
Compilation of DNA sequences of *Escherichia coli* (update 1993)

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ABSTRACT

We have compiled the DNA sequence data for *E.coli* available from the GENBANK and EMBL data libraries and over a period of several years independently from the literature. This is the fifth listing replacing and increasing the former listings substantially. However, in order to save space this printed version contains DNA sequence information only, if they are publically available in electronic form. The complete compilation including a full set of genetic map data and the *E.coli* protein index can be obtained in machine readable form from the EMBL data library (ECD release 15) as a part of the CD-ROM issue of the EMBL sequence database, released and updated every three months. After deletion of all detected overlaps a total of 2 353 635 individual bp is found to be determined till the end of April 1993. This corresponds to a total of 49.87% of the entire *E.coli* chromosome consisting of about 4,720 kbp. This number may actually be higher by 9161 bp derived from other strains of *E.coli*.

INTRODUCTION

Within this sequence supplement issue we were able to publish a compilation of DNA sequences of *Escherichia coli* in four contiguous years since 1989 and asked our colleagues from all over the world for additions and corrections [1–4]. Over the recent years the number of newly published *E.coli* sequence data increased substantially (see Fig. 1). The velocity of adding new data increased also. A rough calculation allows the prediction, that the complete sequence of *E.coli* may be known by 1998, using a noncoordinate effort only. This target may be reached earlier, because at least two groups have devoted their research to systematic sequencing of certain areas of the *E.coli* chromosome. According to our data a total of 2 353 636 bp is sequenced till April 1993. Almost one half of these nucleotides is published more than once. The data presented here may serve as a basis for encouragement to our colleagues to either send us their unpublished, mostly flanking material or to determine additionally the sometimes very small gaps towards known neighbouring sequences. This may finally help to produce the *Escherichia coli* K12 DNA sequence as the first complete sequence of a living organism. This compilation is available in its full form quarterly from EMBL data library together with their current release on tape (ECD) or from the EMBL file server [5]. It may also be received from the EMBL data library on CD-

ROM together with a service stand alone program for quick database search and direct access to collected sequences.

PREVIOUS AND SUPPORTING EFFORTS

The most famous collection of *E.coli* data is the linkage map compiled by B.Bachmann [6]. These data were updated for the last time in 1990 and we tried to follow this update as close as possible. Thus the electronic full version of ECD contains all known genes, except the open reading frames with no genetic function known, but including all recent updates found in the literature. Three other groups [7–13] started a program to fit the DNA sequence data directly onto the physical map compiled by Y.Kohara et al. [14]. We still prefer the genetic map positions rather than the physical map coordinates, since it seems to be more comfortable to find the most important genetic cross references within the Bachman map, directly. However these numbers are often subject to small changes, if a new contig could be formed. In general one may obtain the physical data simply by multiplying the genetic 'map' data by a factor of 47.2. This operation needs to pay attention to a large inversion within the Kohara restriction map, which however is considered in two other cosmidbanks [15,16]. In order to merge our data with those regarding the Kohara map data directly [7–13] we have compared our data with those of K.Rudd (Bethesda,MD) and paid attention to all other collections as far as possible. Thus, we also included the unpublished material available exclusively to us or to K.Rudd. However, these data were given to us for statistical purposes only; for an example see references 17 and 18. The respective information may be available on personal request from the authors named in Listing 1. Additions and corrections of several colleagues are indicated in the main list within the comment column (see Listing 1; for abbreviations see Table 1).

Although the sequence is only semifinished now, a number of refined functional analyses of the sequence data are performed, namely on promoter [19] and terminator structures [20], as well as on ribosomal binding sites [21] and on the distribution of REP sequences [22].

SYSTEMATIC SEQUENCING EFFORTS

1992 the first two reports on systematic sequencing of the *E.coli* chromosome were released [23,24]. According to announcements made on international conferences at Madison, Wisconsin and

at Paris dealing with the chromosomal organisation of small genomes, these projects have reached a fairly advanced status, already. One group headed by F. Blattner (Madison, WI) has almost finished the systematic sequencing of about 20% of the genome located between min 80 and 100. This group has performed their sequencing independently from any sequence data known from other laboratories. Thus, their first report was upon 91.4 kb with about 75% sequenced in other laboratories before. A second report from this group increases the size of this contig to 245 kb [25].

Another group is formed by a number of independent laboratories in Japan. They are devoted to systematic sequencing of the area between min 0 and 33. The coordinator is K. Isono (Kobe University). The first reports are released from the laboratory of M. Mizobuchi (Tokyo) [24]. This group uses a completely different strategy by sequencing gaps only. According to a most recent personal communication, the group of Dr Mizobuchi finished a contig of 274 kb spanning the entire area from min 0 to 6.4. Their first report on 111 kb included about 65% sequence data from other laboratories [24]. The other areas finished now contain considerably more new data.

PERFORMED COMPILATION

The general scope of this collection is to allow a compilation of all uncoordinated sequence information to finally end up with a complete *Escherichia coli* nucleotide sequence data bank, including all sequenced mutants. In order to give a visual impression about the availability of sequence information of *E. coli* DNA we include an appropriate figure. This Figure 1 is printed automatically on a high resolution printer and is to scale as far as possible. The extent of the black bars represents the mainly

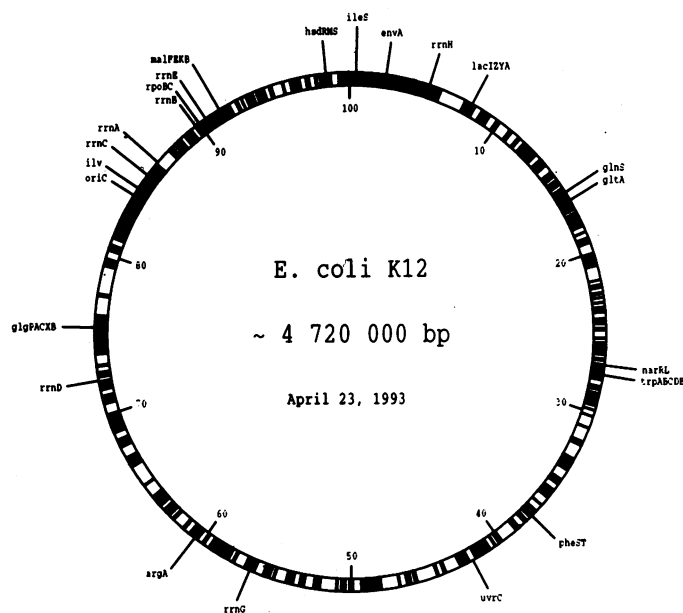


Figure 1. To date sequenced areas within the circular chromosome of *Escherichia coli* K12. The sequenced areas are calculated in percent of the total chromosome according to the main list. All contigs over 2000 bp are shown in scale black bars at the respective genetic map position. Some prominent markers are included as well. The areas between min 0 and 33, and between min 80 and 100 are subject to systematic sequencing efforts in Japan and the U.S.A., respectively (see text).

sequenced areas. All sequences with more than 2000 contiguous basepairs are shown. The final print may not give enough resolution, thus the comparison with the main list (Listing 1) is strongly recommended.

Besides the pure sequence information some specified additions are introduced, mostly if restriction maps could be found in the original paper. We introduced B. Bachmann's genetic map data completely and used them to sort the sequences roughly by a tenth of a minute. Fine assortment was by a hundredth of a minute, if the sequences overlap. A hundredth of a minute corresponds to 472 bp, which seems to be a sufficient resolution. If the sequences were mapped in either of the compilations using the Kohara map [7-13], we preferred to use their assignment including the respective orientation. However, these numbers may not be used as experimentally determined data, as long as we deal with interrupts of any kind. Contigs are only accepted, if either sequence extends over the respective restriction site.

