	<i>Escherichia coli</i>
o411#16	156190	154655	53.6	512	-	3323	100.0	512	<i>emrY</i>		P52600	Multidrug resistance protein Y.	<i>Escherichia coli</i>
o412#1	157362	156193	53.6	390	-	2448	100.0	390	<i>emrK</i>		P52599	Multidrug resistance protein K.	<i>Escherichia coli</i>
o412#2	157769	158380	53.6	204	+	1300	100.0	204	<i>evgA</i>		JU0220	EvgA protein	<i>Escherichia coli</i>
o412#3	158388	161978	53.6	1197	+	7721	99.0	1197	<i>evgS</i>		P30855	Putative sensor protein EvgS precursor (EC 2.7.3.-).	<i>Escherichia coli</i>
o412#4	163182	162040	53.7	381	-	391	25.9	351	(<i>baiF</i>)		P19413	Bile acid-inducible operon protein F.	<i>Eubacterium sp. (strain vpi 12708)</i>
o412#5	163480	163259	53.7	74	-	226	25.3	190	(<i>ywkB</i>)		P45869	Hypothetical 33.6 Kd protein in <i>tdk-prfA</i> intergenic region.	<i>Bacillus subtilis</i>
o412#6	164199	163816	53.7	128	-	208	30.4	115	(<i>ywkB</i>)		P45869	Hypothetical 33.6 Kd protein in <i>tdk-prfA</i> intergenic region.	<i>Bacillus subtilis</i>
o412-414#1	165963	164272	53.8	564	-	2078	55.1	559	<i>OXC</i>		P40149	Oxalyl-CoA decarboxylase (EC 4.1.1.8).	<i>Oxalobacter formigenes</i>
o414#2	167267	166020	53.8	416	-	202	26.9	424	(<i>baiF</i>)		P19413	Bile acid-inducible operon protein F.	<i>Eubacterium sp. (strain vpi 12708)</i>
o414#3	168415	167783	53.8	211	-	no_similarity							
o414#4	169305	169066	53.9	80	-	no_similarity							
o414#5	169658	170575	53.9	306	+	1235	54.2	308	(<i>htrB</i>)		P24187	Heat shock protein B.	<i>Escherichia coli</i>
o414#6	172308	171073	53.9	412	-	877	35.8	394	(<i>ywJG, IPA-85D</i>)		P39643	Probable aspartate aminotransferase (EC 2.6.1.1)	<i>Bacillus subtilis</i>
o414#7	172702	174378	53.9	559	+	422	28.8	569		(<i>yehU</i>)	P33357	Hypothetical 62.1 Kd protein in <i>molR-bglX</i> intergenic region precursor.	<i>Escherichia coli</i>
o414#8	174396	175127	54.0	244	+	1044	82.6	195	(<i>mrkE</i>)		P21649	MrkE protein.	<i>Klebsiella pneumoniae</i>
o414#9	175143	175997	54.0	285	+	545	35.4	271		(<i>yijO</i>)	P32677	Hypothetical transcriptional regulator in <i>gldA-ppc</i> intergenic region (F283).	<i>Escherichia coli</i>
o414#10	178498	176006	54.0	831	-	2066	45.8	714	(<i>ptsA</i>)		P32670	Phosphoenolpyruvate-protein phosphotransferase PtsA (EC 2.7.3.9)	<i>Escherichia coli</i>
o414#11	179560	178526	54.1	345	-	565	35.2	358	(<i>frvX</i>)		P32153	Putative frv operon protein FrvX.	<i>Escherichia coli</i>
o414#12	180348	179563	54.1	262	-	885	39.8	354	(<i>yqhT</i>)		P54518	Putative peptidase in <i>gevT-spoIIIA</i> intergenic region (EC 3.4.-.-).	<i>Bacillus subtilis</i>
o414#13	181906	180662	54.1	415	-	422	28.2	397	(<i>fruA, HI0446</i>)		P44714	PTS system, fructose-specific IIBC component (EIIBC-FRU) (EC 2.7.1.69)	<i>Haemophilus influenzae</i>
o414#14	182305	181931	54.1	125	-	306	45.5	101	(<i>frwB</i>)		P32673	PTS system, fructose-like-2 IIBC component I (EC 2.7.1.69).	<i>Escherichia coli</i>
o414#15	183438	182476	54.2	321	-	2107	98.8	321	<i>gIk</i>		P46880	Glucokinase (EC 2.7.1.2).	<i>Escherichia coli</i>
o416#1	183642	184895	54.2	418	+	no_similarity							
o416#2	185013	185336	54.2	108	+	no_similarity							

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o416#3	186718	185483	54.2	412	-	480	31.6	443	(SPAC27F1.08)		Q10177	Hypothetical 57.6 Kd protein C27F1.08 in chromosome I.	<i>Schizosaccharomyces pombe</i> (fission yeast)
o416#4	187054	188253	54.2	400	+	2441	99.5	401	<i>nupC, cru</i>		P33031	Nucleoside permease NupC	<i>Escherichia coli</i>
o416#5	188331	189452	54.3	374	+	2343	96.2	369	<i>IS186</i>		P08409	Insertion element IS186 47 Kd Hypothetical protein (ORF1).	<i>Escherichia coli</i>
o416#6	189075	188770	54.3	102	-	701	99.0	102	<i>IS421</i>		S04881	hypothetical protein II (insertion sequence IS421)	<i>Escherichia coli</i>
o416#7	189400	189615	54.3	72	+	478	100.0	71	<i>IS186</i>		P08409	Insertion element IS186 47 Kd Hypothetical protein (ORF1).	<i>Escherichia coli</i>
o416#8	191970	189658	54.3	771	-	877	100.0	131		<i>yfeA</i>	P23842	Hypothetical 19.0 Kd protein in <i>glxX</i> 5' region.	<i>Escherichia coli</i>
o416#10	192428	192820	54.3	131	+	271	69.8	116		(<i>yfeC</i>)	P27239	Hypothetical 12.1 Kd protein in <i>gluY-alaW</i> intergenic region.	<i>Escherichia coli</i>
o416#11	192507	192710	54.4	68	+	219	64.9	57		(<i>yfeC</i>)	P27239	Hypothetical 12.1 Kd protein in <i>gluY-alaW</i> intergenic region.	<i>Escherichia coli</i>
o416#12	192825	193214	54.4	130	+	855	100.0	130			S11409	hypothetical protein 130	<i>Escherichia coli</i>
o416#13	194684	193272	54.4	471	-	3198	100.0	471	<i>gluX</i>		A25956	Glutamate-tRNA ligase (EC 6.1.1.17)	<i>Escherichia coli</i>
o416#14	196489	195608	54.4	294	-	1925	100.0	294	<i>xapR, pndR</i>		P23841	Xanthosine operon regulatory protein.	<i>Escherichia coli</i>
o416#15	197997	196744	54.5	418	-	2545	94.8	420	<i>xapB</i>		P45562	Xanthosine permease	<i>Escherichia coli</i>
o416#16	198890	198060	54.5	277	-	1450	87.5	263	<i>xapA, pndA</i>		P45563	Xanthosine phosphorylase (EC 2.4.2.-).	<i>Escherichia coli</i>
o417#1	199139	199900	54.5	254	+	1779	100.0	254		<i>yfeN</i>	P45564	Hypothetical 29.2 Kd protein in <i>xapA-lig</i> intergenic region	<i>Escherichia coli</i>
o417#2	200868	199945	54.5	308	-	387	27.5	269	(<i>yybE</i>)		P37499	Hypothetical transcriptional regulator in <i>cotF-tetB</i> intergenic region.	<i>Bacillus subtilis</i>
o417#3	200958	202001	54.5	348	+	1650	100.0	255		<i>yfeH</i>	P39836	Hypothetical protein in <i>xapB-lig</i> intergenic region .	<i>Escherichia coli</i>
o417#4	202262	202026	54.6	79	-	no_similarity							
o417#5	204186	202174	54.6	671	-	4333	99.9	671	<i>lig, ligA, dnaL, pdeC, lop</i>		P15042	DNA ligase (EC 6.5.1.2)	<i>Escherichia coli</i>
o417#6	205243	204260	54.6	328	-	332	29.0	335	(<i>HI1101</i>)		P44113	Hypothetical protein HI1101.	<i>Haemophilus influenzae</i>
o417-418#1	205474	206232	54.6	253	+	1369	100.0	196	<i>cysZ</i>		E28181	CysZ protein	<i>Escherichia coli</i> (fragment)
o418#2	206423	207388	54.7	322	+	2029	100.0	322	<i>cysK, cysZ</i>		P11096	Cysteine synthase A (EC 4.2.99.8)	<i>Escherichia coli</i>
o418#3	207775	208029	54.7	85	+	516	100.0	85	<i>ptsH, hpr</i>		P07006	PhosphocARRIER protein HPR (Histidine-containing protein).	<i>Escherichia coli, and Salmonella typhimurium</i>
o418#4	208077	209801	54.7	575	+	3617	100.0	575	<i>ptsI</i>		P08839	Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9)	<i>Escherichia coli</i>
o418#5	209845	210351	54.7	169	+	1057	100.0	169	<i>crr</i>		C29785	Phosphotransferase system enzyme II (EC 2.7.1.69), glucose-specific, factor III	<i>Escherichia coli</i>
o418#6	211248	210400	54.8	283	-	218	100.0	34		<i>yfeI</i>	P40191	Hypothetical protein in <i>crr-ptsI</i> intergenic region .	<i>Escherichia coli</i>
o418#7	211353	211724	54.8	124	+	647	83.2	119	(<i>yfeK</i>)		P40195	Hypothetical 13.3 Kd protein in <i>ptsI-cysM</i> intergenic region.	<i>Salmonella typhimurium</i>
o418#8	211760	212491	54.8	244	+	199	45.7	70	(<i>molR</i>)		P33345	Molybdate metabolism regulator.	<i>Escherichia coli</i>
o418#9	213594	212686	54.8	303	-	1977	99.7	303	<i>cysM</i>		D35402	Cysteine synthase (EC 4.2.99.8) B	<i>Escherichia coli</i>
o418#10	214825	213731	54.8	365	-	2409	99.5	365	<i>cysA</i>		C35402	Sulfate/thiosulfate transport protein CysA	<i>Escherichia coli</i>
o418#11	215690	214818	54.9	291	-	1913	100.0	291	<i>cysW</i>		B35402	Sulfate/thiosulfate transport protein CysW	<i>Escherichia coli</i>
o418#12	216523	215693	54.9	277	-	1764	100.0	277	<i>cysU, cysT</i>		P16701	Sulfate transport system permease protein CysT.	<i>Escherichia coli</i>
o418#13	217539	216526	54.9	338	-	2228	100.0	338	<i>cysP</i>		A35403	Thiosulfate-binding protein CysP precursor	<i>Escherichia coli</i>
o419#1	218700	217846	54.9	285	-	535	100.0	84		<i>yfeF</i>	P37440	Hypothetical oxidoreductase in <i>cysP</i> 5' region (EC 1.-.-.-).	<i>Escherichia coli</i>
o419#2	219620	218766	54.9	285	-	533	35.1	282		(<i>yfhH</i>)	P37767	Hypothetical 30.7 Kd protein in <i>purL-dpj</i> intergenic region	<i>Escherichia coli</i>
o419#3	219784	220050	54.9	89	+	335	62.2	82	(<i>HI0754</i>)		P44862	Hypothetical protein HI0754.	<i>Haemophilus influenzae</i>
o419#4	220032	220676	54.9	215	+	701	54.3	210	(<i>HI0754</i>)		P44862	Hypothetical protein HI0754.	<i>Haemophilus influenzae</i>
o419#5	220683	222104	55.0	474	+	602	29.0	465	(<i>sacP, IPA-49D</i>)		P05306	PTS system, sucrose-specific IIBC component (EIIBC-SCR) (EC 2.7.1.69)	<i>Bacillus subtilis</i>
o419#6	222025	223413	55.0	463	+	151	25.9	232	(<i>ampC</i>)		P24735	β -lactamase precursor (EC 3.5.2.6)	<i>Pseudomonas aeruginosa</i>
o419#7	224555	223659	55.0	299	-	no_similarity							
o419#8	225226	224654	55.1	191	-	no_similarity							
o419#9	225736	225290	55.1	149	-	no_similarity							
o420#1	226148	225726	55.1	141	-	no_similarity							
o420#2	226362	227228	55.1	289	+	1831	100.0	289	<i>amiA</i>		P36548	Probable N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28).	<i>Escherichia coli</i>
o420#4	227235	228131	55.1	299	+	2126	100.0	299	<i>hemF</i>		P36553	Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o420#5	229192	228143	55.1	350	-	2354	99.4	350		<i>yfrG</i>	P36547	Hypothetical transcriptional regulator in <i>hemF</i> 3'region	<i>Escherichia coli</i>
o420#6	229738	229241	55.2	166	-	248	48.2	83	(<i>cchA</i>)		P41791	CchA protein precursor.	<i>Salmonella typhimurium</i>
o420#7	230410	229754	55.2	219	-	no_similarity							
o420#8	231307	230423	55.2	295	-	91	100.0	15	<i>eutC</i>		P19636	Ethanolamine ammonia-lyase light chain (EC 4.3.1.7)	<i>Escherichia coli</i>
o420#9	232689	231331	55.2	453	-	179	96.7	30	<i>eutB</i>		P19635	Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7)	<i>Escherichia coli</i>
o421#1	234104	232704	55.2	467	-	no_similarity							
o421#2	235342	234104	55.3	413	-	2295	94.9	372	(<i>eutH</i>)		P41796	Ethanolamine utilization protein EutH	<i>Salmonella typhimurium</i>
o421#3	236731	235547	55.3	395	-	2038	80.7	394	(<i>eutG</i>)		P41795	Ethanolamine utilization protein EutG	<i>Salmonella typhimurium</i>
o421#4	237557	236724	55.3	278	-	1678	89.2	278	(<i>eutJ</i>)		P41794	Ethanolamine utilization protein EutJ	<i>Salmonella typhimurium</i>
o421#5	238971	237571	55.4	467	-	2805	93.8	467	(<i>eutE</i>)		P41793	Ethanolamine utilization protein EutE	<i>Salmonella typhimurium</i>
o421#6	239270	238986	55.4	95	-	600	90.8	98	(<i>cchB</i>)		P41792	CchB protein.	<i>Salmonella typhimurium</i>
o421#7	239712	239380	55.4	111	-	587	96.8	95	(<i>cchA</i>)		P41791	CchA protein precursor.	<i>Salmonella typhimurium</i>
o421#8	240725	239712	55.4	338	-	1457	91.3	242	(<i>eutI</i>)		P41790	Ethanolamine utilization protein EutI	<i>Salmonella typhimurium</i>
o421#9	241525	240725	55.4	267	-	no_similarity							
o421#10	242223	241525	55.4	233	-	no_similarity							
o421#11	242677	242201	55.4	159	-	no_similarity							
o421#12	243064	242693	55.4	124	-	no_similarity							
o421-422#1	245597	243321	55.5	759	-	3559	68.7	757	(<i>HI1245</i>)		P43837	Putative malate oxidoreductase (NAD) (EC 1.1.1.38)	<i>Haemophilus influenzae</i>
o422#2	245886	246833	55.5	316	+	1334	64.6	311	(<i>talA</i>)		S40535	Hypothetical protein	<i>Escherichia coli</i>
o422#3	246856	248856	55.5	667	+	4484	100.0	667	(<i>tkrB</i>)		A48660	Transketolase (EC 2.2.1.1)	<i>Escherichia coli</i>
o422#4	249997	248957	55.6	347	-	no_similarity							
o422#5	250698	250126	55.6	191	-	1018	100.0	157		<i>yffH</i>	P37128	Hypothetical protein in <i>narQ</i> 5'region	<i>Escherichia coli</i>
o422#6	252781	250769	55.7	671	-	4299	95.8	661		<i>yffG</i>	P37127	Hypothetical 71.5 Kd protein in <i>narQ</i> 5'region (AEG53.0).	<i>Escherichia coli</i>
o422#8	252951	254648	55.7	566	+	3634	99.8	566	(<i>narQ</i>)		P27896	Nitrate/nitrite sensor protein NarQ (EC 2.7.3.-)	<i>Escherichia coli</i>
o422#9	254815	257925	55.7	1037	+	266	100.0	40	(<i>acrD</i>)		C42959	<i>envD</i> gene product homolog	<i>Escherichia coli</i>
o422#10	258467	258820	55.8	118	+	794	100.0	118			B42959	14K hypothetical protein (5' of <i>dapE</i>)	<i>Escherichia coli</i>
o422#11	258827	259951	55.8	375	+	2506	100.0	375	(<i>dapE</i> , <i>msxB</i>)		A42959	Succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	<i>Escherichia coli</i>
o422#12	259982	260179	55.8	66	+	212	100.0	31			D42959	Hypothetical protein (3' of <i>dapE</i>)	<i>Escherichia coli</i>
o422#13	261014	260295	55.8	240	-	no_similarity							
o423#1	263080	261125	55.9	652	-	654	37.9	327	(<i>HI1254</i>)		P44140	Hypothetical protein HI1254 precursor.	<i>Haemophilus influenzae</i>
o423#2	263958	263098	55.9	287	-	no_similarity							
o423#3	264839	264129	55.9	237	-	1556	100.0	237	(<i>purC</i>)		C36146	Phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6)	<i>Escherichia coli</i>
o423#4	266086	265055	55.9	344	-	2219	100.0	344	(<i>nlpB</i> , <i>dapX</i>)		P21167	Lipoprotein-34 precursor.	<i>Escherichia coli</i>
o423#5	266981	266106	56.0	292	-	1873	99.3	292	(<i>dapA</i>)		A30381	Dihydrodipicolinate synthase (EC 4.2.1.52)	<i>Escherichia coli</i>
o423#6	267061	267696	56.0	212	+	909	99.3	139	(<i>gcvR</i>)		P23483	<i>gcv</i> operon transcriptional regulator.	<i>Escherichia coli</i>
o423#7	267563	267718	56.0	52	+	285	93.9	49	(<i>gcvR</i>)		P23483	<i>gcv</i> operon transcriptional regulator.	<i>Escherichia coli</i>
o423#8	267699	268166	56.0	156	+	1072	100.0	156	(<i>bcp</i>)		B49749	Bacterioferritin comigratory protein	<i>Escherichia coli</i>
o423#9	268422	269036	56.0	205	+	1447	100.0	205			C49749	Hypothetical protein 1(<i>bcp</i> 3' region)	<i>Escherichia coli</i>
o423#10	269039	271054	56.0	672	+	205	100.0	34			D49749	Hypothetical protein 2(<i>bcp</i> 3' region)	<i>Escherichia coli</i>
o423#11	271047	272012	56.0	322	+	1054	52.2	301	(<i>hycD</i> , <i>hevD</i>)		P16430	Formate hydrogenlyase subunit 4	<i>Escherichia coli</i>
o424#1	272032	273468	56.1	479	+	453	30.1	409	(<i>ndh5</i> , <i>ndhF</i>)		A00454	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5	<i>common tobacco chloroplast</i>
o424#2	273483	274130	56.1	216	+	204	25.5	216	(<i>MTCY251.03</i>)		Q10882	Hypothetical 23.0 Kd protein CY251.03.	<i>Mycobacterium tuberculosis</i>
o424#3	274138	275715	56.1	526	+	211	30.2	397	(<i>hycC</i> , <i>hevC</i>)		P16429	Formate hydrogenlyase subunit 3	<i>Escherichia coli</i>
o424#4	275663	277372	56.1	570	+	2004	70.9	563	(<i>hycE</i> , <i>hevE</i>)		P16431	Formate hydrogenlyase subunit 5 precursor	<i>Escherichia coli</i>
o424#5	277385	277927	56.2	181	+	554	45.3	170	(<i>hycF</i> , <i>hevF</i>)		P16432	Formate hydrogenlyase subunit 6	<i>Escherichia coli</i>
o424#6	277927	278679	56.2	251	+	1041	62.4	250	(<i>hycG</i>)		S08625	Probable hydrogenase 3 protein 7	<i>Escherichia coli</i>
o424#7	278679	279089	56.2	137	+	398	48.1	131	(<i>hycH</i> , <i>hevH</i>)		P16434	Formate hydrogenlyase maturation protein HycH.	<i>Escherichia coli</i>
o425#1	279122	281131	56.2	670	+	1515	51.2	566	(<i>fhlA</i>)		P19323	Formate hydrogenlyase transcriptional activator.	<i>Escherichia coli</i>
o425#3	281156	282001	56.3	282	+	947	50.5	281	(<i>focA</i>)		P21501	Probable formate transporter	<i>Escherichia coli</i>
o425#4	283103	282045	56.3	353	-	663	69.0	142	(<i>HI0238</i>)		P43970	Hypothetical protein HI0238.	<i>Haemophilus influenzae</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o425#5	283316	284419	56.3	368	+	no_similarity							
o425#6	284305	284784	56.3	160	+	no_similarity							
o425#7	284808	285188	56.3	127	+	285	46.2	93	(<i>arsC</i> , <i>arsG</i> , <i>HI0236</i>)		P44589	Putative arsenate reductase	<i>Haemophilus influenzae</i>
o425#8	285900	285310	56.4	197	-	227	26.7	281	(<i>dnaA</i>)		P22837	Chromosomal replication initiator protein DnaA.	<i>Proteus mirabilis</i>
o425#9	287392	286106	56.4	429	-	2710	100.0	429	(<i>uraA</i>)		A56265	Uracil transport protein UraA	<i>Escherichia coli</i>
o425#10	288104	287481	56.4	208	-	1322	100.0	208	(<i>upp</i> , <i>uraP</i>)		P25532	Uracil phosphoribosyltransferase (EC 2.4.2.9)	<i>Escherichia coli</i>
o425#11	288429	289463	56.4	345	+	2291	99.7	345	(<i>purM</i> , <i>purG</i>)		P08178	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)	<i>Escherichia coli</i>
o425#12	289466	290101	56.4	212	+	1404	100.0	212	(<i>purN</i>)		A28486	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	<i>Escherichia coli</i>
o425#13	290276	292339	56.5	688	+	4496	100.0	688	(<i>ppk</i>)		A44306	Polyphosphate kinase (EC 2.7.4.1)	<i>Escherichia coli</i>
o425#14	292347	293885	56.5	513	+	3391	100.0	513	(<i>ppx</i>)		A45333	Exopolyphosphatase PPX	<i>Escherichia coli</i>
o427#1	296170	293930	56.6	747	-	424	26.4	477			Q04855	Hypothetical 80.5 Kd protein in <i>nrcC</i> 5'region	<i>Azorhizobium caulinodans</i>
o427#2	297027	297539	56.6	171	+	no_similarity							
o427#3	297377	297096	56.6	94	-	no_similarity							
o427#4	297558	298094	56.6	179	+	no_similarity							
o427#5	299767	298193	56.7	525	-	3512	100.0	525	(<i>guaA</i>)		A24640	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2)	<i>Escherichia coli</i>
o427#6	301371	299839	56.7	511	-	3235	99.8	511	(<i>guaB</i>)		A93555	IMP dehydrogenase (EC 1.1.1.205)	<i>Escherichia coli</i>
o427#7	301464	302831	56.7	456	+	2968	99.8	456	(<i>xseA</i>)		A25940	exodeoxyribonuclease VII (EC 3.1.11.6) large chain	<i>Escherichia coli</i>
o427#8	304627	303119	56.8	503	-	1536	70.6	500	(<i>HI0136</i>)		P44536	Hypothetical GTP-binding protein HI0136.	<i>Haemophilus influenzae</i>
o427#9	305884	304709	56.8	392	-	141	32.8	119	(<i>afsK</i>)		P54741	Serine/threonine protein kinase AfsK (EC 2.7.1.-).	<i>Streptomyces coelicolor</i>
o427#10	306284	305898	56.8	129	-	253	39.5	114	(<i>HI0370</i>)		P43989	Hypothetical protein HI0370.	<i>Haemophilus influenzae</i>
o427#11	306516	306220	56.8	99	-	200	34.1	85	(<i>HI0370</i>)		P43989	Hypothetical protein HI0370.	<i>Haemophilus influenzae</i>
o427#12	307808	306537	56.8	424	-	2798	99.8	424	(<i>hisS</i>)		A23890	Histidine-tRNA ligase (EC 6.1.1.21)	<i>Escherichia coli</i>
o427-428#1	309037	307922	56.9	372	-	2388	100.0	372	(<i>gcpE</i>)		S23058	GcpE protein	<i>Escherichia coli</i>
o428#2	310077	309067	56.9	337	-	2188	100.0	337		<i>yfgA</i>	P27434	Hypothetical 36.2 Kd protein in <i>ndk-gcpE</i> intergenic region.	<i>Escherichia coli</i>
o428#3	311516	310365	56.9	384	-	2543	100.0	384		<i>yfgB</i>	P36979	Hypothetical 43.1 Kd protein in <i>ndk-gcpE</i> intergenic region.	<i>Escherichia coli</i>
o428#4	312097	311669	56.9	143	-	926	100.0	143	(<i>ndk</i>)		JH0495	Nucleoside-diphosphate kinase (EC 2.7.4.6)	<i>Escherichia coli</i>
o429#1	314198	312249	57.0	650	-	291	28.5	477	(<i>phpF</i> , <i>ponA</i>)		P38050	Penicillin-binding protein 1A (PBP-1A).	<i>Bacillus subtilis</i>
o429#2	314557	314090	57.0	156	-	no_similarity							
o429#3	319518	314575	57.1	1648	-	no_similarity							
o429#4	319728	320567	57.1	280	+	1893	100.0	280	(<i>sseA</i>)		P31142	Putative thiosulfate sulfurtransferase (EC 2.8.1.1)	<i>Escherichia coli</i>
o429#5	322029	321391	57.1	213	-	1379	99.5	213	(<i>sseB</i>)		JC2271	Rhodanese-like protein SseB	<i>Escherichia coli</i>
o429#6	323589	322309	57.2	427	-	266	97.6	42		<i>yfhI</i>	P37095	Hypothetical protein in <i>fdx</i> 3'region .	<i>Escherichia coli</i>
o429#7	323967	323770	57.2	66	-	463	100.0	66		<i>yfhJ</i>	P37096	Hypothetical 7.7 Kd protein in <i>fdx</i> 3'region.	<i>Escherichia coli</i>
o429#8	324314	323982	57.2	111	-	769	100.0	111	(<i>fdx</i>)		JC1110	Ferredoxin [2Fe-2S]	<i>Escherichia coli</i>
o430#1	326166	324319	57.2	616	-	3886	99.8	616	(<i>hscA</i>)		A53488	Heat shock cognate protein 66	<i>Escherichia coli</i>
o430#2	326698	326186	57.2	171	-	1106	100.0	171		<i>yfhE</i>	P36540	Hypothetical 20.1 Kd protein in <i>hscA</i> 5'region (ORF-1).	<i>Escherichia coli</i>
o430#3	326864	326709	57.2	52	-	no_similarity							
o430#4	327117	326797	57.3	107	-	647	91.6	107		<i>yfhF</i>	P36539	Hypothetical 11.5 Kd protein in <i>hscA</i> 5'region.	<i>Escherichia coli</i>
o430#5	327520	327137	57.3	128	-	401	50.0	124	(<i>nifU</i>)		P05340	NifU protein.	<i>Azotobacter vinelandii</i>
o430#6	328762	327551	57.3	404	-	77	100.0	12		<i>yczO</i>	P39171	Unknown protein from 2D-PAGE (spot M92) .	<i>Escherichia coli</i>
o430#7	329362	328877	57.3	162	-	591	63.8	141	(<i>HI0379</i>)		P44675	Hypothetical protein HI0379.	<i>Haemophilus influenzae</i>
o430#8	330554	329817	57.3	246	-	800	54.0	239	(<i>HI0380</i>)		P44676	Hypothetical protein HI0380.	<i>Haemophilus influenzae</i>
o430#9	330673	331473	57.3	267	+	1722	99.6	267	(<i>stbB</i> , <i>ssyA</i>)		P22783	Extragenic suppressor protein SuhB.	<i>Escherichia coli</i>
o430#10	331594	332472	57.4	293	+	381	29.6	233	(<i>BEM46</i>)		P54069	BEM46 protein .	<i>Schizosaccharomyces pombe</i> (fission yeast)
o430#11	332666	334054	57.4	463	+	3097	99.8	463	(<i>csiE</i>)		P54901	CsiE protein.	<i>Escherichia coli</i>
o430#12	335078	333942	57.4	379	-	854	36.5	378	(<i>HI0308</i>)		P44629	Hypothetical protein HI0308.	<i>Haemophilus influenzae</i>
o430#13	336131	335241	57.4	297	-	548	34.1	287	(<i>alsR</i>)		Q04778	<i>als</i> operon regulatory protein.	<i>Bacillus subtilis</i>
o431#1	336264	337622	57.5	453	+	1351	48.9	440	(<i>bedC1</i>)		Q07944	Benzene 1,2-dioxygenase α subunit (EC 1.14.12.3).	<i>Pseudomonas putida</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o431#3	337622	338137	57.5	172	+	353	32.6	172	<i>bncB</i>		P08085	Benzene 1,2-dioxygenase β subunit (EC 1.14.12.3)	<i>Pseudomonas putida</i>
o431#4	338140	338457	57.5	106	+	322	43.7	103	<i>bphF</i>		P37332	Biphenyl dioxygenase system ferredoxin component.	<i>Burkholderia cepacia</i> (<i>Pseudomonas cepacia</i>)
o431#5	338457	339266	57.5	270	+	904	47.9	267	<i>bphB</i>		P50206	Biphenyl-2,3-dihydro-2,3-diol dehydrogenase (EC 1.3.1.-)	<i>Pseudomonas sp. (strain KKS102)</i>
o431#6	339279	340478	57.5	400	+	670	31.3	399	<i>bphG</i>		P37337	Biphenyl dioxygenase system ferredoxin-NAD(+) reductase component (EC 1.18.1.3).	<i>Burkholderia cepacia</i> (<i>Pseudomonas cepacia</i>)
o431#7	340506	340997	57.5	164	+	296	43.2	125		<i>(yqjF)</i>	P42619	Hypothetical 17.2 Kd protein in <i>exuR-tdcC</i> intergenic region	<i>Escherichia coli</i>