Note, the given map coordinate may vary somehow within different issues of this collection, due to increasing number of recognized overlaps. If the numbers are not consecutive within collected entries, you may find the missing entries within the electronic ECD data bank only. Numbers higher than 100 within this line refer to DNA sequences, which could not be localized within the chromosome yet. The numbers refer to the following type of information:

- 101-126 Unlocalized structural genes in alphabetical order
- >200 Insertion sequences in quasi numerical order (e.g. 200.05 is IS5; 201.50 is IS150)
- >300 tRNAs filed as RNA sequences and unlocalized tRNA genes in alphabetical order of the corresponding amino acids (RNA sequences neglected here)
- >400 unlocalized RNAs
- >500 reviews and summaries (neglected here)

The gene symbols are either according to the Bachmann list or to the respective paper. Several symbols have been changed in the past for different reasons. In order to provide a basis for comparison, we added Listing 2, which is part of the main list but sorted on names. Note, some names denoted by '*' seem to be biased. Thus the given entry names within the EMBL or GenBank entries differ sometimes from the given gene symbol. These differences are indicated as much as possible mostly using the '=' symbol in the last position of the name column pointing to the comment column. If more than two gene symbols are necessary to describe the content either of a single or a condensed entry, the '&' symbol points to the comment column, in order to indicate that this area consists of more than two genes. Thus the two columns should be read as one consecutive item. We tried to use each gene symbol at least once in the first position. Since a fairly compressed form had to be used within this databank, some terms and abbreviations had to be used and are explained in Table 1.

This fourth edition of ECD contains a major increase of information by adding the exact coordinates for the performed overlaps, the entire genetic map data [6] and the 2D-protein index numbers [26]. In order to make the calculations transparent, we preferred to keep all references with contributions to the respective area. However, we can only give one reference per data bank entry in this printed version. The full set of information

is provided in the electronic ECD version, which also includes some structural information and other functional data, restriction map data, corrections or sequenced mutations. Most tRNA sequences are compiled together with their respective anticodon sequence. For crossreferences to the tRNA collection [27] see our previous listing [1]. Most ribosomal operons are not fully sequenced within their 16S and 23S RNA genes. Thus the compiled sequences are sometimes only analogs. Insertion sequences are compiled using the known copy number within *E. coli* K12 strain W3110 [28,29]. Only those insertion elements which are sequenced together with flanking areas may be found at the respective genetic locus.

Strains other than *E. coli* K12 are indicated. However, the respective sequence data are not included in the final calculation. Names not found within the Bachmann list or not genetically defined within the original paper are abbreviated but explained with the full name. Undetermined or open reading frames (urf or orf) are indicated mostly according to the original paper and the resulting protein size. Regions with no specific genetic function are marked as intergenic or flanking regions. Some reviews on the genetic or functional structure as well as on cosmid banks are included, but neglected in this printed version.

The accession number column gives the first accession number for any EMBL entry. This number remains constantly with the quoted nucleotide sequence. It is therefore the most important cross reference. According to the general databank policies the accession number will even be part of any condensed entry after removing overlaps. Thus an EMBL EC entry may be found via different accession numbers, but each accession number points to one individual EC entry only. If the EMBL-accession number differs from the GenBank accession number, the GenBank accession number is given in the comment column. Published sequences, which are not yet included into EMBL databank are now added and received internal accession numbers either from K. Rudd's [8] or our own collection. Unpublished material still not publically available, may be obtained directly from those individuals, who are named in the comment column (see Listing 1).

The EMBL column gives the EMBL entry name for the given reference, usually beginning with the identification EC..... The respective GenBank entry name usually begins with ECO....., and is given in the respective column. This may be used to find *Escherichia coli* sequences directly either within the EMBL databank or GenBank. However, this identification may also point to plasmid borne and other sequences (for a list of these entries see our previous listing [1]).

Note, that the EC or ECO entry name may have been changed between different database releases, especially due to compressing overlapping sequences or to changing preliminary names (usually the respective accession number). Numbers in brackets after the name point to the position of this reference within the list of references of the respective GenBank/EMBL entry. Incorporation of these numbers is still incomplete. In order not to depend on these changes the respective invariant accession number is always given in the accession number column.

There are five columns giving different types of numbers of basepairs:

1) The basepair ('bp') column gives the number of basepairs found in the reference quoted. The number is mostly consistent with the respective number given in the EMBL or GenBank entry. If it is clear from the original text, that the given sequence

information is used as illustration only and not originally determined here, the entry within this column is 0. If the text allows to complete restriction sites the flanking nucleotides are added, or if it allows to recognize vector sequences, these sequences are omitted. Thus the given number may differ from the EMBL or GenBank entry. This is mostly indicated in the comment column.

2) The 'offset' column is a control number for ascending order in the map column and describes the number of nucleotides collected up to the previous entry. This column is deleted in the printed version now.

3) The 'from' column defines the address number of the nucleotide to begin with in the respective collection.

4) The 'to' column defines the respective nucleotides to terminate the respective collection. If the *from* number is higher than the *to* number our program automatically inverses the sequence.

5) The total column gives the number of basepairs added to a total number after deletion of all repeats and overlaps from different entries. This number is given only once per added area in the first entry after a sort by the genetic map position. Data from strains other than *E. coli* K12 are ignored in this calculation. If there is no overlap to other entries the numbers given in the bp and total column are identical. Adding up all entries in this column we arrive at the actual number of sequenced basepairs of the entire *E. coli* genome. The actual number of total basepairs sequenced up to April 1993 is 2 353 635 bp = 49.87%

In order to distinguish between the different entries, e.g. for this printed version of the data base, an additional one letter column (*) is included as well. T defines the start of a completely collectable entry. P defines the start of an entry only partially collectable. F defines an entry missing in the EMBL data base. C defines any collectable entry other than the starting one. B, J, U, and W define entries from strains other than *E. coli* K12.

The article column line gives the references for the quoted sequence information in a fairly condensed format and indicates the volume and first page of each entry, only. The appropriate year is added in a special year column to allow the calculation of an annual index given in Table 2. A list of abbreviations for the respective journals is given in Table 3.

The gene-protein database of *Escherichia coli* (Edition 5) of VanBogelen et al. [26] is included in a separate column. Only very few proteins addressed in the 2D gels are not found in the genetic map. Note, the full information is again given in the electronic version only.

DATA DISTRIBUTION IN MACHINE READABLE FORM

This compilation is available as a flat file (ECD) from the EMBL data library [4] and is automatically distributed with the each release the EMBL data library. In addition, this compilation is available together with a stand alone service program on the CD-ROM version of the EMBL data library. This CD-ROM is produced in cooperation with IRL-Press and contains the other collections of this supplement issue, too. However our version may also be available on disk on request from Gießen; email address KROEGER@EMBL-HEIDELBERG.DE. Using our service program one may assemble the entire nucleotide sequence directly from the CD-ROM or may extract each single or collected entry individually.