o431#8	341920	341051	57.6	290	-	no_similarity							
o431#9	343026	341935	57.6	364	-	518	31.6	361	<i>gutB</i>		Q06004	Sorbitol dehydrogenase (EC 1.1.1.14)	<i>Bacillus subtilis</i>
o431#10	344057	343062	57.6	332	-	587	33.0	309	<i>araH</i>		P08532	L-arabinose transport system permease protein AraH.	<i>Escherichia coli</i>
o431#11	345593	344085	57.7	503	-	1126	37.2	492	<i>mgIA</i>		P23199	Galactoside transport ATP-binding protein MglA.	<i>Escherichia coli</i>
o432#1	346599	345619	57.7	327	-	227	26.3	323	<i>mgIB</i>		P23905	D-galactose-binding periplasmic protein precursor (GBP)	<i>Salmonella typhimurium</i>
o432#2	349977	346699	57.7	1093	-	no_similarity							
o432#3	350095	350553	57.8	153	+	no_similarity							
o432#4	350553	351284	57.8	244	+	233	28.4	201	<i>(HI0144)</i>		P44541	Hypothetical protein HI0144.	<i>Haemophilus influenzae</i>
o432#5	352738	351488	57.8	417	-	2752	100.0	417	<i>glaA</i>		P00477	Serine hydroxymethyltransferase (EC 2.1.2.1)	<i>Escherichia coli</i>
o432#6	353066	354253	57.8	396	+	2657	100.0	396	<i>hmpA, hmp, fsrB</i>		P24232	Flavo-hemoprotein (EC 1.6.99.7)	<i>Escherichia coli</i>
o432#7	354639	354304	57.8	112	-	717	100.0	112	<i>glnB</i>		C49940	Regulatory protein P-II	<i>Escherichia coli</i>
o432#8	356034	354703	57.9	444	-	2812	98.9	444			B49940	Nitrogen regulator I homolog	<i>Escherichia coli</i>
o432-436#1	356737	356027	57.9	237	-	1607	100.0	237			A49940	Orf1 5' of <i>glnB</i>	<i>Escherichia coli</i>
o432-436#2	358284	356905	57.9	460	-	2966	100.0	460		<i>yfhK</i>	P52101	Probable sensor protein YfhK (EC 2.7.3.-).	<i>Escherichia coli</i>
o432-436#3	362774	358890	58.0	1295	-	8641	99.9	1295	<i>purL, purI</i>		P15254	Phosphoribosylformylglycinamide synthase (EC 6.3.5.3)	<i>Escherichia coli</i>
o432-436#4	363170	364585	58.0	472	+	3069	99.4	472		<i>yfhD</i>	P30135	Hypothetical 53.2 Kd protein in <i>purL-dpj</i> intergenic region (O472).	<i>Escherichia coli</i>
o432-436#5	365121	364588	58.1	178	-	1199	100.0	178		<i>yfhC</i>	P30134	Hypothetical 20.0 Kd protein in <i>purL-dpj</i> intergenic region (ORF178)	<i>Escherichia coli</i>
o432-436#6	365718	365149	58.1	190	-	1305	100.0	190			S20973	Hypothetical protein 190	<i>Escherichia coli</i>
o432-436#7	365990	366835	58.1	282	+	1774	100.0	282		<i>yfhH</i>	P37767	Hypothetical 30.7 Kd protein in <i>purL-dpj</i> intergenic region (O306).	<i>Escherichia coli</i>
o432-436#8	366894	367151	58.1	86	+	628	100.0	86		<i>yfhL</i>	P52102	Putative ferredoxin-like protein in <i>purL-dpj</i> intergenic region (O86).	<i>Escherichia coli</i>
o432-436#9	368229	367852	58.1	126	-	818	100.0	126	<i>acpS, dpj</i>		P24224	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	<i>Escherichia coli</i>
o432-436#10	368960	368232	58.2	243	-	1558	100.0	243	<i>pdxJ</i>		A42293	Vitamin B-6 biosynthesis protein PdxJ	<i>Escherichia coli</i>
o432-436#11	369700	368975	58.2	242	-	1570	99.2	242	<i>recO</i>		JS0116	RecO protein	<i>Escherichia coli</i>
o432-436#12	370617	369715	58.2	301	-	1940	100.0	301	<i>era, rbaA</i>		P06616	GTP-binding protein Era.	<i>Escherichia coli</i>
o432-436#13	371294	370617	58.2	226	-	1468	100.0	226	<i>rnc</i>		A26023	Ribonuclease III (EC 3.1.26.3)	<i>Escherichia coli</i>
o432-436#14	372537	371569	58.2	323	-	2182	100.0	323	<i>lepB</i>		P00803	Signal peptidase I (EC 3.4.21.89)	<i>Escherichia coli</i>
o432-436#15	374349	372556	58.3	598	-	3901	100.0	598	<i>lepA</i>		P07682	GTP-binding protein LepA.	<i>Escherichia coli</i>
o432-436#17	375026	374550	58.3	159	-	1045	100.0	159	<i>rseC</i>		P46187	Sigma-E factor regulatory protein RseC.	<i>Escherichia coli</i>
o432-436#19	375979	375026	58.3	318	-	2066	100.0	318	<i>rseB</i>		P46186	Sigma-E factor regulatory protein RseB precursor.	<i>Escherichia coli</i>
o432-436#20	376629	375982	58.3	216	-	1443	100.0	216	<i>rseA, mclA</i>		P38106	Sigma-E factor negative regulatory protein.	<i>Escherichia coli</i>
o432-436#21	377237	376665	58.3	191	-	1219	100.0	191	<i>rpoE, sigE</i>		P34086	RNA polymerase sigma-E factor (Sigma-24).	<i>Escherichia coli</i>
o432-436#22	377645	379264	58.3	540	+	3638	99.8	540	<i>nadB, nicB</i>		P10902	L-aspartate oxidase (EC 1.4.3.16)	<i>Escherichia coli</i>
o432-436#23	379988	379329	58.4	220	-	1466	100.0	220		<i>yfiC</i>	P31825	Hypothetical 24.5 Kd protein in <i>nadB-srmB</i> intergenic region.	<i>Escherichia coli</i>
o432-436#24	380120	381451	58.4	444	+	2881	100.0	444	<i>srmB, rbaB</i>		P21507	ATP-dependent RNA helicase SrmB.	<i>Escherichia coli</i>
o432-436#26	381890	381666	58.4	75	-	no_similarity							
o432-436#27	382548	381904	58.5	215	-	1422	100.0	215		<i>yfiE</i>	P33634	Hypothetical transcriptional regulator in <i>srmB-ung</i> intergenic region.	<i>Escherichia coli</i>
o436#28	382651	383235	58.5	195	+	1265	99.5	195		<i>yfiK</i>	P38101	Hypothetical 21.2 Kd protein in <i>srmB-ung</i> intergenic region.	<i>Escherichia coli</i>
o436#29	383677	383297	58.5	127	-	812	100.0	127		<i>yfiD</i>	P33633	Hypothetical 14.3 Kd protein in <i>srmB-ung</i> intergenic region.	<i>Escherichia coli</i>
o436#30	383982	384668	58.5	229	+	1578	100.0	229	<i>ung</i>		A28175	Uacil-DNA glycosylase (EC 3.2.2.-)	<i>Escherichia coli</i>
o436#31	385839	384505	58.5	445	-	2228	100.0	330		<i>yfiF</i>	P33635	Hypothetical 37.8 Kd protein in <i>srmB-ung</i> intergenic region.	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o436#32	385935	386165	58.5	77	+	215	96.7	30		<i>yfiG</i>	P33636	Hypothetical thioredoxin-like protein in <i>ung</i> 3' region.	<i>Escherichia coli</i>
o436#33	386215	386379	58.5	55	+	269	51.4	74	(<i>TRXA</i>)		P06544	Thioredoxin I (TRX-1)	<i>Anabaena sp. (strain pcc 7119)</i>
o436#34	386427	387146	58.5	240	+	no_similarity							
o436#35	387181	389838	58.6	886	+	no_similarity							
o436#36	389934	391307	58.6	458	+	2956	98.0	452	<i>psxA, psx</i>		P23830	CDP-diacylglycerol-serine o-phosphatidyltransferase (EC 2.7.8.8)	<i>Escherichia coli</i>
o436#37	391407	391676	58.6	90	+	628	100.0	90		<i>yfiM</i>	P46126	Hypothetical 9.9 Kd protein in <i>psxA-kgiP</i> intergenic region.	<i>Escherichia coli</i>
o436#38	392974	391679	58.7	432	-	2799	100.0	432	<i>kgiP, witA</i>		P17448	Alpha-ketoglutarate permease.	<i>Escherichia coli</i>
o437#1	398218	398472	58.8	85	+	no_similarity							
o437#2	401400	398830	58.9	857	-	5452	99.6	857	<i>clpB, htpM</i>		P03815	ClpB protein (heat shock protein F84.1).	<i>Escherichia coli</i>
o437#3	402261	401533	58.9	243	-	1671	100.0	243		<i>yfiH</i>	P33644	Hypothetical 26.3 Kd protein in <i>clpB</i> 5' region.	<i>Escherichia coli</i>
o437#4	402725	402261	58.9	155	-	390	77.5	80		<i>yfiI</i>	P33643	Hypothetical protein in <i>clpB</i> 5' region.	<i>Escherichia coli</i>
o437#5	403372	402317	58.9	352	-	1546	100.0	231		<i>yfiI</i>	P33643	Hypothetical protein in <i>clpB</i> 5' region.	<i>Escherichia coli</i>
o437#6	403375	404109	58.9	245	+	678	43.3	245	(<i>HI0177</i>)		P44553	Hypothetical protein HI0177.	<i>Haemophilus influenzae</i>
o437#7	404383	404721	58.9	113	+	720	100.0	113		<i>yfiA</i>	A30275	Hypothetical 13K protein (<i>pheA</i> 5' region)	<i>Escherichia coli</i>
o438#1	404974	406131	58.9	386	+	2477	100.0	386	<i>pheA</i>		A30261	Chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51)	<i>Escherichia coli</i>
o438#2	407298	406180	59.0	373	-	2458	100.0	373	<i>tyrA</i>		A30274	Chorismate mutase (EC 5.4.99.5) T / prephenate dehydrogenase (EC 1.3.1.12)	<i>Escherichia coli</i>
o438#3	408379	407312	59.0	356	-	2345	100.0	356	<i>aroF</i>		P00888	Phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive (EC 4.1.2.15)	<i>Escherichia coli</i>
o438#4	408589	408951	59.0	121	+	596	100.0	89			A30262	Hypothetical protein 89	<i>Escherichia coli (fragment)</i>
o438#5	409104	409619	59.0	172	+	no_similarity							
o438#6	409612	410202	59.0	197	+	no_similarity							
o438#7	410018	410299	59.0	94	+	no_similarity							
o438#8	410193	410366	59.0	58	+	no_similarity							
o438#9	410338	410838	59.0	167	+	510	100.0	79		<i>yfiN</i>	P46139	Hypothetical protein in <i>rplS</i> 5' region.	<i>Escherichia coli</i>
o438#10	410857	411336	59.1	160	+	1041	100.0	160		<i>yfiB</i>	P07021	Hypothetical 17.2 Kd protein in <i>rplS</i> 5' region.	<i>Escherichia coli</i>
o438#11	411762	411418	59.1	115	-	731	100.0	115	<i>rplS</i>		S07951	Ribosomal protein L19	<i>Escherichia coli</i>
o438#12	412570	411806	59.1	255	-	1715	100.0	255	<i>trmD</i>		A30380	tRNA (guanine-N1-)-methyltransferase (EC 2.1.1.31)	<i>Escherichia coli</i>
o438#13	413158	412604	59.1	185	-	1249	99.5	185		<i>yfiA</i>	P21504	Hypothetical 21.0 Kd protein in <i>trmD-rpsP</i> intergenic region.	<i>Escherichia coli</i>
o438#14	413493	413197	59.1	99	-	469	100.0	71	<i>rpsP</i>		P02372	30S ribosomal protein S16.	<i>Escherichia coli</i>
o438#15	415025	413667	59.2	453	-	2901	100.0	453	<i>ffh</i>		P07019	Signal recognition particle protein	<i>Escherichia coli</i>
o438#16	415117	415980	59.2	288	+	no_similarity							
o438#17	416049	417287	59.2	413	+	380	85.7	70		<i>yfiD</i>	P37908	Hypothetical 8.7 Kd protein in <i>grpE</i> 3' region.	<i>Escherichia coli</i>
o438#18	417938	417348	59.2	197	-	1231	100.0	197	<i>grpE</i>		S01240	Heat shock protein B25.3	<i>Escherichia coli</i>
o438#19	418246	417938	59.2	103	-	324	93.3	60		<i>yfiC</i>	P37907	Hypothetical 7.0 Kd protein in <i>grpE-recN</i> intergenic region.	<i>Escherichia coli</i>
o438#20	418061	418936	59.2	292	+	1921	99.7	292		<i>yfiB</i>	P37768	Hypothetical 32.6 Kd protein in <i>grpE-recN</i> intergenic region.	<i>Escherichia coli</i>
o438#21	419025	420683	59.2	553	+	3564	99.8	553	<i>recN, radB</i>		P05824	DNA repair protein RecN (recombination protein N).	<i>Escherichia coli</i>
o438#22	420835	421173	59.3	113	+	739	100.0	113	<i>smpA</i>		P23089	Small protein A.	<i>Escherichia coli</i>
o438#23	421528	421241	59.3	96	-	598	99.0	96		<i>yfiF</i>	P52119	Hypothetical 10.8 Kd protein in <i>smpA-smpB</i> intergenic region	<i>Escherichia coli</i>
o438#24	421994	421521	59.3	158	-	1020	100.0	158		<i>yfiG</i>	P52121	Hypothetical 17.8 Kd protein in <i>smpA-smpB</i> intergenic region	<i>Escherichia coli</i>
o438#25	422126	422605	59.3	160	+	1057	100.0	160	<i>smpB</i>		JS0701	SmpB protein	<i>Escherichia coli</i>
owisc1#1	423389	424627	59.3	413	+	2712	100.0	413	<i>intA, slpA, intX</i>		P32053	Prophage CP4-57 integrase.	<i>Escherichia coli</i>
owisc1#2	425830	424877	59.4	318	-	2143	100.0	318		<i>yfiH</i>	P52123	Hypothetical 37.1 Kd protein in <i>intA-ulpA</i> intergenic region	<i>Escherichia coli</i>
owisc1#3	425874	426083	59.4	70	+	474	100.0	70	<i>alpA, alp</i>		P33997	Prophage CP4-57 regulatory protein AlpA.	<i>Escherichia coli</i>
owisc1#4	426215	427621	59.4	469	+	3119	100.0	469		<i>yfiI</i>	P52124	Hypothetical 54.0 Kd protein in <i>alpA-gubD</i> intergenic region	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