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Table 1. Databank cross references and abbreviations. Some differences between the two databases or repeated entries, as well as accession numbers given in most recent papers are indicated directly

Gb	points to a difference mostly in the accession number between GenBank and EMBL databanks [see also AC line].
GbNew	is introduced, if the actual issue of GenBank data bank may not contain this more recent entry. However, caused by a certain difference in updating these entries, they may already be incorporated into the most actual GenBank version. They are always available using the EMBL/GenBank file server.
KR	indicates entries primarily found by K. Rudd [3]
BB	acknowledges the contribution of Bobby Baum, 6607 Pyle Road, Bethesda, Maryland 20817, USA. Entries marked by BB are added [new] or corrected [length, map location, overlap] using a listing compiled by Bobby Baum. His collection may be available as Ec.lis file via the National Biomedical Research Foundation (USA).
RVB	[Ruth VanBogelen]
MK	[Manfred Kröger] and
HD	[Peter Rice or other colleagues at EMBL] point to unresolved differences to the databases found by these individuals.
char	characterization of genetic elements
comp	comparison with other organisms
corr	correction of published data
func	functional description
gap	small undetermined gaps
gene map	genes not sequenced till now
map	restriction or genetic map data
mut	sequenced mutations
prom	characterized promoter sequences
regul	characterized regulatory sequences
summ	summation or review
unpub	unpublished material quoted in the respective article or in either of the databases referred to

Table 2. Annual growing of the *E. coli* DNA-sequence information. This table compiles all published sequence information according to the annual growth in number of publications (entries) and nucleotides given therein. The final number for total information (bp) exceeds the actual number of sequenced nucleotides (2 353 635 bp) roughly by one third

Year	annual entries	total entries	annual information (bp)	total information (bp)
1967	1	1	600	600
1968	2	3	205	805
1969	4	7	349	1154
1970	3	10	249	1403
1971	10	20	841	2244
1972	5	25	426	2670
1973	6	31	434	3104
1974	4	35	205	3309
1975	9	44	820	4129
1976	7	51	530	4659
1977	9	60	1116	5775
1978	22	82	6911	12686
1979	43	125	20122	32808
1980	56	180	36312	68934
1981	72	252	101793	170727
1982	95	347	83314	254041
1983	135	482	131952	385993
1984	141	623	178748	564741
1985	167	790	163921	728662
1986	176	966	248308	976970
1987	150	1116	204359	1181329
1988	186	1302	248615	1429944
1989	206	1508	291660	1721604
1990	205	1713	327797	2049401
1991	244	1957	402797	2452198
1992	277	2234	617365	3069563
1993	96	2330	479262	3548825

Table 3. List of abbreviations for journals

ABB	Archives of Biochemistry and Biophysics
AcMB	Archives of Microbiology
AdER	Advances in Enzyme Regulation
AgrB	Agricultural Biochemistry (Tokyo)
AEMb	Applied Environmental Microbiology
AInP	Annales Institute Pasteur Microbiologie
AMbP	Acta Microbiologica Polonica
AnMi	Annales of Microbiology
ANYA	Annales of New York Academy of Science
BBA	Biochemica Biophysica Acta
BBRC	Biochemical Biophysical Research Communications
BChF	Biochimie (France)
BCHS	Biological Chemistry Hoppe Seyler's
BiCh	Biochemistry (USA)
BInt	Biochemistry International
BioE	BioEngineering – Forschung und Praxis (VAAM-Germany)
Bioo	Bioorganic Chemistry (UdSSR)
BiRp	Bioscience Report
BJ	Biochemical Journal (UK)
CJMi	Canadian Journal of Microbiology
CRC	Carlsberg Research Communication
CSHQ	Cold Spring Harbour Symposium of Quantitative Biology
Cell	Cell
DANs	Doklady Akademia Nauk (UdSSR)
DNA	DNA
DNAS	DNA Sequence – Journal of DNA Sequencing and Mapping
EJB	European Journal of Biochemistry
Elph	Electrophoresis
EMBO	EMBO Journal
FEBS	FEBS Letters
FedP	Federation Proceedings
G	Genetics
GAnT	Gene Analysis Techniques
GeDV	Genes and Development
Gene	Gene
Geno	Genomics
GlyB	Glycobiology
JBCh	Journal of Biological Chemistry
JBac	Journal of Bacteriology
JBio	Journal of Biochemistry (Japan)
JBSc	Journal of Biological Sciences
JCBc	Journal of Cellular Biochemistry
JGMi	Journal of General Microbiology
JJGe	Japanese Journal of Genetics
JMAG	Journal of Molecular and Applied Genetics
JMB	Journal of Molecular Biology
MBE	Molecular Biology and Evolution
MGG	Molecular General Genetics
MoMB	Molecular Microbiology
MuRs	Mutation Research
N	Nature
NBio	New Biology
NAR	Nucleic Acids Research
NNB	Nature New Biology
PNAS	Proceedings of the National Academy of Science (USA)
Prot	PROTEINS: Structure, Function and Genetics
PSDA	Protein Sequence Data Analysis
PRSB	Proceedings of the Royal Society B; Biol. Sciences
Scie	Science
Unpub.	unpublished material quoted in the databanks or quoted in the collection of K.Rudd (not yet available)
ZNfC	Zeitschrift für Naturforschung Part C (Biological Sciences)