owise1#5	427777	428400	59.4	208	+	1426	100.0	208		<i>yffJ</i>	P52125	Hypothetical 24.6 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#6	430770	428584	59.5	729	-	4770	100.0	729		<i>yffK</i>	P52126	Hypothetical 83.1 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#8	432383	430770	59.5	538	-	3573	100.0	538		<i>yffL</i>	P52127	Hypothetical 62.0 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#9	433006	432746	59.5	87	-	584	100.0	87		<i>yffM</i>	P52128	Hypothetical 10.0 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#10	433148	434218	59.5	357	+	2302	99.7	357		<i>yffN</i>	P52129	Hypothetical 40.1 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#11	434265	434582	59.6	106	+	684	100.0	106		<i>yffO</i>	P52130	Hypothetical 11.9 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#12	434934	435800	59.6	289	+	1904	99.3	289		<i>yffP</i>	P52131	Hypothetical 32.5 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#14	435895	436713	59.6	273	+	1817	100.0	273		<i>yffQ</i>	P52132	Hypothetical 31.3 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#16	436933	437631	59.6	233	+	1559	100.0	233		<i>yffR</i>	P52133	Hypothetical transcriptional regulator in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#17	437519	438352	59.6	278	+	1836	100.0	278		<i>yffS</i>	P52134	Hypothetical 30.3 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1#18	438379	438843	59.7	155	+	1046	100.0	155		<i>yffT</i>	P52135	Hypothetical 17.1 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
owise1-442#1	439385	439074	59.7	104	-	342	100.0	51		<i>yffU</i>	P52136	Putative arsenate reductase	<i>Escherichia coli</i>
o442#2	440066	439401	59.7	222	-	1410	100.0	222		<i>yffV</i>	P52137	Putative arsenical pump membrane protein .	<i>Escherichia coli</i>
o442#3	440351	440070	59.7	94	-	467	100.0	77		<i>yffV</i>	P52137	Putative arsenical pump membrane protein .	<i>Escherichia coli</i>
o442#4	440449	440210	59.7	80	-	238	100.0	39		<i>yffV</i>	P52137	Putative arsenical pump membrane protein .	<i>Escherichia coli</i>
o442#5	440549	442249	59.7	567	+	3583	100.0	567		<i>yffW</i>	P52138	Hypothetical 64.2 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
o442#8	443150	443605	59.8	152	+	1090	100.0	152		<i>yffX</i>	P52139	Hypothetical 17.3 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
o442#9	443617	444096	59.8	160	+	1021	100.0	160		<i>yffY</i>	P52140	Hypothetical 18.0 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
o442#12	444346	444660	59.8	105	+	721	100.0	105		<i>yffZ</i>	P52141	Hypothetical 11.7 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
o442#13	444684	445010	59.8	109	+	no_similarity							
o442#14	448226	445380	59.9	949	-	6108	99.8	949		<i>ypjA</i>	P52143	Hypothetical 98.4 Kd protein in <i>alpA-gabD</i> intergenic region	<i>Escherichia coli</i>
o442#17	450535	450299	59.9	79	-	232	69.6	56 (<i>pin</i>)			P03014	DNA-invertase PIN.	<i>Escherichia coli</i>
o442#18	453992	454663	60.0	224	+	158	28.7	122			P22630	α -amylase precursor (EC 3.2.1.1)	<i>Aeromonas hydrophila</i>
o443#1	456112	457191	60.0	360	+	no_similarity							
o443#2	457214	458479	60.1	422	+	1370	100.0	204		<i>ygaF</i>	P37339	Hypothetical protein in <i>gabP</i> 3'region .	<i>Escherichia coli</i>
o443#3	458505	459950	60.1	482	+	3150	100.0	482 <i>gabD</i>			P25526	Succinate-semialdehyde dehydrogenase (NADP+) (EC 1.2.1.16)	<i>Escherichia coli</i>
o443#4	459967	461244	60.1	426	+	2803	100.0	426 <i>gabT</i>			A37846	4-aminobutyrate transaminase (EC 2.6.1.19)	<i>Escherichia coli</i>
o443#5	461485	462882	60.2	466	+	3031	100.0	466 <i>gabP</i>			P25527	GabA permease (4-amino butyrate transport carrier)	<i>Escherichia coli</i>
o443#6	462906	463565	60.2	220	+	719	100.0	114		<i>ygaE</i>	P37338	Hypothetical transcriptional regulator in <i>gabP</i> 3'region .	<i>Escherichia coli</i>
o443#7	464015	463572	60.2	148	-	80	100.0	12		<i>yzzM</i>	P39169	Unknown protein from 2D-PAGE (spot LM6) .	<i>Escherichia coli</i>
o443#8	464260	464105	60.2	52	-	145	52.4	42 (ZK632.10)			P34655	Hypothetical 8.7 Kd protein ZK632.10 in chromosome III.	<i>Caenorhabditis elegans</i>
o443#9	464443	464739	60.2	99	+	247	41.1	95 (<i>hlyU</i>)			P52695	Transcriptional activator HlyU.	<i>Vibrio cholerae</i>
o443#10	464752	465273	60.2	174	+	no_similarity							
o445#1	465727	465326	60.2	134	-	859	100.0	134 <i>stpA</i> , <i>hnsB</i>			P30017	DNA-binding protein StpA.	<i>Escherichia coli</i>
o445#2	466396	466842	60.3	149	+	no_similarity							
o445#3	467238	466885	60.3	118	-	634	97.9	97		<i>ygaC</i>	P36931	Hypothetical 12.1 Kd protein in <i>stpA</i> 5'region.	<i>Escherichia coli</i>
o445#4	467366	467704	60.3	113	+	223	41.1	95		(<i>sqjD</i>)	P42617	Hypothetical 11.1 Kd protein in <i>exuR-tdcC</i> intergenic region	<i>Escherichia coli</i>
o445#5	467955	468605	60.3	217	+	470	55.0	129 (MG230)			P47472	Hypothetical protein MG230.	<i>Mycoplasma genitalium</i>
o445#6	468620	470173	60.3	518	+	3098	88.8	528 (<i>nrdE</i>)			Q08698	Ribonucleoside-diphosphate reductase 2 α chain (EC 1.17.4.1)	<i>Salmonella typhimurium</i>
o445#7	470034	470723	60.3	230	+	1143	86.8	197 (<i>nrdF</i>)			S34271	Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	<i>Salmonella typhimurium</i>
o445#8	470736	471692	60.4	319	+	734	100.0	110 <i>nrdF</i>			P37146	Ribonucleoside-diphosphate reductase 2 β chain (EC 1.17.4.1)	<i>Escherichia coli</i>
o445#9	472049	473248	60.4	400	+	2552	100.0	400 <i>proV</i>			P14175	Glycine betaine/l-proline transport ATP-binding protein ProV.	<i>Escherichia coli</i>
o445#10	473244	474305	60.4	354	+	2323	100.0	354 <i>proW</i>			JS0129	Glycine betaine/proline transport system protein ProW	<i>Escherichia coli</i>
o445#11	474366	475355	60.4	330	+	2218	100.0	330 <i>proX</i> , <i>proU</i>			P14177	Glycine betaine-binding periplasmic protein precursor.	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
o445#12	475550	475813	60.5	88	+	no_similarity							
o445#13	475843	476172	60.5	110	+	no_similarity							
o445#14	475946	476725	60.5	260	+	no_similarity							
o445#15	476852	477586	60.5	245	+	no_similarity							
o445#16	477579	477911	60.5	111	+	300	87.3	55		<i>ygaH</i>	P43667	Hypothetical protein in <i>emrR</i> 5'region.	<i>Escherichia coli</i>
o445#17	478005	478532	60.5	176	+	1160	100.0	176	<i>emrR</i> , <i>mprA</i>		P24201	EmrR protein.	<i>Escherichia coli</i>
o445#18	478662	479831	60.5	390	+	2454	99.5	390	<i>emrA</i>		JC1344	Multidrug resistant protein EmrA	<i>Escherichia coli</i>
o445#20	479851	481386	60.5	512	+	3361	99.6	512	<i>emrB</i>		JC1345	Multidrug resistant protein EmrB	<i>Escherichia coli</i>
o445#21	481968	481456	60.6	171	-	795	100.0	119		<i>ygaG</i>	P45578	Hypothetical protein in <i>emrB</i> 3'region.	<i>Escherichia coli</i>
o446#1	483674	482121	60.6	518	-	3434	99.2	518	<i>gshA</i> , <i>gshI</i> ,		A24136	Glutamate-cysteine ligase (EC 6.3.2.2)	<i>Escherichia coli</i>
o446#2	484082	483750	60.6	111	-	375	47.1	136	(<i>HI0489</i>)		P44005	Hypothetical protein HI0489.	<i>Haemophilus influenzae</i>
o446#3	484738	484175	60.7	188	-	533	42.0	188	(<i>HI0488</i>)		P44004	Hypothetical protein HI0488.	<i>Haemophilus influenzae</i>
o446#4	485834	485553	60.7	94	-	no_similarity							
o446#5	486380	486198	60.7	61	-	376	100.0	61	<i>csrA</i> , <i>zfa</i>		P31803	Carbon storage regulator.	<i>Escherichia coli</i>
o446#6	489245	486618	60.8	876	-	5621	98.7	876	<i>alaS</i> , <i>lovB</i>		P00957	Alanyl-tRNA synthetase (EC 6.1.1.7)	<i>Escherichia coli</i>
o446#8	489873	489376	60.8	166	-	1103	98.8	166	<i>oraA</i> , <i>recX</i>		P33596	Regulatory protein RecX (OraA protein).	<i>Escherichia coli</i>
o446#9	491000	489945	60.8	352	-	2233	99.7	352	<i>recA</i> , <i>lexB</i> , <i>umuB</i> , <i>recH</i> , <i>rnmB</i> , <i>tif</i> , <i>zab</i>		P03017	RecA protein.	<i>Escherichia coli</i> , and <i>Shigella flexneri</i>
o446#10	491580	491086	60.8	165	-	1067	100.0	165		<i>ygaD</i>	P41053	Hypothetical 17.6 Kd protein in <i>mltB-recA</i> intergenic region.	<i>Escherichia coli</i>
o446#11	492810	491728	60.8	361	-	2467	100.0	361	<i>mltB</i>		P41052	Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)	<i>Escherichia coli</i>
o446#12	493066	494583	60.8	506	+	3344	100.0	506	<i>srlA</i> , <i>gutA</i> , <i>sbl</i>		P05705	PTS system, glucitol/sorbitol-specific IIBC component (EC 2.7.1.69)	<i>Escherichia coli</i>
o446#13	494597	494965	60.9	123	+	819	100.0	123	<i>srlB</i> , <i>gutB</i>		B26725	Phosphotransferase system enzyme II (EC 2.7.1.69), sorbitol-specific, factor III	<i>Escherichia coli</i>
o446#14	494972	495748	60.9	259	+	1676	100.0	259	<i>srlD</i> , <i>gutD</i>		P05707	Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140)	<i>Escherichia coli</i>
o446#15	495857	496213	60.9	119	+	791	100.0	119	<i>gutM</i> , <i>srlM</i>		P15081	Glucitol operon activator protein.	<i>Escherichia coli</i>
o446-wisc2#1	496283	497053	60.9	257	+	1637	100.0	257	<i>srlR</i> , <i>gutR</i>		P15082	Glucitol operon repressor.	<i>Escherichia coli</i>
owisc2#2	497037	498011	60.9	325	+	1297	93.2	220	<i>gutQ</i> , <i>srlQ</i>		P17115	GutQ protein.	<i>Escherichia coli</i>
owisc2#3	498556	498014	61.0	181	-	1185	100.0	181		<i>ygaA</i>	P37013	Hypothetical 58.1 Kd protein in <i>gutQ</i> 3'region.	<i>Escherichia coli</i>
owisc2#4	499619	498546	61.0	358	-	2238	100.0	348		<i>ygaA</i>	P37013	Hypothetical 58.1 Kd protein in <i>gutQ</i> 3'region.	<i>Escherichia coli</i>
owisc2#5	500240	499686	61.0	185	-	398	100	60		<i>ygaB</i>	P37015	Hypothetical protein in <i>gutQ</i> 3'region.	<i>Escherichia coli</i>
owisc2#6	499713	501149	61.0	479	+	151	30.8	52	(<i>alkG</i>)		P00272	Rubredoxin 2.	<i>Pseudomonas oleovorans</i>
owisc2#7	501149	502279	61.0	377	+	2425	99.7	377		<i>ygbD</i>	P37596	Hypothetical 41.4 Kd protein in <i>hydA</i> 3'region (EC 1.18.1.-)	<i>Escherichia coli</i>
owisc2#8	504860	502413	61.1	816	-	4999	96.7	750	<i>hypF</i> , <i>hydA</i>		P30131	Transcriptional regulatory protein HypF.	<i>Escherichia coli</i>
owisc2#9	505342	504818	61.1	175	-	1236	100	175	<i>hydN</i>		P30132	Electron transport protein HydN.	<i>Escherichia coli</i>
owisc2#10	506597	505494	61.1	368	-	1960	93.8	339	<i>ascG</i>		S27551	Regulatory protein AscG	<i>Escherichia coli</i>
owisc2#12	506761	508215	61.1	485	+	3037	99	485	<i>ascF</i>		B44070	Phosphotransferase system enzyme II (EC 2.7.1.69) Asc	<i>Escherichia coli</i>
owisc2#13	508227	509648	61.2	474	+	3207	98.9	474	<i>ascB</i>		C44070	Phospho- β -glucosidase	<i>Escherichia coli</i>
owisc2#14	510280	509813	61.2	156	-	no_similarity							
owisc2#15	510683	510276	61.2	136	-	900	100	136	<i>hycH</i> , <i>hevH</i>		P16434	Formate hydrogenlyase maturation protein HycH.	<i>Escherichia coli</i>
owisc2#16	511447	510683	61.2	255	-	1745	100	255	<i>hycG</i>		S08625	Probable hydrogenase 3 protein 7	<i>Escherichia coli</i>
owisc2#17	511989	511450	61.2	180	-	1260	100	180	<i>hycF</i> , <i>hevF</i>		P16432	Formate hydrogenlyase subunit 6 (Fhl subunit 6).	<i>Escherichia coli</i>
owisc2#18	513708	512002	61.3	569	-	3849	99.6	569	<i>hycE</i> , <i>hevE</i>		P16431	Formate hydrogenlyase subunit 5 precursor (Fhl subunit 5)	<i>Escherichia coli</i>
owisc2#19	514649	513729	61.3	307	-	1973	100	307	<i>hycD</i> , <i>hevD</i>		P16430	Formate hydrogenlyase subunit 4 (Fhl subunit 4)	<i>Escherichia coli</i>