Listing 1: Main list sorted on map position

map name	comment	protein	bp *	from	to	total	journal	vol	page	year	EMBL	AccNr	GenBank
0.01 thrA	operator		349 T	1	123	129425	JBCh	257	3896	1982	ECTHRPRO	X68872	-
0.02 thrA	-		2463 C	1	196	0	PNAS	77	5730	1980	ECTHR	J01706	ECOTHR
0.03 thrABC	-		208 C	0	0	0	PNAS	76	1706	1979	ECTHR	J01706	ECOTHR
0.04 0-2.4 min	Japan-EC genome project		111402 C	1	19058	0	NAR	20	3305	1992	ECAPAH01	D10483	ECOMORI
0.22 hcgA,orf	5 open reading frames		3171 C	0	0	0	DNAS	0	0	1992	ECTGA	X67700	-
0.24 dnaK,orf	E.coli B comparison		2141 B	0	0	0	PNAS	174	3715	1992	ECDNAKB	D10765	-
0.25 dnaKJ	promoter		182 C	0	0	0	PNAS	82	2679	1985	ECDNAK	M10420	ECODNAKA
0.26 dnaK	corr	B066.0	1920 C	0	0	0	PNAS	81	848	1984	ECDNAK	K01298	ECODNAK
0.27 dnaKJ	corr		1623 C	0	0	0	JBCh	261	1778	1986	ECDNAJK	M12544	ECODNAJK
0.30 IS186A	location A		1336 C	0	0	0	FBS	192	47	1985	IS186	X03123	INS186ECB
0.31 gef	cell killing		780 C	0	0	0	MCMB	3	1463	1989	ECGEGENEX17311	ECGEGFGENE	-
0.46 ant	new KR		1349 C	0	0	0	JBCh	263	10408	1988	ECANTAPA	J03879	ECOANTAPA
0.49 nhaR	KR		270 C	1	18	0	JBCh	267	10433	1992	--NHAR	0036MK	-
0.50 0-2.4 min	correction of 28kd		0 C	19090	111402	0	NAR	20	3305	1992	ECAPAH01	D10483	ECOMORI
0.51 rpsT	14 bp to be deleted		2881 C	0	0	0	NAR	14	6965	1986	ECRPSTB	V00345	ECORPST
0.53 rpsT	also EORPSTB		1806 C	0	0	0	JBCh	260	5616	1985	ECRPSTB	M10428	ECORPST
0.54 rpsT	part. aa-sequence only		2073 C	0	0	0	Sci	226	1315	1984	--ILS	0018MK	ECORPSTA
0.59 lspA,orf	corr BB		1138 C	0	0	0	FBS	173	264	1984	ECLIFEP	X00776	ECOLSPA
0.61 lspA,orf	corr BB		2696 C	0	0	0	NAR	19	180	1991	ECLIFEP	X00776	ECOLSPA
0.62 dapB	orf 149,316,304,dapB		1281 C	0	0	0	JBCh	259	14829	1984	ECDAPB	M10611	ECODAPB
0.63 carA		G041.4	5227 C	0	0	0	PNAS	81	4139	1984	ECCARAB	J01597	ECOCARAB
0.96 kefC	& apaGH,kegA,pdxA,surA		2253 C	0	0	0	MCMB	5	607	1991	ECKEFC	X56742	ECOKEFC
1.10 spaH			2396 C	0	0	0	MGG	205	515	1986	ECAPAH	X04711	ECOPAH
1.11 spaG			1200 C	0	0	0	NAR	8	2255	1980	ECFOLA	J01609	ECOFOLA
1.13 pdxA			1469 C	0	0	0	JBac	171	4767	1989	--PDXA	0019MK	-
1.15 surA			1666 C	0	0	0	Unpub.	0	K.Rudd	1991	--	ES3143	surAeco
1.43 polII	orf1 = surA acc. 0.96		4081 C	0	0	0	MGG	226	24	1991	ECPOLB	X54847	ECOPOLD
1.45 polB	M.Almiron/R.Kolter		4666 C	0	0	0	NAR	18	7185	1990	ECPOLEDA	M35371	ECOPOLBDA
1.49 araA	131 differences	MK	4478 C	0	0	0	Gene	47	231	1986	ECARAABD	M15263	ECARAABD
1.52 araB	E.coli B	2D:araA	175 C	0	0	0	PNAS	78	752	1981	ECARACZ	V00257	ECORABOP
1.58 araC	E.coli B J01641 in Gb		1162 C	0	0	0	NAR	8	5267	1980	ECARACZ	V00257	ECORABOP
1.59 araCBA	E.coli B J01641 in Gb		1172 C	0	0	0	NAR	8	649	1982	ECARACZ	V00257	ECORABOP
1.83 leuA	corr BB		305 C	0	0	0	JMB	154	579	1981	ECARAX	V00259	ECORARACK
1.84 leuP	overlap HD, BB		855 C	0	0	0	JMB	149	1113	1986	ECLYVA	J01642	ECOLEVA
1.85 leuO	analog to lysR		960 C	0	0	0	PNAS	86	6602	1988	ECLYVA	M21150	ECOLEVO
1.86 ilvI			2323 C	0	0	0	NAR	11	5299	1983	ECLYVA	M21150	ECOLEVO
1.87 ilvH			389 C	0	0	0	JBac	163	186	1985	ECLYVA	M21150	ECOLEVO
1.96 orfB	next to orfB, Hind3 id?		1820 C	0	0	0	JBac	172	4696	1990	ECLYVA	M21150	ECOLEVO
2.04 pbpB	next to shl, Hind3 id?		1500 T	0	0	0	NAR	18	2813	1990	ECLYVA	M21150	ECOLEVO
2.07 murF	= ftsI		2759 C	0	0	0	MGG	191	1	1983	ECBPBB	X52063	ECOPBPBB
2.08 murF			1656 C	0	0	0	CJMI	35	1051	1989	ECBPBB	X52063	ECOPBPBB
2.11 mray	mray = orfY		1491 C	0	0	0	NAR	17	5379	1989	ECMURF	X15432	ECOMURF
2.12 murD	corr in ECMURD okay		2608 C	0	0	0	NAR	18	1058	1990	ECMURF	X15432	ECOMURF
2.13 ftsW			1629 C	0	0	0	NAR	18	183	1990	ECMURD	X17609	ECOMURD
2.15 murC			2745 C	0	0	0	JBac	171	6375	1989	ECFTSW	M30807	ECOFTSW
2.16 ddl			1152 C	0	0	0	NAR	18	4014	1990	ECMURC	X52644	ECOMURC
2.17 ftsQ			2490 C	0	0	0	JBac	167	809	1986	ECDDLFTS	M14029	ECODDLFTS
2.26 ftsZ			1870 C	0	0	0	JMB	184	399	1985	ECFTSOA	X02821	ECOFTSOA
2.29 envA	= sulB, sfiB	corr BB	2048 C	0	0	0	Gene	36	241	1985	ECFTSOAB	M10429	ECOFTSOAB
2.30 secA			3811 C	0	0	0	JBac	169	5408	1987	ECENVAA	M19211	ECOENVAA
2.31 mutT			867 C	0	0	0	JBac	170	3404	1988	ECSECA	M20791	ECOSECA
2.40 2.4 - 4.2 min region	wrong BB		82680 C	0	0	0	Unpub.	0	9	1993	ECMUTT	X04831	ECOMUTT
2.41 intergenic	min region		2000 C	0	0	0	Unpub.	0	30280	1992	--	--	--
2.70 quac	K.Mizobuchi		1991 C	1	2000	0	Unpub.	0	35	1988	ECQUAC	M33020	ECOGUAC
2.80 nadC	X07917 identical new BB		3607 C	1	1991	0	Unpub.	0	1091	1992	--	--	--
2.90 ampD	K.Mizobuchi & aceEF, lpd		1983 C	1	1844	0	MCMB	3	1091	1989	ECAMPDE	X15237	ECOAMPDE

Listing 1: (continued)