owisc2#20	516478	514655	61.3	608	-	3972	99.7	608	<i>hycC</i> , <i>hevC</i>		P16429	Formate hydrogenlyase subunit 3 (Fhl subunit 3)	<i>Escherichia coli</i>
owisc2#21	517086	516478	61.4	203	-	1418	99	203	<i>hycB</i> , <i>hevB</i>		P16428	Formate hydrogenlyase subunit 2 (Fhl subunit 2).	<i>Escherichia coli</i>
owisc2#22	517672	517214	61.4	153	-	1019	100	153	<i>hycA</i> , <i>hevA</i>		P16427	Formate hydrogenlyase regulatory protein HycA.	<i>Escherichia coli</i>
owisc2#23	517884	518231	61.4	116	+	811	100	116	<i>hypA</i>		S15197	HypA protein	<i>Escherichia coli</i>
owisc2#24	518238	519107	61.4	290	+	1936	99.7	290	<i>hypB</i>		S15198	Hydrogenase isozyme HypB	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score*	%	overlap*	gene*	y gene*	accession*	description	species
owise2#25	519101	519370	61.4	90	+	612	100	90	<i>hypC</i>		S15199	Hydrogenase isozyme HypC	<i>Escherichia coli</i>
owise2#26	519373	520491	61.4	373	+	2562	99.7	373	<i>hypD</i>		S15200	Hydrogenase isozyme HypD	<i>Escherichia coli</i>
owise2#27	520533	521498	61.4	322	+	2074	99.7	322	<i>hypE</i>		S15201	HypE protein	<i>Escherichia coli</i>
owise2#28	521575	523650	61.4	692	+	4486	100	692	<i>fhIA</i>		S12079	Transcriptional activator FhIA	<i>Escherichia coli</i>
owise2#30	524043	523693	61.5	117	-	840	100	117		<i>ygbA</i>	P25728	Hypothetical 13.9 Kd protein in <i>fhIA-mutS</i> intergenic region.	<i>Escherichia coli</i>
owise2#32	524330	526888	61.5	853	+	5504	100	853	<i>mutS, fdv</i>		P23909	DNA mismatch repair protein MutS.	<i>Escherichia coli</i>
owise2#33	526997	527650	61.6	218	+	656	45.8	214			P03772	Serine/threonine protein phosphatase (EC 3.1.3.16).	<i>Bacteriophage lambda</i>
owise2#34	528501	527707	61.6	265	-	1668	100	265		<i>ygbI</i>	P52598	Hypothetical transcriptional regulator in <i>mutS-rpoS</i> intergenic region (F265).	<i>Escherichia coli</i>
owise2#35	528668	529573	61.6	302	+	1335	72.9	292	(HI1010)		P44979	Hypothetical protein HI1010.	<i>Haemophilus influenzae</i>
owise2#36	529573	530736	61.6	388	+	1360	55.2	382	(HI1011)		P44093	Hypothetical protein HI1011.	<i>Haemophilus influenzae</i>
owise2#37	530658	530831	61.6	58	+	148	58.3	36	(HI1011)		P44093	Hypothetical protein HI1011.	<i>Haemophilus influenzae</i>
owise2#38	530831	531466	61.6	212	+	276	35.2	165	(<i>ficA</i> , HI0611)		P44777	L-fucose phosphate aldolase (EC 4.1.2.17).	<i>Haemophilus influenzae</i>
owise2#39	531474	532247	61.7	258	+	708	40.3	258	(<i>gip</i>)		P30147	Glyoxylate-induced protein.	<i>Escherichia coli</i>
owise2#40	532339	533700	61.7	454	+	426	33.3	450	(<i>gatU</i>)		P46858	Low-affinity gluconate transporter (Gluconate permease) (GNT-I system).	<i>Escherichia coli</i>
owise2#41	534789	533800	61.7	330	-	2101	100	330	<i>rpoS, katF, appR, sigS, otsX, nur</i>		P13445	RNA polymerase sigma factor RpoS (Sigma-38).	<i>Escherichia coli</i>
owise2#42	535991	534855	61.8	379	-	2465	100	379	<i>nlpD</i>		P33648	Lipoprotein NlpD precursor.	<i>Escherichia coli</i>
owise2#44	536757	536134	61.8	208	-	1369	100	208	<i>pcm</i>		JH0242	Protein-L-isواسpartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) precursor	<i>Escherichia coli</i>
owise2#45	537512	536754	61.8	253	-	1712	100	253	<i>surE</i>		P36664	Survival protein SurE.	<i>Escherichia coli</i>
owise2#46	538542	537496	61.8	349	-	945	44	341	(HI0701)		P44039	Hypothetical protein HI0701.	<i>Haemophilus influenzae</i>
owise2#47	539018	538542	61.8	159	-	1057	100	159		<i>ygbB</i>	P36663	Hypothetical 16.9 Kd protein in <i>surE-cysC</i> intergenic region	<i>Escherichia coli</i>
owise2#48	539728	539021	61.8	236	-	436	37	219	(<i>yacM</i>)		Q06755	Hypothetical 25.8 Kd protein in <i>mecB-gltX</i> intergenic region.	<i>Bacillus subtilis</i>
owise2#49	540058	539750	61.8	103	-	250	42.9	91	(HI0673)		P44035	Hypothetical protein HI0673.	<i>Haemophilus influenzae</i>
owise2#50	540648	540253	61.9	132	-	451	84.1	82		<i>ygbE</i>	P46141	Hypothetical protein in <i>surE-cysC</i> intergenic region	<i>Escherichia coli</i>
owise2#51	541225	540626	61.9	200	-	1308	99.5	200	<i>cysC</i>		P23846	Adenylylsulfate kinase (EC 2.7.1.25)	<i>Escherichia coli</i>
owise2#52	542655	541231	61.9	475	-	3075	100	475	<i>cysN</i>		JN0327	Sulfate adenylyltransferase (EC 2.7.7.4) large chain	<i>Escherichia coli</i>
owise2#53	543565	542660	61.9	302	-	2054	99.7	302	<i>cysD</i>		JN0326	Sulfate adenylyltransferase (EC 2.7.7.4) small chain	<i>Escherichia coli</i>
owise2#54	543817	544851	61.9	345	+	2282	100	345	<i>iap</i>		A28382	Alkaline phosphatase isozyme conversion protein (EC 3.4.11.-)	<i>Escherichia coli</i>
owise2#55	545335	545721	62.0	129	+	no_similarity							
owise2#56	546155	545808	62.0	116	-	770	100	116		<i>ygbF</i>	P45956	Hypothetical 13.2 KD protein in <i>iap</i> 3'region.	<i>Escherichia coli</i>
owise2#57	547008	546094	62.0	305	-	no_similarity							
owise2#58	547623	547027	62.0	199	-	no_similarity							
owise2#59	547279	547437	62.0	53	+	no_similarity							
owise2#60	548284	547613	62.0	224	-	no_similarity							
owise2#61	549378	548290	62.0	363	-	no_similarity							
owise2#62	551373	549868	62.1	502	-	no_similarity							
owise2#64	554499	551791	62.2	903	-	2308	99.7	333		<i>ygcB</i>	P38036	Hypothetical protein in <i>cysH</i> 3'region	<i>Escherichia coli</i>
owise2#65	555547	554816	62.2	244	-	1630	100	244	<i>cysH</i>		S14221	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (EC 2.8.2.-)	<i>Escherichia coli</i>
owise2#66	557334	555625	62.2	570	-	3805	99.8	570	<i>cysI, cysQ</i>		B34354	Sulfite reductase (NADPH) (EC 1.8.1.2) hemoprotein	<i>Escherichia coli</i>
owise2#67	559133	557337	62.3	599	-	3907	99.5	599	<i>cysJ</i>		B34231	Sulfite reductase (NADPH) (EC 1.8.1.2)	<i>Escherichia coli</i>
owise2#68	559449	559811	62.3	121	+	no_similarity							
owise2#69	559892	561160	62.3	423	+	1085	40.7	430	(<i>fixC</i>)		P31575	FixC protein.	<i>Escherichia coli</i>
owise2#70	561154	561411	62.3	86	+	272	48.6	72	(<i>fixX</i>)		P31576	Ferredoxin like protein.	<i>Escherichia coli</i>
owise2#71	561431	562003	62.3	191	+	361	28.1	185	(<i>glpP</i>)		P30300	Glycerol uptake operon antiterminal regulatory protein.	<i>Bacillus subtilis</i>
owise2#72	563047	562157	62.3	297	-	305	33.9	218	(<i>ETF A</i>)		P38974	Electron transfer flavoprotein α -subunit (α -ETF)	<i>Paracoccus denitrificans</i>
owise2#74	563791	563084	62.4	236	-	178	29.4	119	(<i>ETF B</i>)		P38117	Electron transfer flavoprotein β -subunit (β -etf).	<i>Homo sapiens (Human)</i>
owise2#75	565178	563772	62.4	469	-	334	37.6	141		(<i>yaaU</i>)	P31679	Hypothetical 18.4 Kd protein in <i>fixC-kefC</i> intergenic region	<i>Escherichia coli</i>
owise2#76	565994	565203	62.4	264	-	no_similarity							
owise2#77	566362	566000	62.4	121	-	no_similarity							

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
owisc2#78	566652	566374	62.4	93	-	no_similarity							
owisc2#79	567582	566725	62.4	286	-	699	46.4	252	(<i>kdsD</i>)		P50842	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) (2-keto-3-deoxygluconate oxydoreductase).	<i>Bacillus subtilis</i>
owisc2#80	567826	569100	62.4	425	+	603	25.5	408		(<i>yihN</i>)	P32135	Hypothetical 46.3 Kd protein in <i>glnA-fdhE</i> intergenic region	<i>Escherichia coli</i>
owisc2#81	569484	570605	62.5	374	+	2528	99.5	374		(<i>ycE</i>)	P55138	Hypothetical 41.5 Kd protein in <i>cysJ-eno</i> intergenic region	<i>Escherichia coli</i>
owisc2#82	572653	571985	62.6	223	-	1506	99.6	223		(<i>ycF</i>)	P55139	Hypothetical 25.0 Kd protein in <i>cysJ-eno</i> intergenic region	<i>Escherichia coli</i>
owisc2#83	572877	573815	62.6	313	+	2085	100	313		(<i>ycG</i>)	P55140	Hypothetical 34.9 Kd protein in <i>cysJ-eno</i> intergenic region	<i>Escherichia coli</i>
owisc2#85	575173	573881	62.6	431	-	2725	100	431	<i>eno</i>		P08324	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)	<i>Escherichia coli</i>
owisc2#86	576898	575267	62.6	544	-	3571	100	544	<i>pyrG</i>		P08398	CTP synthase (EC 6.3.4.2) (UTP-ammonia ligase)	<i>Escherichia coli</i>
owisc2#87	577920	577132	62.7	263	-	1725	100	263	<i>mazG</i>		P33646	MazG protein.	<i>Escherichia coli</i>
owisc2#88	578326	577994	62.7	111	-	752	100	111	<i>chpA, mazF, chpAK</i>		P33645	PemK-like protein 1 (MazF protein).	<i>Escherichia coli</i>
owisc2#89	578574	578329	62.7	82	-	551	100	82	<i>chpR, mazE, chpAI</i>		P18534	PemI-like protein 1 (MazE protein).	<i>Escherichia coli</i>
owisc2#90	580886	578655	62.7	744	-	4957	100	744	<i>relA</i>		P11585	GTP pyrophosphokinase (EC 2.7.6.5) (ATP:GTP 3'-pyrophosphotransferase) (ppGpp synthetase I).	<i>Escherichia coli</i>
owisc2#91	582235	580937	62.8	433	-	2857	100	433		(<i>ycA</i>)	P55135	Hypothetical RNA methyltransferase in <i>relA-barA</i> intergenic region (EC 2.1.1.-).	<i>Escherichia coli</i>
owisc2#92	582292	585045	62.8	918	+	5936	100	918	<i>barA</i>		S20550	Sensor-regulator protein BarA	<i>Escherichia coli</i>
owisc2#93	586620	585283	62.9	446	-	2253	70.4	452	(<i>ycbF</i>)		P42238	Probable glucarate dehydratase (EC 4.2.1.40) (GDH).	<i>Bacillus subtilis</i>
owisc2#94	587996	586644	62.9	451	-	2022	66	441	(<i>ycbF</i>)		P42238	Probable glucarate dehydratase (EC 4.2.1.40) (GDH).	<i>Bacillus subtilis</i>
owisc2#95	589335	587986	62.9	450	-	1978	65.8	433	(<i>ycbE</i>)		P42237	Probable glucarate transporter.	<i>Bacillus subtilis</i>
owisc2#96	590219	589773	62.9	149	-	261	30.7	150	(<i>mioC</i>)		P03817	MioC protein.	<i>Escherichia coli</i>
owisc2#97	591019	590240	62.9	260	-	687	65.8	161	(HI1435)		P44197	Hypothetical protein HI1435.	<i>Haemophilus influenzae</i>
owisc2#98	591348	591022	63.0	109	-	no_similarity							
owisc2#99	592515	591973	63.0	181	-	1212	99.4	181	<i>syd, ydr</i>		P43526	Syd protein.	<i>Escherichia coli</i>
owisc2#100	592583	593428	63.0	282	+	1152	61.4	280	(HI1291)		P44153	Hypothetical protein HI1291.	<i>Haemophilus influenzae</i>
owisc2#101	593543	594904	63.0	454	+	538	98.8	81		(<i>ygdH</i>)	P37350	Hypothetical protein in <i>sdaC</i> 5' region	<i>Escherichia coli</i>
owisc2#102	595464	596750	63.0	429	+	2745	100	429	<i>sdaC</i>		S45633	Probable serine transport protein	<i>Escherichia coli</i>
owisc2#103	596811	598175	63.1	455	+	2887	97.4	455	<i>sdaB</i>		S30351	L-serine deaminase	<i>Escherichia coli</i>
owisc2#104	598290	599042	63.1	251	+	1704	99.6	251	<i>exo</i>		P38506	Potential 5'-3' exonuclease (EC 3.1.11.-).	<i>Escherichia coli</i>
owisc2#105	600251	599103	63.1	383	-	2520	100	383	<i>ficO</i>		A32883	Lactaldehyde reductase (EC 1.1.1.77)	<i>Escherichia coli</i>
owisc2#106	600923	600279	63.2	215	-	1406	100	215	<i>ficA, ficC, prd</i>		P11550	L-fuculose phosphate aldolase (EC 4.1.2.17).	<i>Escherichia coli</i>
owisc2#107	601470	602783	63.2	438	+	2851	100	438	<i>ficP</i>		JS0184	Fucose permease	<i>Escherichia coli</i>
owisc2#108	602819	604591	63.2	591	+	4008	100	591	<i>ficI</i>		JS0185	Isomerase <i>ficI</i> (EC 5.-.-.-)	<i>Escherichia coli</i>
owisc2#109	604673	606118	63.2	482	+	3212	100	482	<i>ficK</i>		JS0186	Fucokinase (EC 2.7.1.52)	<i>Escherichia coli</i>