9.00 orf_araJ	-	4355 T	2688	9532	JBac 173	7765	1991	ECARAJ	M64787	ECOARAJ
9.03 sbcc	-	5125 C	200	0	NAR	8033	1989	ECBCC	X15981	ECOSBCC
9.05 phob	-	1972 C	966	0	JMB	37	1986	ECPHOB	X04026	ECOPHOB
9.10 malZ	-	2345 T	1972	10236	JBCh 266	549	1986	ECPHORG	X04704	ECOPHORG
9.12 queA	-	3013 T	2345	0	JMB	19450	1991	ECMALZ	X59839	ECOMALZ
9.13 tgt	-	1488 C	3013	0	JBac 173	2256	1991	ECQBIO	M37702	ECQBIO
9.16 secD	-	1823 C	1823	0	JBac 173	2256	1991	ECQTGT	M63939	ECQTGT
9.18 orf6, tsx	-	4435 C	4435	0	EMBO 9	3209	1990	ECSECDF	X56175	ECOSECDF
9.19 tsx	-	6 C	0	0	JBac 174	1709	1992	map		map
9.50 ispa	-	1474 C	1474	0	Gene 96	55	1990	ECTSX	M57685	ECOTSX
9.55 pppA	-	1452 T	1452	1452	JBio 108	99	1990	ECTSPA	D00694	ECOTSPA
9.80 cyoABCDE	-	704 T	711	705	JBac 170	5110	1988	M23546	M23546	M23546
9.90 bola	-	5813 T	5813	5813	JBCh 265	11185	1990	ECYOXA	J05492	ECOCYOXA
9.92 tig	-	1597 T	893	7719	EMBO 8	3923	1989	ECOBOLA	X17642	ECOBOLA
9.93 clpp	-	1809 C	1352	0	JBac 172	5555	1990	ECTIG	M34066	ECOTIG
9.94 clpX	-	1236 C	1236	0	JBCh 265	12536	1990	ECCLPPA	J05534	ECOCLPPA
9.95 lon	-	903 C	903	0	Unpub.	K.Rudd	1991	-	ES3012	clpXeco
9.97 lon	-	2812 C	6	0	Bio 14	408	1988	ECLONA	M38347	ECOLONA
10.01 HU-1(hupB)	-	3002 C	3002	0	JBCh 263	11718	1988	ECLON	J03896	ECOLON
10.20 ffs	-	460 C	460	0	MGG 201	360	1985	ECHUPB	X16540	ECOHUPB
10.30 teab	-	764 T	764	764	JMB 178	509	1984	ECRNA45	X01074	ECOSGK
10.40 nusB	-	1455 T	1455	1455	JBCh 266	11044	1991	ECTESB	M63308	ECOTESB
10.70 prfC	-	683 T	683	683	NAR 12	4987	1984	ECNUSB1	X00681	ECONUSB
10.80 apt, dnaX & orf12, recR, hptG, adk	-	1225 T	1225	1225	JBCh 266	13988	1991	ECOPRIC	D00727	ECOPRIC
10.90 vlnA, adk	-	0 T	6819	9848	JBac 172	6042	1990	ECAPTADK	M38777	ECOAPTADK
10.92 orf203, 312	-	1867 C	1867	0	JMB 219	393	1991	ECADKVIS	D90259	ECOADKVIS
11.30 usha	-	1708 C	3575	0	Unpub.		1991	ECADKVIS	D90259	ECOADKVIS
11.45 rhmD	-	1819 T	1819	1819	NAR 14	4325	1986	ECUSHA	X03895	ECOUSHA
11.50 rhmD	-	300 T	300	300	NAR 19	7177	1991	ECRHSDRS	X60997	ECORHSDRS
11.60 gcl, orf258	-	4846 T	4846	4846	NAR 19	7177	1990	ECRHSDG	X60999	ECORHSDG
11.90 ads (fold)	-	2762 T	2762	2762	JBCh 268	3911	1993	-	L03845	-
11.91 fold	-	1769 T	1769	1769	Unpub.		1992	ECADS	D10588	ECADS
12.00 pufE	-	1044 T	1044	2449	JBCh 266	23953	1991	ECFOLD	M74789	ECOFOLD
12.20 ppiB	-	2449 T	2449	2449	JBac 171	198	1989	ECOPURE01	M19657	ECOPUREK
12.23 cvs	-	949 T	398	2746	Bich 30	3041	1991	ECAPP1B	M55430	ECOAPP1B
12.30 orf, dnaY	-	2194 C	2194	0	NAR 19	265	1991	ECQYSSG	X56234	ECQYSSG
12.34 argU, IS3	-	2520 T	967	5048	MGG 220	325	1990	ECINXY	X51662	-
12.35 IS3C	-	2269 C	244	0	JBac 171	6197	1989	ECINTD01	M31074	ECINTDLP
12.37 mvrc	-	1002 C	1002	4017	NAR 20	2127	1985	ECIS3	X02311	INS3
12.60 PA-2 lc	-	1060 T	1060	0	NAR	3159	1992	ECVRC	M62732	ECOVRC
12.61 rmpC	-	1303 C	1472	0	JBCh 261	12723	1986	STPAZLC	J02580	PAZLC
12.63 IS5B	-	1195 C	2816	0	N	159	1982	IS5LAM	M13457	ECOEFNMP
12.64 PA-2 RZ	-	290 C	2527	0	JBCh 261	12723	1986	STPAZLC	J02580	PAZLC
12.65 mureine	-	1000 F	1000	1000	BioE 9	5100	1993	-	-	-
12.75 ecos2	-	690 T	690	690	NAR 20	3357	1992	EC52G	D00928	ECOS2G
12.80 M5 protein	-	753 T	1296	0	NAR 15	3924	1987	ECM5	Y00138	ECOM5
12.81 appY = M5	-	1874 C	1874	0	JBac 171	1683	1989	ECAPPYAA	M24530	ECOAPPYAA
12.82 cmpt	-	2035 C	2035	0	NAR 16	1209	1988	ECOMPT1	X06903	ECOOMPT1
12.90 envY	-	945 T	945	0	NAR 17	800	1989	ECENVY	X13548	ECORNVY
13.00 pheP	-	2256 T	2256	2256	NAR 17	3622	1991	ECPHEPA	M58000	ECOPHEPA
13.10 gsk	-	1756 T	1756	1756	Unpub.		1992	ECGSK	D00798	ECOGSK
13.30 bent 104	-	279 T	279	279	MGG 226	367	1991	ECBENT104	X63981	ECOBENT104
13.40 IS186B	-	1341 T	1341	24622	FEB5 192	47	1985	IS186CO	M11300	INS186ECO
13.41 entD	-	943 C	941	0	MOMB 3	757	1989	ECENTD	X17426	ECOENTD
13.43 fepA	-	2624 C	2469	0	JBCh 261	10797	1986	ECFEPAA	M13748	ECOFEPAA
13.44 fepA	-	1997 C	231	0	JBCh 263	18857	1988	ECFR6	J04216	ECOFER6
13.47 entF	-	4753 C	497	0	Bich 30	2916	1991	ECENTF	M60177	ECOENTF
13.48 fepE	-	813 C	813	0	Unpub.		1991	-	ES3030	fepEeco
13.49 fepC	-	2961 C	2961	0	MOMB 5	1415	1991	ECFEPDGG	X57471	ECOFEPDGG
13.52 p43	-	1391 C	1391	0	MOMB 5	1415	1991	ECP43MP	X57470	ECOP43MP

Listing 1: (continued)

18.95 artP	periplasmatic transport	1	909	909	Unpub.	1993	ECARTP	X69108	-
19.00 potFPHGI	putrescine transport	1	5877	5877	JBCh 268	1993	ECOPTFGH	X69108	-
19.05 rimK	-	1	1559	1559	MGG 217	1989	ECRIMK	X15859	ECORIMK
19.10 clpA	-	1	3380	3380	JBCh 265	1990	ECCLPAA	M31045	ECOCLPAA
19.15 aat,mdrA	-	3572	1	1	0 Unpub.	1993	ECMAAT	L10383	-
19.20 htrD, trxB	-	1288	350	350	JBCh 175	1993	ECHTRD	M95935	ECOHTRD
19.22 trxB	-	1202	1	1	0 JBCh 263	1988	ECTRB	J03762	ECOTRB
19.30 artIQMJ	arg periplasm. transport	1	3708	3708	Unpub.	1993	ECAPTS	X67753	-
19.40 aIB (lrp)	leucine response	1	1174	1174	PNAS 272	1990	ECLRP	D11105	ECLRP
19.50 cmlA ?	chloramphenicol transf.	1	930	930	BJ 272	1990	ECLICAT	X53796	ECLICAT
20.00 serS	-	1	729	729	Prot 1	1986	ECLIVRA	M36020	ECLIVRA
20.01 dnsABC	-	1	1854	1854	0 MOMB 2	1988	ECSDMS	X05017	ECOSERS
20.10 orf, pfl	-	770	6492	6492	JBAC 171	1988	ECFLZ	J03412	ECODMS
20.11 pfl	-	140	3592	3592	0 EJB 177	1988	ECDFL	X08035	ECOPFL
20.24 serC, arnA	-	1	1490	1490	2983 BJ 234	1988	ECRSP	M25608	ECAROA
20.25 arnA	-	1	1284	1284	0 FEBS 170	1984	ECAROA	X00557	ECAROA
20.26 arnA	-	1	1760	1760	0 BJ 234	1986	M25608	X25608	ECAROA
20.40 rpsA s1	2. part of divided seq.	1	977	977	3032 MGG 196	1984	ECRSPA01	X00785	ECORPSAL
20.42 rpsA s1	28 bp difference MK	1	977	977	0 NAR 10	1982	ECRSPA	V00352	ECORSPA
20.43 hlp (hmbD)	122 bp lambda	1	2287	2287	0 JMB 183	1985	ECHIP	X04864	EOHIP
20.50 mba	-	1	475	475	0 MOMB 7	1993	ECMSBAG	Z11796	ECOMSBAG
20.60 mukB	-	1	3468	3468	5353 EMBO 10	1991	ECMUKB	X57550	ECOMUKB
20.65 aspC, ompF	& ansS, pcnB, pepB BB	1	5353	5353	9133 BJ 234	1986	ECASPC	X03629	ECOASPC
20.69 ompF	-	1	1	1	0 NAR 10	1982	ECOMPF	J01655	ECOMPF
20.74 ansS	-	1415	1	1	0 Gene 84	1989	ECTGASNS	M33145	ECOTGASNS
20.76 pncB	-	1592	1	1	0 JBCh 265	1990	ECPNCB	J05568	ECOPNCB
20.77 pepN	-	1928	417	417	0 EJB 155	1986	ECPEPNS	X03709	ECOPEPNS
20.78 pepN	-	1	3409	3409	0 Gene 48	1986	ECPEPN	M15273	ECOPEPN
20.90 bent 103	corr	1	238	238	238 MGG 226	1991	ECBENT103	XK63980	ECOBENT103
21.20 pycD	no neighboring gene	1	1357	1357	1357 EJB 151	1985	ECPYRD	X02826	ECOPYRD
21.65 rnf	-	1	600	600	1209 EMBO 12	1993	-	-	-
21.67 fabA	ribosome modulation fac	1	2271	2271	0 JBCh 263	1988	ECFABAA	J03186	ECOFABAA
21.71 ompA, sulA	mut only 726 bp acc.BB	1	2821	2821	2271 NAR 8	1980	ECOMPAA	V00307	ECOOMPA
22.00 hsdR	helicase V	1	6023	6023	2821 JBCh 264	1989	ECHLIV	J04726	EOHELIV
22.10 hysABCDEF	loc acc KR	1	1336	1336	6023 JBAC 172	1990	ECHYA	M34825	EOHYA
22.30 serT	= divs ser tRNA	1	2690	2690	1336 EMBO 3	1984	ECDIVE	X00547	ECOTGS
22.50 appCB	-	1	1901	1901	4591 MGG 229	1992	-	-	-
22.52 appA	correction of 22.60	1	1674	1674	0 JBAC 172	1990	ECAPPAA	M58708	EOAPPAA
22.60 app	glucose-1-phosphatase	1	1674	1674	1674 JBAC 172	1990	ECAGPA	M33807	EOAGPA
22.80 putACP	also ECPUTC M35174	1	2212	2212	2212 MGG 210	1987	ECPUTP	X05653	ECOPUTC
23.00 terE	near Pyc	1	22	22	22 JBAC 173	1991	ECTERE	X64000	ECOTERE
23.10 mmyB, orf	multicopy suppression	1	2676	2676	2676 JBAC 174	1992	ECMSYB	X59939	ECMSYB
23.20 serX	2. tRNA Ser5 locus	1	649	649	649 MOMB 7	1990	ECTRNS5	X52787	ECOTRNS5
23.30 IS3D	flanking sequences	1	1000	1000	1000 JMB 212	1993	ECIS3D	D12597	ECOTRNS5
23.40 htrB	-	1	563	563	563 Unpubl.	1993	ECIS3D	D12597	ECOTRNS5
23.50 pycC	-	1	3129	3129	3129 Unpub.	1991	ECHTRB	X61000	ECOHTRB
23.60 g20.3, tcp	-	1	2046	2046	2046 EJB 160	1986	ECPYRC	X04469	ECOPYRH
23.61 rimJ	new BB	0	1609	1609	1609 JBAC 174	1992	ECRIMJA	M92278	-
23.70 phoH, orf1	= psiH	1	2250	2250	0 MGG 209	1987	ECRIMJ	X06118	ECORIMJ
24.00 mopA*	= groE = ans ?	1	595	595	2250 JBAC 175	1993	-	-	-
24.11 ans	correction	1	541	541	595 JBAC 161	1985	ECANS	M11294	ECOGROELA
24.15 g30k, orfYX	& orf	1	8929	8929	0 JBCh 266	1992	ECANS	X67470	ECOGAMS
24.16 rnfL, L32	-	1	784	784	0 Unpub.	1989	ECRPMFA	M29698	ECORPMFA
24.17 plxX, fabH	-	1	1059	1059	0 JBAC 171	1992	ECG30K	M96791	ECOG30K
24.18 fabD	-	1	1428	1428	0 JBCh 267	1992	ECFABH	M77744	ECOFABH
24.40 fabD	-	1	1395	1395	0 JBCh 267	1992	ECFABD	M87040	ECOFABD
24.41 fabDG, scpP	bad name fabG (71.13)	1	1378	1378	2773 JBAC 174	1992	ECFABAC	M84991	ECOFABAC
24.70 ptsG	-	1	1523	1523	4124 JBCh 261	1986	ECPTSG	J02618	ECOPTSG