owisc2#110	606123	606542	63.3	140	+	693	92.2	116	<i>ficU</i>		P11555	Fucose operon <i>FucU</i> protein.	<i>Escherichia coli</i>
owisc2#111	606603	607331	63.3	243	+	1571	100	243	<i>ficR</i>		JS0188	<i>fic</i> operon regulatory protein	<i>Escherichia coli</i>
owisc2#112	608478	607381	63.3	366	-	2537	100	366			I41067	Hypothetical protein 3 (<i>gcvA</i> region)	<i>Escherichia coli</i>
owisc2#113	607574	607768	63.3	65	+	416	100	63			PS0038	Hypothetical protein 63 (<i>fucR</i> 3' region)	<i>Escherichia coli</i> (fragment)
owisc2#114	608866	608474	63.3	131	-	858	100	131			I41066	Hypothetical protein 2 (<i>gcvA</i> region)	<i>Escherichia coli</i>
owisc2#115	609802	608888	63.4	305	-	1989	100	305	<i>gcvA</i>		I41065	Glycine cleavage activator protein	<i>Escherichia coli</i>
owisc2#116	610383	610156	63.4	76	-	no_similarity							
owisc2#117	610572	611774	63.4	401	+	301	28.8	392	(<i>nifS</i>)		Q01179	NifS protein.	<i>Rhodobacter sphaeroides</i> (<i>Rhodopseudomonas sphaeroides</i>)
owisc2#118	611777	612217	63.4	147	+	156	35.5	76	(HI1293)		P44155	Hypothetical protein HI1293.	<i>Haemophilus influenzae</i>
owisc2#119	613077	612274	63.4	268	-	395	31.2	202	(<i>YK1.027W</i>)		P36101	Hypothetical 50.3 Kd protein in <i>TFAI-URA6</i> intergenic region.	<i>Saccharomyces cerevisiae</i> (<i>Baker's yeast</i>)
owisc2#120	614413	613319	63.5	365	-	2486	99.7	365	<i>mltA, mlt</i>		P46885	Membrane-bound lytic murein transglycosylase a precursor (EC	<i>Escherichia coli</i>
owisc2#121	616335	614995	63.5	447	-	564	30.3	416	(<i>amiB</i>)		P26365	N-acetylmuramoyl-L-alanine amidase precursor (EC 3.5.1.28).	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
owisc2#122	616477	617805	63.5	443	+	2856	99.8	443	<i>argA</i>		P08205	Amino-acid acetyltransferase (EC 2.3.1.1)	<i>Escherichia coli</i>
owisc2#123	619696	617873	63.6	608	-	3937	99.3	608	<i>recD</i>		P04993	Exodeoxyribonuclease V 67 Kd polypeptide (EC 3.1.11.5)(Exonuclease V α chain).	<i>Escherichia coli</i>
owisc2#124	623238	619699	63.6	1180	-	7830	100	1180	<i>recB, rorA</i>		P08394	Exodeoxyribonuclease V 135 Kd polypeptide (EC 3.1.11.5) (Exonuclease V β chain).	<i>Escherichia coli</i>
owisc2#125	626119	623234	63.7	962	-	6288	99.9	962	<i>ptr</i>		P05458	Protease III precursor (EC 3.4.24.55) (Pitriylisin) (Protease P1).	<i>Escherichia coli</i>
owisc2#126	629663	626298	63.8	1122	-	7637	100	1122	<i>recC</i>		P07648	Exodeoxyribonuclease V 125 Kd polypeptide (EC 3.1.11.5) (Exonuclease V γ chain).	<i>Escherichia coli</i>
owisc2#127	629999	629679	63.8	107	-	720	100	107			E24137	Hypothetical 12K protein (<i>thyA-recC</i> intergenic region)	<i>Escherichia coli</i>
owisc2#128	630349	629987	63.8	121	-	824	100	121			D24137	Hypothetical 13K protein	<i>Escherichia coli</i>
owisc2#129	631191	630391	63.8	267	-	1802	100	267			C24137	Hypothetical 30K protein (<i>thyA-recC</i> intergenic region)	<i>Escherichia coli</i>
owisc2#130	631412	630945	63.8	156	-	1091	99.4	156	<i>ppdA</i>		P33554	Prepilin peptidase dependent protein A precursor.	<i>Escherichia coli</i>
owisc2#131	632390	631599	63.8	264	-	1851	99.6	264	<i>thyA</i>		A00549	Thymidylate synthase (EC 2.1.1.45)	<i>Escherichia coli</i>
owisc2#132	633272	632400	63.9	291	-	1986	99	291	<i>lgt, umpA</i>		P37149	Prolipoprotein diacylglycerol transferase (EC 2.4.99.-).	<i>Escherichia coli</i>
owisc2#133	635669	633426	63.9	748	-	4816	100	748	<i>ptsP</i>		P37177	Phosphoenolpyruvate-protein phosphotransferase PtsP (EC 2.7.3.9)	<i>Escherichia coli</i>
owisc2#134	636212	635685	63.9	176	-	152	32.8	64	<i>(y2gD)</i>		P46351	Hypothetical 45.4 Kd protein in thiaminase I 5' region.	<i>Bacillus subtilis</i>
owisc2#135	636900	637583	63.9	228	+	1501	100	228	<i>mutH, mutR, prv</i>		P06722	DNA mismatch repair protein MutH.	<i>Escherichia coli</i>
owisc2#136	637655	638365	64.0	237	+	931	61.4	236	(HI0056)		P43932	Hypothetical protein HI0056.	<i>Haemophilus influenzae</i>
owisc2#137	638506	638721	64.0	72	+	no_similarity							
owisc2#138	638832	639869	64.0	346	+	300	36.6	279		<i>ygeD</i>	P40690	Aldo-keto reductase	<i>Babesia bovis</i>
owisc2#139	641115	639907	64.0	403	-	484	96.2	78			P39196	Hypothetical 8.7 Kd protein in <i>mutH-aas</i> intergenic region.	<i>Escherichia coli</i>
owisc2#140	643249	641093	64.1	719	-	4708	99.6	719	<i>aas</i>		P31119	2-acylglycerophosphoethanolamine acyltransferase / Acyl-acyl carrier protein synthetase (2-acyl-GPE acyltransferase / acyl-acyl synthetase).	<i>Escherichia coli</i>
owisc2#141	643834	644862	64.1	343	+	2220	100	343	<i>galR</i>		A93910	<i>gal</i> repressor	<i>Escherichia coli</i>
owisc2#142	646134	644875	64.1	420	-	2799	100	420	<i>lysA</i>		P00861	Diaminopimelate decarboxylase (EC 4.1.1.20)	<i>Escherichia coli</i>
owisc2#143	646256	647188	64.1	311	+	1990	99.7	311	<i>lysR</i>		A03565	Regulatory protein LysR	<i>Escherichia coli</i>
owisc2#144	647870	647181	64.2	230	-	1511	100	230			A04438	Hypothetical protein (<i>lys</i> operon)	<i>Escherichia coli</i>
owisc2#145	649417	648002	64.2	472	-	3009	99.8	472	<i>araE</i>		B26430	Arabinose transport protein	<i>Escherichia coli</i>
owisc2#146	650493	649735	64.2	253	-	1642	100	253	<i>kduD</i>		P37769	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) (2-Keto-3-deoxygluconate oxydoreductase).	<i>Escherichia coli</i>
owisc2#147	651359	650526	64.2	278	-	1460	73.7	278	<i>(kdu)</i>		Q05529	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17) (5-Keto-4-deoxyuronate isomerase) (DK1 isomerase).	<i>Erwinia chrysanthemi</i>
owisc2#148	652830	651649	64.3	394	-	1610	61.6	393	<i>(phbA)</i>		P45363	Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA	<i>Thiocystis violacea</i>
owisc2#149	653082	654308	64.3	409	+	1043	38.8	415	<i>(sdaC)</i>		P36559	Serine transporter.	<i>Escherichia coli</i>
owisc2#150	658470	658991	64.4	174	+	374	36.7	139	<i>(yppI)</i>		P18008	IppI protein.	<i>Shigella flexneri, and Shigella dysenteriae</i>
owisc2#151	659329	660702	64.4	458	+	596	28.9	408	<i>(iagA, hila)</i>		P43015	Invasion protein IagA (protein HilA).	<i>Salmonella typhimurium</i>
owisc2#152	661235	661648	64.5	138	+	294	38.7	137	<i>(iagB)</i>		P43018	Invasion protein IagB.	<i>Salmonella typhi</i>
owisc2#153	662142	661699	64.5	148	-	243	31.9	144	<i>(bvGA)</i>		P16574	Virulence factors putative positive transcription regulator BvGA.	<i>Bordetella pertussis, Bordetella bronchiseptica, and Bordetella</i>
owisc2#154	664513	663611	64.5	301	-	2068	99.7	301	<i>IS2</i>		JQ0040	Hypothetical 34K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#155	664037	664465	64.5	143	+	956	99.3	143	<i>IS2</i>		JQ0042	Hypothetical 16K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#156	664440	664150	64.5	97	-	688	99	97	<i>IS2</i>		JQ0041	Hypothetical 11K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#157	664881	664474	64.5	136	-	855	99.3	136	<i>IS2</i>		S56497	Hypothetical 13K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#158	666106	665273	64.6	278	-	no_similarity							
owisc2#159	667127	666375	64.6	251	-	566	45	262	<i>(nlpD)</i>		P33648	Lipoprotein NlpD precursor.	<i>Escherichia coli</i>
owisc2#161	667542	669836	64.6	765	+	524	26	761	<i>(RY, XDH)</i>		P22811	Xanthine dehydrogenase (EC 1.1.1.204) (XD) (Rosy locus protein).	<i>Drosophila pseudoobscura (Fruit fly)</i>
owisc2#163	669850	670725	64.6	292	+	no_similarity							
owisc2#164	670725	671201	64.7	159	+	404	45.6	147	<i>(coxS)</i>		B56279	Carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain	<i>Pseudomonas carboxydovorans</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
owisc2#165	673022	671247	64.7	592	-	804	45.7	317	(<i>src</i>)		P26047	Signal-transduction and transcriptional-control protein	<i>Clostridium beijerinckii</i> (<i>Clostridium mp</i>)
owisc2#166	673569	674657	64.7	363	+	150	25.5	369	(<i>argF</i>)		P18186	Ornithine carbamoyltransferase chain F (EC 2.1.3.3)	<i>Bacillus subtilis</i>
owisc2#167	674744	675937	64.8	398	+	188	27.8	324	(<i>ilvA</i>)		P20506	Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine deaminase).	<i>Salmonella typhimurium</i>
owisc2#168	675998	677206	64.8	403	+	289	28.5	376	(<i>argE</i>)		P23908	Acetylornithine deacetylase (EC 3.5.1.16) (Acetylornithinase) (AO) (N-Acetylornithinase) (NAO).	<i>Escherichia coli</i>
owisc2#169	677262	678644	64.8	461	+	937	35.8	464			P47942	Turned on after division, 64 KD protein (TOAD-64).	<i>Rattus norvegicus</i> (<i>Rat</i>)
owisc2#170	678695	679624	64.8	310	+	731	44.6	314	(<i>arcC</i> , HI0595)		P44769	Carbamate kinase (EC 2.7.2.2).	<i>Haemophilus influenzae</i>
owisc2#171	681473	679851	64.9	541	-	no_similarity							
owisc2#172	682192	681524	64.9	223	-	no_similarity							
owisc2#173	682394	682969	64.9	192	+	no_similarity							
owisc2#174	683294	686389	64.9	1032	+	337	31.2	426	(<i>gltD</i> , <i>aspB</i>)		P09832	Glutamate synthase (NADPH) small chain (EC 1.4.1.13) (Glutamate synthase β subunit) (NADPH-GOGAT) (GLTS β chain).	<i>Escherichia coli</i>
owisc2#176	686395	687720	65.0	442	+	no_similarity							
owisc2#177	687774	688550	65.0	259	+	no_similarity							
owisc2#178	688550	691417	65.1	956	+	451	25	768	(<i>xdh</i>)		P08793	Xanthine dehydrogenase (EC 1.1.1.204) (XD).	<i>Calliphora vicina</i> (<i>Blue blowfly</i>) (<i>Calliphora erythrocephala</i>)
owisc2#179	691585	692982	65.1	466	+	1269	44.2	452		(<i>vicE</i>)	P27432	Hypothetical 48.9 Kd protein in <i>gltS</i> 3'region.	<i>Escherichia coli</i>
owisc2#180	692880	694316	65.1	479	+	no_similarity							
owisc2#181	694355	694921	65.2	189	+	958	83.8	173		(<i>ycjD</i>)	P32702	Hypothetical 45.7 Kd protein in <i>soxR-acs</i> intergenic region	<i>Escherichia coli</i>
owisc2#182	694927	695718	65.2	264	+	1450	81.3	278		(<i>ycjD</i>)	P32702	Hypothetical 45.7 Kd protein in <i>soxR-acs</i> intergenic region	<i>Escherichia coli</i>
owisc2#183	696248	695760	65.2	163	-	385	40.7	167	(<i>hydN</i>)		P30132	Electron transport protein HydN.	<i>Escherichia coli</i>
owisc2#184	698179	696248	65.3	644	-	1861	59.7	449	(<i>gltD</i> , <i>aspB</i>)		P09832	Glutamate synthase (NADPH) small chain (EC 1.4.1.13)	<i>Escherichia coli</i>
owisc2#185	698531	700045	65.3	505	+	1224	41.8	428	(<i>pbuX</i>)		P42086	Xanthine permease.	<i>Bacillus subtilis</i>
owisc2#186	700298	700843	65.3	182	+	161	27	196	(<i>IDH1</i> , <i>BOT2</i> , <i>YPL117C</i> , <i>LPH10C</i>)		P15496	Isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) (IPP isomerase) (<i>Baker's yeast</i>)	<i>Saccharomyces cerevisiae</i> (<i>Baker's yeast</i>)
owisc2#187	702404	700893	65.3	504	-	3309	100	504	(<i>lysS</i> , <i>herC</i> , <i>asuD</i>)		P13030	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine-tRNA ligase) (LysRS).	<i>Escherichia coli</i>
owisc2#188	703493	702420	65.4	358	-	2209	98.6	345	(<i>prfB</i> , <i>supK</i>)		P07012	Peptide chain release factor 2 (RF-2).	<i>Escherichia coli</i>
owisc2#190	705198	703609	65.4	530	-	3805	99.5	578	(<i>recJ</i>)		P21893	Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-).	<i>Escherichia coli</i>