24.71 fhuE	Fe recep M16186 Gb	KR	2601	1	2057	0	MOMB	4	427	1990	ECFHUE1	X17615	ECOFHUE1
24.80 ndh	J01653 in Gb; loc acc	KR	1	1	1667	0	EJB	116	165	1981	ECNDHX	V00306	ECONDHX
25.00 pabC	aminodeoxychorismate ly		1	1	439	0	JBac	174	5317	1992	ECFABC	M93135	ECOPABC
25.20 att e14R	M19689 in Gb?		1	0	0	0	JBac	170	2040	1988	ECATTE	M19683	ECOATTE
25.30 mfd	mutation frequ. decline		1	0	1568	0	Scie	260	53	1993	-	-	-
25.40 icd		C043.8	1	1	1772	0	JBch	262	10422	1987	ECICD	J02799	ECOICD
25.50 lit			1	1	1772	0	JBac	170	2056	1988	ECLIT	M19634	ECOLIT
25.60 phoQ, phoP			4097	1	1	0	Unpub.	4	492	1992	ECFHOPQ	D90393	ECOPHOPQ
25.63 purB, phoP			1864	1	2613	0	EMBO	4	237	1985	ECFNB	X59307	ECOPURB
25.70 pinI	att e14	K03521 in Gb	1	1	1040	0	JBSC	17	217	1992	ECMCRAGNA219104	-	-
25.80 mcrA	bad coding sequence		840	1	853	0	JBac	173	7368	1991	ECMCR	M76667	ECOMCRA
25.81 mcrA	224 bp lambda in Em	BB	1070	1	74	0	NAR	16	7995	1988	ECFADR	X08087	ECOFADR
25.90 fadR			2072	1	2072	0	JBch	267	11064	1992	ECFHAB	M83655	ECONHAB
25.92 nahB			2454	1	4386	0	PNAS	82	4336	1985	ECMUCD	M10107	ECOMUCD
26.00 dadX, orf	(minCDE)	loc ?	1	1	2400	0	Unpub.	56	641	1989	ECMADAX	L02948	ECODADAX
26.10 minBCDE	= osma		1	1	2538	0	Cell	217	347	1989	ECMNB	J03153	ECOMINB
26.30 treA	next to hema	acc KR	1785	1	1620	0	EMBO	10	3549	1991	ECPTHG	X15868	ECOTREA
26.40 rap, pth	sequencing across BamHI		1	1	1440	0	Gene	82	209	1989	ECHEMA	M30785	ECOHEMA
26.60 prs	last 83 bp from lambda		1333	1	1504	0	PNAS	82	3616	1985	ECRF1X	M11519	ECORF1X
26.62 orf1, 2, prs	compilation of nar data		4160	0	950	0	MGG	207	369	1987	ECRDSA	X05552	ECONDSA
26.64 hema, pfrA		H021.6	1	1	1504	0	MGG	207	369	1987	ECRDSA	X05552	ECONDSA
26.67 prfA (RF1)			1	1	1504	0	MGG	207	369	1987	ECRDSA	X05552	ECONDSA
26.70 kdsA			1	1	1504	0	MGG	207	369	1987	ECRDSA	X05552	ECONDSA
26.93 narLXK			1	1	1504	0	MGG	207	369	1987	ECRDSA	X05552	ECONDSA
26.99 narX			1	1	1504	0	MGG	207	369	1987	ECRDSA	X05552	ECONDSA
27.00 narX(R)KG	correction; narQ ??		599	0	2482	0	NAR	17	2947	1989	ECNARXL	X13360	ECONARXL
27.01 narX(narQ)			1	1	2482	0	NAR	17	2947	1989	ECNARXL	X13360	ECONARXL
27.02 narG			1	1	2482	0	NAR	17	2947	1989	ECNARXL	X13360	ECONARXL
27.05 narH			135	0	509	0	Unpubl.	0	139	1992	ECNARK	X15996	ECONARK
27.07 narJI			5400	0	447	0	FEBB	177	260	1984	ECNARG1	X01164	ECONARG
27.16 tyrTV, tpr	K01197 in Gb		595	1	1890	0	JBac	170	1721	1988	ECNARI	M20147	ECONARI
27.26 hnr	1305 kb		1	1	1303	0	JMB	155	83	1982	ECNARYSU	X04168	ECOTGYI
27.30 galU	orf1 of X59940 is galU		1	1	1161	0	Unpub.	0	1161	1992	ECNRNG	X66003	-
27.31 msyA	multicopy suppression		1288	1	1288	0	Unpub.	0	1288	1992	ECGALU	M98830	ECOGALU
27.38 tdk	thymidine kinase		1	1	1095	0	JBac	174	1454	1992	ECMSYA	X59940	ECOMSYA
27.40 orf	A.Danchin		1790	1	2928	0	MOMB	5	373	1991	ECFDKG	X53733	ECOTDKG
27.42 adHE	alcohol DH		2759	0	2928	0	Unpub.	0	1992	ECFKAD	ECOTKAD	X67326	ECOTKAD
27.43 adHE			2023	1	3739	0	Gene	85	209	1989	ECADHEX	M33504	ECOADHEX
27.44 oppA	S.Short		1	1	3739	0	FEBB	281	59	1991	ECADHEG	X59263	ECOADHEG
27.45 oppA	oligopeptide binding		1	1	3739	0	FEBB	281	59	1991	ECADHEG	X59263	ECOADHEG
27.55 lpd, kch	att phi80, tonB		3951	1	1920	0	Unpub.	265	K. Rudd	1991	-	-	-
27.57 tonB	summ KR		1	1	1697	0	JBch	265	8387	1990	ECOPPA	J05433	ECOOPPA
27.59 tonA, P14			1	1	1697	0	Unpub.	80	5235	1983	ECXCH	L12044	-
27.60 trp - tonB	intergenic region		3641	1	3641	0	Cell	41	577	1985	ECTONB	K00431	ECOTONB
27.61 trpE			7134	1	7134	0	Cell	41	577	1985	ECTONB	K00431	ECOTONB
27.79 trpBCDE			1068	0	0	0	NAR	9	6647	1981	ECTGP	J01714	ECOTGP
27.87 trp 5' end			952	1	1588	0	Blo	10	415	1984	ECTRPZ	M38366	ECOTRPZ
28.20 btuR	gap of 300 bp to sohB		1	1	4071	0	JBac	171	154	1989	ECBTUR	M21528	ECOBTUR
28.30 sohB, topA	suppressor of htrA		784	1	4071	0	JBac	173	5763	1991	ECSOHB	M73320	ECOSOHB
28.31 topA		I115.0	668	1	1691	0	JMB	191	321	1986	ECTOPA	X04475	ECOTOPA
28.32 cysB			232	1	3972	0	JBch	262	5999	1987	ECYSB	M15041	ECOCYSB
28.34 acn, ribA	GTP cyclohydrolase II		1323	1	1113	0	EJB	204	599	1992	ECACN	X60293	ECOACN
28.35 ribA			1	1	1113	0	Unpub.	0	5117	1988	ECRIBA	X67876	-
28.50 pppB	bad name EMBL		1	1	2181	0	JBac	170	43	1993	ECRMBG	X67913	-
28.75 rnb	within pyrF		364	1	488	0	Cell	55	467	1988	ECTERC1A	M23250	ECOTERC1A
28.80 terC1			481	1	1366	0	JBac	171	511	1989	ECOSMB	M22859	ECOOSMB
28.81 pyrF	osmotic. ind. lipoprot.		1	1	1366	0	JGM1	138	209	1992	ECENVM	M97219	-
28.83 osmB			1	1	1366	0	JGM1	138	209	1992	ECENVM	M97219	-
28.91 envM	stress induced operon		1	1	2424	0	JMB	220	35	1991	ECFSP	X57560	ECOPSP
29.10 pspABCDE			1	1	2424	0	JMB	220	35	1991	ECFSP	X57560	ECOPSP

Listing 1: (continued)