owisc2#191	706055	705348	65.4	236	-	1557	100	236	(<i>dsbC</i> , <i>xprA</i>)		P21892	Thiol-disulfide interchange protein DsbC precursor.	<i>Escherichia coli</i>
owisc2#192	706976	706083	65.4	298	-	1943	99.7	298	(<i>xerD</i> , <i>xprB</i>)		P21891	Integrase/recombinase XerD.	<i>Escherichia coli</i>
owisc2#193	707088	707606	65.4	173	+	1183	99.4	173	(<i>fldB</i>)		P41050	Flavodoxin 2.	<i>Escherichia coli</i>
owisc2#194	708056	707652	65.5	135	-	no_similarity							
owisc2#195	708303	708040	65.5	88	-	273	54.5	77	(HI0627)		P44025	Hypothetical protein HI0627.	<i>Haemophilus influenzae</i>
owisc2#196	708546	709523	65.5	326	+	427	37.3	308	(HI0466)		P44000	Hypothetical protein HI0466.	<i>Haemophilus influenzae</i>
owisc2#197	710381	709725	65.5	219	-	668	47.3	205	(<i>ypjQ</i>)		P54175	Hemolysin III homolog.	<i>Bacillus subtilis</i>
owisc2#198	710856	710548	65.5	103	-	470	69	100	(HI1394)		P44172	Hypothetical protein HI1394.	<i>Haemophilus influenzae</i>
owisc2#199	710895	712331	65.5	479	+	2246	65.8	476	(<i>hglA</i>)		P42973	6-phospho- β -glucosidase (EC 3.2.1.86).	<i>Bacillus subtilis</i>
owisc2#200	713134	712394	65.6	247	-	605	100	97		(<i>ygjF</i>)	P52037	Hypothetical oxidoreductase in <i>gcvP</i> 5'region (EC 1.-.-)	<i>Escherichia coli</i>
owisc2#201	716274	713404	65.6	957	-	6308	99.9	957	(<i>gcvP</i>)		S36834	Glycine dehydrogenase (decarboxylating) (EC 1.4.4.2)	<i>Escherichia coli</i>
owisc2#202	716782	716396	65.7	129	-	823	100	129	(<i>gcvH</i>)		A56623	Glycine cleavage system protein H	<i>Escherichia coli</i>
owisc2#203	717900	716809	65.7	364	-	2406	100	364	(<i>gcvT</i>)		A56689	Aminomethyltransferase (EC 2.1.2.10)	<i>Escherichia coli</i>
owisc2#204	719550	718351	65.7	400	-	2652	99.5	400	(<i>visC</i>)		D47020	VisC protein	<i>Escherichia coli</i>
owisc2#205	720751	719576	65.7	392	-	2597	99.7	392	(<i>ubiH</i> , <i>visB</i>)		C47020	UbiH protein	<i>Escherichia coli</i>
owisc2#206	722073	720751	65.8	441	-	2920	100	441	(<i>pepP</i>)		JX0067	X-Pro aminopeptidase (EC 3.4.11.9) II	<i>Escherichia coli</i>
owisc2#207	722683	722102	65.8	194	-	1315	100	194		(<i>ygjB</i>)	A47020	Hypothetical 21.5K protein	<i>Escherichia coli</i>
owisc2#208	722845	723171	65.8	109	+	691	100	109		(<i>ygjE</i>)	P45580	Hypothetical 12.6 Kd protein in <i>pepP-ssr</i> intergenic region	<i>Escherichia coli</i>
owisc2#209	723474	724019	65.8	182	+	1260	100	182		(<i>ygjA</i>)	P09160	Hypothetical 21.1 Kd protein in <i>ssr-serA</i> intergenic region	<i>Escherichia coli</i>
owisc2#210	725640	724414	65.9	409	-	2626	100	409	(<i>serA</i>)		P08328	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (PGDH).	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score*	%	overlap†	gene*	y gene†	accession†	description	species
owisc2#211	726594	725902	65.9	231	-	1474	100	231	<i>rpiA</i>		S22097	Ribose-5-phosphate isomerase (EC 5.3.1.6), constitutive	<i>Escherichia coli</i>
owisc2#212	726844	726617	65.9	76	-	509	100	76		<i>yqfE</i>	P52038	Hypothetical 8.4 Kd protein in <i>rpiA-iciA</i> intergenic region	<i>Escherichia coli</i>
owisc2#213	726986	727876	65.9	297	+	1967	100	297	<i>iciA</i>		S22098	Regulatory protein IciA	<i>Escherichia coli</i>
owisc2#214	728083	730224	65.9	714	+	4621	99.9	714	<i>sbm</i>		S22099	Sbm protein	<i>Escherichia coli</i>
owisc2#215	730220	731212	65.9	331	+	2144	100	331		<i>yrgD</i>	P27254	Hypothetical 36.7 Kd protein in <i>sbm-fba</i> intergenic region	<i>Escherichia coli</i>
owisc2#216	731226	732008	66.0	261	+	1692	100	261		<i>yrgG</i>	P52045	Hypothetical 29.2 Kd protein in <i>sbm-fba</i> intergenic region	<i>Escherichia coli</i>
owisc2#217	732035	733510	66.0	492	+	3239	100	492		<i>yrgH</i>	P52043	Hypothetical 53.8 Kd protein in <i>sbm-fba</i> intergenic region	<i>Escherichia coli</i>
owisc2#220	734421	733513	66.0	303	-	2004	100	303		<i>yrgI</i>	P52044	Hypothetical transcriptional regulator in <i>sbm-fba</i> intergenic region	<i>Escherichia coli</i>
owisc2#221	735313	734576	66.1	246	-	1551	99.6	246		<i>yrgE</i>	P11668	Hypothetical 26.6 Kd protein in <i>sbm-fba</i> intergenic region	<i>Escherichia coli</i>
owisc2#222	736041	735409	66.1	211	-	1406	99.5	211		<i>yrgA</i>	P11667	Hypothetical 23.2 Kd protein in <i>sbm-fba</i> intergenic region	<i>Escherichia coli</i>
owisc2#223	737040	736183	66.1	286	-	1771	100	286		<i>yrgB</i>	S04735	Hypothetical protein 4 (<i>fda</i> 3' region)	<i>Escherichia coli</i>
owisc2#224	738474	737401	66.1	358	-	2375	100	358	<i>fba</i> , <i>fda</i>		P11604	Fructose-bisphosphate aldolase (EC 4.1.2.13).	<i>Escherichia coli</i>
owisc2#225	739855	738695	66.2	387	-	2438	100	387	<i>pgk</i>		S04733	Phosphoglycerate kinase (EC 2.7.2.3)	<i>Escherichia coli</i>
owisc2#226	740924	739908	66.2	339	-	2217	100	339	<i>gapB</i>		S04732	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) B	<i>Escherichia coli</i>
owisc2#227	741922	741212	66.2	237	-	1599	99.6	237		<i>yrgC</i>	P11664	Hypothetical 27.1 Kd protein in <i>epd-cmtA</i> intergenic region	<i>Escherichia coli</i>
owisc2#228	742428	741922	66.2	169	-	1104	100	169		<i>yrgD</i>	P11663	Hypothetical 19.3 Kd protein in <i>epd-cmtA</i> intergenic region	<i>Escherichia coli</i>
owisc2#229	743415	742453	66.2	321	-	2116	100	321		<i>yrgF</i>	P21437	Hypothetical 34.3 Kd protein in <i>epd-cmtA</i> intergenic region	<i>Escherichia coli</i>
owisc2#230	744431	743415	66.3	339	-	2257	100	339		<i>yrgP</i>	P52048	Hypothetical 45.8 Kd protein in <i>epd-cmtA</i> intergenic region.	<i>Escherichia coli</i>
owisc2#231	744709	744335	66.3	125	-	565	100	87		<i>yrgP</i>	P52048	Hypothetical 45.8 Kd protein in <i>epd-cmtA</i> intergenic region.	<i>Escherichia coli</i>
owisc2#232	746091	744706	66.3	462	-	2989	100	462	<i>cmtA</i>		P32059	PTS system, mannitol (cryptic)-specific IIBC component (EC 2.7.1.69).	<i>Escherichia coli</i>
owisc2#233	746562	746122	66.3	147	-	946	100	147	<i>cmtB</i>		S36122	Phosphotransferase system enzyme II (EC 2.7.1.69) factor III, mannitol-specific	<i>Escherichia coli</i>
owisc2#234	748870	746879	66.4	664	-	4406	100	664	<i>tktA</i> , <i>tkt</i>		P27302	Transketolase 1 (EC 2.2.1.1) (TK 1).	<i>Escherichia coli</i>
owisc2#235	749150	749905	66.4	252	+	1601	100	252		<i>yrgG</i>	P25894	Hypothetical 26.8 Kd protein in <i>tktA-speB</i> intergenic region	<i>Escherichia coli</i>
owisc2#236	751034	750117	66.4	306	-	2067	100	306	<i>speB</i>		C42604	Agmatinase (EC 3.5.3.11)	<i>Escherichia coli</i>
owisc2#237	753148	751175	66.4	658	-	4411	99.8	658	<i>speA</i>		A37771	Arginine decarboxylase (EC 4.1.1.19)	<i>Escherichia coli</i>
owisc2#238	753303	753160	66.4	48	-	307	97.9	48		<i>yrgB</i>	P46877	Hypothetical 5.4 Kd protein in <i>speA-metK</i> intergenic region	<i>Escherichia coli</i>
owisc2#239	753424	753636	66.4	71	+	459	100	71		<i>yrgC</i>	P46878	Hypothetical 8.1 Kd protein in <i>speA-metK</i> intergenic region	<i>Escherichia coli</i>
owisc2#240	753887	753639	66.5	83	-	544	98.8	83		<i>yrgD</i>	P46879	Hypothetical 9.5 Kd protein in <i>speA-metK</i> intergenic region	<i>Escherichia coli</i>
owisc2#241	753943	755094	66.5	384	+	2535	100	384	<i>metK</i>		P04384	S-adenosylmethionine synthetase (EC 2.5.1.6)	<i>Escherichia coli</i>
owisc2#242	755520	756911	66.5	464	+	3012	100	464	<i>galP</i>		P37021	Galactose-proton symport (Galactose transporter).	<i>Escherichia coli</i>
owisc2#243	756991	757485	66.5	165	+	1128	100	165	<i>sprT</i>		P39902	SprT protein.	<i>Escherichia coli</i>
owisc2#245	757583	758287	66.5	235	+	1667	100	235	<i>endA</i>		A38966	Endonuclease I	<i>Escherichia coli</i>
owisc2#246	758370	759098	66.6	243	+	1601	100	243		<i>yrgJ</i>	P37912	Hypothetical 26.9 Kd protein in <i>endA-gshB</i> intergenic region	<i>Escherichia coli</i>
owisc2#247	759114	760061	66.6	316	+	2101	100	316	<i>gshB</i> , <i>gsh-II</i>		P04425	Glutathione synthetase (EC 6.3.2.3)	<i>Escherichia coli</i>
owisc2#248	760173	760733	66.6	187	+	1235	100	187		<i>yqgE</i>	P52049	Hypothetical 20.7 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#249	760736	761149	66.6	138	+	904	100	138		<i>yqgF</i>	P52050	Hypothetical 15.2 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#250	762316	761339	66.6	326	-	2118	100	326		<i>yrgR</i>	P52052	Hypothetical 36.0 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#252	762334	763035	66.6	234	+	1512	100	234		<i>yrgS</i>	P52054	Hypothetical 25.8 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#253	763056	763619	66.7	188	+	1220	100	188		<i>yrgT</i>	P52058	Hypothetical 21.2 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#254	763607	763906	66.7	100	+	638	99	100		<i>yrgU</i>	P52060	Hypothetical 10.9 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#255	763917	764507	66.7	197	+	1281	100	197		<i>yrgV</i>	P52061	Hypothetical 21.0 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#256	764503	765636	66.7	378	+	2597	100	378		<i>yrgW</i>	P52062	Hypothetical 42.6 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#257	766801	765797	66.7	335	-	2210	99.7	335		<i>yrgM</i>	P46142	Hypothetical 38.5 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#259	767964	766921	66.8	348	-	2221	100	348	<i>ansB</i>		A35132	Asparaginase (EC 3.5.1.1) II precursor	<i>Escherichia coli</i>
owisc2#260	768859	768143	66.8	239	-	1529	100	239		<i>yrgN</i>	P46143	Hypothetical 26.4 Kd protein in <i>gshB-ansB</i> intergenic region	<i>Escherichia coli</i>
owisc2#261	769368	769045	66.8	108	-	748	100	108		<i>yrgL</i>	P38521	Hypothetical 12.9 Kd protein in <i>ansB-mutY</i> intergenic region	<i>Escherichia coli</i>
owisc2#262	770087	769371	66.8	239	-	1648	100	239		<i>yrgH</i>	P32049	Hypothetical 27.3 Kd protein in <i>ansB-mutY</i> intergenic region	<i>Escherichia coli</i>
owisc2#263	770248	771297	66.8	350	+	2413	100	350	<i>mutY</i> , <i>micA</i>		P17802	A/G-specific adenine glycosylase (EC 3.2.2.-).	<i>Escherichia coli</i>
owisc2#264	771328	771600	66.8	91	+	617	100	91		<i>yrgX</i>	P52065	Hypothetical 11.0 Kd protein in <i>mutY-nupG</i> intergenic region	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction ^a	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
owisc2#265	771641	772201	66.8	187	+	1117	100	169		ygkZ	P52066	Hypothetical 40.4 Kd protein in <i>mutY-nupG</i> intergenic region precursor	<i>Escherichia coli</i>
owisc2#266	772158	772745	66.9	196	+	1232	100	192		ygkZ	P52066	Hypothetical 40.4 Kd protein in <i>mutY-nupG</i> intergenic region precursor	<i>Escherichia coli</i>
owisc2#267	772950	774203	66.9	418	+	2732	100	418	<i>mapG</i>	A26226	Nucleoside-transporting protein NupG	<i>Escherichia coli</i>	
owisc2#268	776451	774259	66.9	731	-	4956	100	731	<i>speC</i>	P21169	Ornithine decarboxylase, constitutive (EC 4.1.1.17).	<i>Escherichia coli</i>	
owisc2#269	776788	777492	67.0	235	+	no_similarity							
owisc2#270	778361	777828	67.0	178	-	297	32	150	<i>(epsM)</i>		P41851	General secretion pathway protein M (Cholera toxin secretion protein EpsM).	<i>Vibrio cholerae</i>
owisc2#271	779205	778366	67.0	280	-	432	29.6	331	<i>(exeL)</i>		P45789	General secretion pathway protein L.	<i>Aeromonas hydrophila</i>
owisc2#272	780284	779292	67.0	331	-	207	27.4	288	<i>(exeC)</i>		P45790	General secretion pathway protein C.	<i>Aeromonas hydrophila</i>
owisc2#273	780712	780305	67.0	136	-	no_similarity							
owisc2#274	781587	780781	67.1	269	-	686	41.9	272	<i>(outO)</i>		P31712	Type 4 prepilin-like protein specific leader peptidase (EC 3.4.99.-) (Pectic enzymes secretion protein outo).	<i>Erwinia carotovora</i>
owisc2#275	784331	781788	67.1	848	-	no_similarity							
owisc2#276	786346	784322	67.2	675	-	279	54.4	79	<i>(PARPA-BETA)</i>		P09791	Procytic form specific polypeptide α - β precursor (Procyclin) (PARP α - β).	<i>Trypanosoma brucei</i>
owisc2#278	788513	786834	67.2	560	-	2372	63.3	558	<i>(lldP, lctP)</i>		P33231	L-lactate permease.	<i>Escherichia coli</i>
owisc2#279	791036	788871	67.3	722	-	4787	100	722	<i>glcB, glc</i>		P37330	Malate synthase G (EC 4.1.3.2) (MSG).	<i>Escherichia coli</i>
owisc2#280	791465	791064	67.3	134	-	830	100	134	<i>glcG</i>		P45504	GlcG protein.	<i>Escherichia coli</i>
owisc2#281	792693	791473	67.3	407	-	2736	100	407	<i>glcF, gox</i>		P52074	Glycolate oxidase iron-sulfur subunit.	<i>Escherichia coli</i>
owisc2#282	795254	793758	67.4	499	-	3315	100	499	<i>glcD, gox</i>		P52075	Glycolate oxidase subunit GlcD.	<i>Escherichia coli</i>
owisc2#285	795505	796266	67.4	254	+	1635	100	254	<i>glcC</i>		P52072	Glc operon transcriptional activator.	<i>Escherichia coli</i>
owisc2#286	797448	796279	67.4	390	-	no_similarity							
owisc2#288	797411	798424	67.4	338	+	2267	100	338	<i>IS5</i>		A91483	Hypothetical 39K protein (insertion sequence IS5)	<i>Escherichia coli</i>
owisc2#289	798079	797726	67.4	118	-	778	100	118	<i>IS5</i>		B91483	Hypothetical 12K protein (insertion sequence IS5)	<i>Escherichia coli</i>
owisc2#291	799503	798577	67.4	309	-	no_similarity							
owisc2#292	798806	799225	67.4	140	+	no_similarity							
owisc2#293	800445	799690	67.5	252	-	no_similarity							
owisc2#294	801175	800480	67.5	232	-	no_similarity							
owisc2#295	801364	802053	67.5	230	+	no_similarity							
owisc2#296	803604	802108	67.5	499	-	3203	100	499	<i>pitB</i>		P43676	Probable low-affinity inorganic phosphate transporter 2.	<i>Escherichia coli</i>
owisc2#297	805755	803899	67.6	619	-	4251	100	619	<i>gsp</i>		P43675	Glutathionylspermidine synthetase/amidase.	<i>Escherichia coli</i>
owisc2#298	805912	806823	67.6	304	+	no_similarity							
owisc2#299	807197	806952	67.6	82	-	546	100	82	<i>hybG</i>		P37185	Hydrogenase-2 operon protein HybG.	<i>Escherichia coli</i>
owisc2#301	807547	807239	67.6	103	-	689	100	103	<i>hybF</i>		P37184	Hydrogenase-2 operon protein HybF.	<i>Escherichia coli</i>
owisc2#302	808032	807547	67.6	162	-	1093	99.4	162	<i>hybE</i>		P37183	Hydrogenase-2 operon protein HybE.	<i>Escherichia coli</i>
owisc2#303	808519	808028	67.6	164	-	1034	100	164	<i>hybD</i>		P37182	Hydrogenase-2 operon protein HybD.	<i>Escherichia coli</i>
owisc2#304	810222	808522	67.7	567	-	3813	100	567	<i>hybC</i>		P37181	Hydrogenase-2 large chain (EC 1.18.99.1)	<i>Escherichia coli</i>
owisc2#305	811448	810222	67.7	409	-	2603	99.7	392	<i>hybB</i>		P37180	Probable Ni/Fe-hydrogenase 2 B-type cytochrome subunit.	<i>Escherichia coli</i>
owisc2#306	812370	811387	67.7	328	-	2302	99.7	328	<i>hybA</i>		P37179	Hydrogenase-2 small chain precursor (EC 1.18.99.1)	<i>Escherichia coli</i>
owisc2#307	813491	812376	67.7	372	-	1020	41.1	360	<i>(hoxK)</i>		P21950	Uptake hydrogenase small subunit precursor (EC 1.18.99.1)	<i>Azotobacter vinelandii</i>
owisc2#308	813967	813683	67.8	95	-	no_similarity							
owisc2#309	814496	814089	67.8	136	-	no_similarity							
owisc2#310	814921	814499	67.8	141	-	no_similarity							
owisc2#311	815015	814830	67.8	62	-	no_similarity							
owisc2#312	815127	816164	67.8	346	+	368	30.8	328	<i>(iolS, SS92ER)</i>		P46336	IolS protein.	<i>Bacillus subtilis</i>
owisc2#314	816701	816210	67.8	164	-	1041	100	164		ygkA	P52082	Hypothetical 18.6 Kd protein in <i>hybA-exbD</i> intergenic region	<i>Escherichia coli</i>
owisc2#315	816892	817773	67.8	294	+	736	44	277	<i>(SPAC4H3.08)</i>		Q10216	Hypothetical oxidoreductase C4H3.08 in chromosome i (EC 1.-.-.-).	<i>Schizosaccharomyces pombe</i> (Fission yeast)
owisc2#316	817629	817814	67.8	62	+	268	97.3	37		ygkA	P25887	Hypothetical protein in <i>hybA-exbD</i> intergenic region	<i>Escherichia coli</i>
owisc2#317	818473	818051	67.9	141	-	898	100	141	<i>exbD</i>		JV0030	ExbD protein	<i>Escherichia coli</i>

Table 1. Continued.

orf number	start (nt)	end (nt)	map (min)	length (aa)	direction*	score ^b	% ^c	overlap ^d	gene ^e	y gene ^f	accession ^g	description	species
owisc2#318	819214	818483	67.9	244	-	1533	99.6	244	<i>exbB</i>		P18783	Biopolymer transport ExbB protein.	<i>Escherichia coli</i>
owisc2#319	819466	820650	67.9	395	+	2592	99.7	395	<i>metC</i>		A25153	Cystathionine β-lyase (EC 4.4.1.8)	<i>Escherichia coli</i>
owisc2#320	820793	821449	67.9	219	+	1448	100	219		<i>yghB</i>	P33196	Hypothetical 24.1 Kd protein in <i>metC-suffl</i> intergenic region (O219).	<i>Escherichia coli</i>
owisc2#321	822618	821494	67.9	375	-	196	24.8	206	<i>(exsA)</i>		P26993	Exoenzyme S synthesis regulatory protein ExsA.	<i>Pseudomonas aeruginosa</i>
owisc2#322	822584	823744	67.9	387	+	851	39.8	367	<i>(bdhB)</i>		Q04945	NADH-dependent butanol dehydrogenase B (EC 1.1.1.1.-)	<i>Clostridium acetobutylicum</i>
owisc2#323	824217	824675	68.0	153	+	716	44.5	265			A32950	Probable reductase protein	<i>Leishmania major</i>
owisc2#324	824878	825168	68.0	97	+	no_similarity							
owisc2#325	825258	825803	68.0	182	+	no_similarity							
owisc2#326	825857	826111	68.0	85	+	231	48.6	70	<i>(lpp)</i>		P02939	Major outer membrane lipoprotein precursor (Murein-lipoprotein).	<i>Erwinia amylovora</i>
owisc2#327	827254	826160	68.0	365	-	no_similarity							
owisc2#328	828375	827401	68.1	325	-	no_similarity							
owisc2#329	829898	828489	68.1	470	-	3219	100	470	<i>suffl</i>		P26648	Suffl protein precursor.	<i>Escherichia coli</i>
owisc2#330	830710	829976	68.1	245	-	1636	100	245	<i>plsC, parF</i>		P26647	1-acyl-SN-glycerol-3-phosphate acyltransferase (EC 2.3.1.51).	<i>Escherichia coli</i>
owisc2#331	833202	830947	68.2	752	-	4898	100	752	<i>parC</i>		P20082	Topoisomerase IV subunit A (EC 5.99.1.-).	<i>Escherichia coli</i>
owisc2#332	834947	833343	68.2	535	-	1599	45.7	530	<i>(oppA)</i>		P06202	Periplasmic oligopeptide-binding protein precursor.	<i>Salmonella typhimurium</i>
owisc2#333	836460	835981	68.2	160	-	no_similarity							
owisc2#334	836905	836516	68.2	130	-	854	100	130		<i>ygiW</i>	P52083	Hypothetical 14.0 KD protein in <i>parC-mdaB</i> intergenic region precursor	<i>Escherichia coli</i>
owisc2#335	837057	837713	68.3	219	+	1428	100	219		<i>ygiX</i>	P52076	Probable transcriptional regulatory protein YgiX.	<i>Escherichia coli</i>
owisc2#336	837713	839059	68.3	449	+	2921	100	449		<i>ygiY</i>	P40719	Probable sensor protein YgiY (EC 2.7.3.-).	<i>Escherichia coli</i>
owisc2#337	839760	840338	68.3	193	+	1335	100	193	<i>mdaB, mda66</i>		P40717	Modulator of drug activity B.	<i>Escherichia coli</i>
owisc2#338	840372	840683	68.3	104	+	696	100	104		<i>ygiN</i>	P40718	Hypothetical 11.5 Kd protein in <i>parC-parE</i> intergenic region	<i>Escherichia coli</i>
owisc2#339	842626	840737	68.4	630	-	4187	100	630	<i>parE</i>		P20083	Topoisomerase IV subunit B (EC 5.99.1.-).	<i>Escherichia coli</i>
owisc2#340	843236	842658	68.4	193	-	1315	100	193		<i>yqiA</i>	P36653	Hypothetical 21.6 Kd protein in <i>parE-icc</i> intergenic region	<i>Escherichia coli</i>
owisc2#342	844063	843239	68.4	275	-	1891	99.6	275	<i>icc</i>		P36650	Icc protein.	<i>Escherichia coli</i>
owisc2#343	844510	844091	68.4	140	-	951	100	140		<i>yqiB</i>	P36652	Hypothetical 16.5 Kd protein in <i>icc-tolC</i> intergenic region	<i>Escherichia coli</i>
owisc2#344	845140	844514	68.4	209	-	1361	100	209		<i>yqiE</i>	P36651	Hypothetical 23.7 Kd protein in <i>icc-tolC</i> intergenic region	<i>Escherichia coli</i>
owisc2#345	845339	846823	68.4	495	+	3093	99.8	495	<i>tolC, mtcB, mtaA, refI</i>		P02930	Outer membrane protein TolC precursor.	<i>Escherichia coli</i>
owisc2#346	846826	847083	68.5	86	+	604	100	86			S11458	Hypothetical protein (<i>tolC</i> 3' region)	<i>Escherichia coli</i>
owisc2#347	846941	847642	68.5	234	+	1568	100	234		<i>ygiB</i>	S22360	Hypothetical protein D	<i>Escherichia coli</i>
owisc2#348	847651	848808	68.5	386	+	2661	100	386		<i>ygiC</i>	S22361	Hypothetical protein A	<i>Escherichia coli</i>
owisc2#349	849664	848852	68.5	271	-	1876	100	271		<i>ygiD</i>	P24197	Hypothetical 29.9 Kd protein in <i>tolC-ribB</i> intergenic region	<i>Escherichia coli</i>
owisc2#350	849780	850550	68.5	257	+	1631	100	257		<i>ygiE</i>	S22363	Hypothetical protein B	<i>Escherichia coli</i>
owisc2#351	851097	850939	68.6	53	-	296	97.7	44	<i>ribB, htrP</i>		A38159	LuxH protein homolog HtrP	<i>Escherichia coli</i>
owisc2#352	851698	851048	68.6	217	-	1406	100	217	<i>ribB, htrP</i>		P24199	3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase).	<i>Escherichia coli</i>
owisc2#353	852157	852360	68.6	68	+	no_similarity							
owisc2#354	852647	853195	68.6	183	+	481	97.4	78		<i>ygiL</i>	P39834	Hypothetical fimbrial-like protein in <i>ribB</i> 5' region	<i>Escherichia coli</i>
owisc2#355	853375	853782	68.6	136	+	855	99.3	136	<i>IS2</i>		S56497	Hypothetical 13K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#356	853743	854645	68.6	301	+	2068	99.7	301	<i>IS2</i>		JQ0040	Hypothetical 34K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#357	854219	853791	68.6	143	-	956	99.3	143	<i>IS2</i>		JQ0042	Hypothetical 16K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#358	853816	854106	68.6	97	+	688	99	97	<i>IS2</i>		JQ0041	Hypothetical 11K protein (insertion sequence IS2)	<i>Escherichia coli</i>
owisc2#359	854633	855574	68.6	314	+	666	40.1	322	<i>(papC)</i>		P07110	Outer membrane USHER protein PapC precursor.	<i>Escherichia coli</i>
owisc2#360	855402	857096	68.6	565	+	1215	35.1	510	<i>(pmfC)</i>		P53514	Outer membrane USHER protein PmfC precursor.	<i>Proteus mirabilis</i>
owisc2#361	857106	857861	68.7	252	+	470	32.8	256	<i>(pmfD)</i>		P53520	Chaperone protein pmfD precursor.	<i>proteus mirabilis</i>
owisc2#362	858509	858928	68.7	140	+	no_similarity							
owisc2#363	859174	858977	68.7	66	-	469	100	66	<i>glgS</i>		S25201	GlgS protein	<i>Escherichia coli</i>
owisc2#364	859443	860069	68.7	209	+	no_similarity							
owisc2#365	860099	861757	68.8	553	+	192	25.1	331			P12957	Caldesmon, smooth muscle (CAD).	<i>Gallus gallus (chicken)</i>

a, + and - represent clockwise and counterclockwise directions of transcription in the *E.coli* genetic map, respectively

b, fasta optimal score in the overlapped region

c, amino acid identity in the overlapped region

d, size of the region where significant similarity is detected

e, genes in parenthesis indicate the homologues of the genes identified in *E. coli* or other organisms.

f, hypothetical genes designated by K.E. Rudd et al.

g, accession number in the SWISSPROT or PIR database