Gene	Description	Accession	Length	Year	Source	Accession	Length	Year	Source
29.20 tyrR	-	1964 T	1	1964	1964 JBCh	261	403	1986	ECTYRR
29.22 tyrR	-	1964 T	1	1964	0 JBac	175	1767	1993	M12114
29.30 prrBCD	-	3853 T	1	3853	3853 EMBO	9	1383	1990	ECOPRBCD
29.50 ALDH	similar to mamm. aldh	2883 T	1	2883	2883 Gene	99	15	1991	ECALDHQ3
29.80 fnr (nirR)	-	1641 T	1	1641	2019 NAR	10	6119	1982	ECFNRR
29.81 ogt, fnr	summ BB	718 C	1	341	0 NAR	15	9177	1987	ECOGT
29.90 dbpA	-	1668 T	1	1668	1668 NAR	18	5413	1990	ECBEADA
30.00 bent 108	no neighboring gene	315 T	1	315	315 MGG	226	367	1991	ECBENT108
30.20 racC, recE	-	2475 T	1	2475	2475 JBac	171	2101	1989	ECRECEA
30.50 trkG	within rac prophage	1817 T	1	1817	1817 JBac	173	3170	1991	ECRCKG
30.95 dcp	-	2906 T	1	2906	2906 JBac	174	1698	1992	ECDCPG
31.00 cybB	-	1439 T	1	1439	1439 MGG	212	1	1988	ECCYBB
31.10 try	-	1722 T	1	1722	1722 PNAS	81	3287	1984	ECG
31.85 ori-H	flanking seq. of rhsE	1331 T	1	1331	1331 Unpub.			1992	ECRHESEA
32.00 rhsE	-	2440 T	1	2440	2440 NAR	19	7177	1991	ECRHSRG
32.00 orf, IS2, 30	near repl. terminus	9415 T	1	9415	9415 BchF	0	0	1991	ECIS2IS30
32.10 ald	-	1764 T	1	1764	1764 JBac	173	6118	1991	ECALD
32.20 attP2 III	-	497 T	1	493	497 JBac	174	4086	1992	ECBP2ASC
32.40 osmC	-	998 T	1	998	998 JMB	220	959	1991	ECOSMC
32.60 rimL	map acc. KR	1248 T	1	1248	1248 MGG	217	289	1989	ECRIML
33.10 narXyW	second nar operon	7080 T	1	7080	7080 MGG	222	104	1990	ECNARZYW
33.40 fdnGHI	fdnGHI ?	4981 T	1	4981	4981 JBCh	266	22380	1991	ECFDNGHI
33.50 sfcA	new KR, fusion with rec	1765 C	1	1765	1765 G	125	261	1990	ECSBCAS
33.60 marR	-	7876 T	1	7876	7876 JBac	175	1484	1993	ECMARAR
33.70 gadB	map (1589) and sequence	1421 T	1	1421	1421 JBac	174	5820	1992	ECGADB
33.90 hip	hip operon orf1 & orf2	2235 T	1	2235	2235 JBac	173	5732	1991	ECHIPO
34.00 terC3	-	454 T	1	454	454 Cell	55	467	1988	ECTERC3A
34.50 uraB	-	286 T	1	286	286 JGM1	132	697	1986	ECUXAB
34.60 ecos1	within qin at ca. 35.1	2078 T	1	2078	2078 NAR	20	3357	1992	ECs1G
34.70 relB	-	2142 T	1	2141	2141 EMBO	4	1059	1985	ECRELB
34.90 dicBAC	-	968 T	1	4440	4440 NAR	14	6821	1986	ECDICABC
35.60 tus	& fumCA, manA	3524 T	1	3524	3524 Unpub.			1992	ECPNT
35.61 tau	tus term.pr.	2416 T	1	520	6149 PNAS	86	1593	1989	TAU
35.65 fumCA	-	2079 C	1	2079	0 JBCh	264	21031	1989	ECTAU
35.66 fuma	-	2250 C	1	430	0 BJ	237	547	1986	ECFUMC
35.67 manA	-	2408 C	1	550	0 NAR	12	3631	1984	ECFUMA
35.70 uida	-	1604 C	1	1604	0 Gene	32	41	1984	ECMANAA
35.71 uida	-	460 T	0	0	2439 MGG	199	101	1985	ECUIDAI
35.80 hdhA	-	2439 C	1	2439	0 PNAS	83	8447	1986	ECUIDAI
35.82 malIX	correction within malX	1785 T	1	845	6319 JBac	173	2173	1991	ECSHDH
35.83 add	-	3119 C	1	4197	0 JBac	173	4862	1991	ECMALAA
36.00 tyrS	-	1200 C	1	1200	0 Bich	30	2273	1991	ECADD
36.01 pdxH	-	1275 T	1	1	2369 FEBS	150	419	1982	ECTYRS
36.10 rnt	& RNA helicase like pr.	1142 C	1	1323	0 JBac	174	6033	1992	ECTYSPDH
36.20 valV, valW	new tRNA Val2A,B locus	1323 T	1	300	1323 JBCh	267	25609	1992	ECRNTASET
36.40 nth	map	780 T	1	300	300 JMB	212	579	1990	ECRNTAV2
36.50 sodB	loc BB	970 T	1	780	800 Bich	28	4444	1989	ECNTH
36.60 purR	correction for J04212	1575 T	1	2041	2041 EJB	187	1555	1988	ECsODB
36.65 cfa	-	814 T	1	1575	1575 Bich	31	11020	1992	ECCFAX
36.80 lpp	-	1798 T	1	814	814 Cell	18	1109	1979	ECCLPP
37.00 aroD	near aroH	3312 T	1	1798	1798 BJ	238	475	1986	ECAROD
37.10 ppaA	strain W3110	3662 C	1	3312	3668 MGG	231	332	1992	ECPPGENEX
37.20 aroH, urfa	-	2054 T	1	3662	0 Unpub.			1991	ECPEPSYN
37.43 btud	-	5972 C	1	2054	2054 Gene	102	87	1991	ECAROHA
37.47 hma	-	3060 C	1	378	10765 JBac	167	928	1986	ECBTUCED
37.50 pheST, infC	also M10430	409 T	1	5784	0 Unpub.			1985	ECCHIMA
37.70 pfrB	-	1249 C	1	423	0 JBac	163	787	1985	ECTHRINF
37.71 pfrB	-	3466 T	1	1249	0 Gene	28	285	1983	ECPFKB
37.90 katE	catalase HPII	3466 T	1	1249	10563 JBac	173	514	1991	ECOKATE

37.91 kate, cele	588 C	488	101	0	Unpub.	1992	ECCELKATEX66725	ECOCELKATE
37.92 celABCDf	4989 C	4989	1	0	G	1990	ECCELOPE X52890	ECOCCELOPE
37.94 anr	520 C	436	1	0	Unpub.	1991	ECANRG X60186	ECOANRG
37.95 ntr-like	1493 C	102	1384	0	JBac 169	1987	ECENTRLA M15328	ECENTRLA
38.00 bnt 106	302 T	1	302	302	MGG 226	1991	ECENTR106X63983	ECOBENTR106
38.30 xthA	1246 T	1	1246	1246	Unpub.	1988	ECXTHA X13002	ECOXTHA
38.40 gdhA map	1937 T	1	1937	1937	Gene 27	1984	ECGDHAK K02499	ECOGDTHAK
38.55 topB, seld	2540 T	2540	1	1	Gene 264	1984	ECGTOPB J05076	ECOTOPB
38.56 seld	1202 C	741	1	0	PNAS 87	1990	ECSELD M30184	ECOSELD
38.57 orf183	780 C	736	288	1	JBac 173	1989	ECORF183 M68961	ECORF183
38.58 sppA	2156 T	1	2156	1	JBCh 261	1986	ECOSPPA M13359	ECOSPPA
38.80 ansA	1523 T	1	1523	1	Gene 78	1989	ECANSORA M26934	ECOANSORA
39.35 gapDH	1354 C	0	0	0	NAR 16	1985	ECOGAP X02662	ECOGAP
39.60 rnd	1623 T	1	1623	1	JBac 159	1984	ECRABBB K02673	ECOPABBB
39.80 pabB	2230 T	1	2230	1	JBCh 267	1992	ECFADD L02649	-
39.90 fadD	3179 T	1	3188	1	JBCh 262	1987	ECFTSLPM J02699	ECOPTSLPM
40.10 ptmPL	1224 T	1	954	1	JBac 173	1991	ECHTPX M58470	ECOHTPX
40.40 htpX	3178 C	1224	1	1	JBac 173	1991	ECERC D00674	ECOPRC
40.41 prc	2937 T	2937	73	1	JBac 174	1992	ECEDDEDA M87458	ECOEDEDEDA
40.80 eda, edd	2330 C	2330	1	1	JBac 173	1991	ECZWF M55005	ECOZWF
40.82 zwf	1640 C	1	1105	1	Unpub.	1991	ECYKAA M63703	ECOPYKAA
40.85 pykA	2589 C	2589	1	1	JBac 174	1992	ECMSBBA M77039	ECOMSBBA
40.96 msbB	2685 T	2685	1	1	JBac 170	1988	ECRUVA01 M21298	ECORUVABA
41.10 ruvBA	3255 C	2850	1	1	JBac 173	1991	ECRUVC D10165	ECORUVVC
41.13 ruvC, orf23	3866 C	2751	1	1	NAR 18	1990	ECASPS X53863	ECOASPS
41.14 aspS	3063 T	1	2372	1	NAR 17	1989	ECARGS X15320	ECOARGS
41.30 argS	2372 T	1	17	1	JBac 165	1986	ECCHB3 M13463	ECOCHEB3
41.45 cheZYBR	3465 C	3465	1	1	Cell 33	1983	ECTARK V01504	ECOCHEA
41.49 tap	1198 C	1198	1	1	JBac 165	1986	ECHE1 M13462	ECOCHE1
41.51 cheA	1393 C	1393	1	1	Unpub.	1990	ECCHBA M34669	ECOCHEA
41.54 motB	974 C	0	0	0	JBac 166	1986	ECMOTAB J01652	ECOMOTAB
41.55 motA, flhD	1076 C	1883	1	1	JBac 159	1984	ECMOTAB M12914	ECOMOTAB
41.57 flhB, flhD	0 C	1155	1	1	JBac 170	1988	ECFLBA M19439	ECOFLEBA
41.57 flhB, flhD	0 C	4200	5	1	JBac 170	1988	ECARAFGH X06091	ECOARAFGH
41.80 araFGH	530 C	15	1	1	JMB 197	1990	ECARAFGH X58969	ECOARAFGH
41.82 araFGH	823 T	1	823	1	JMB 215	1991	ECRSGA X53513	ECORSGA
42.00 gen-165	1935 T	890	1947	1	MGG 225	1988	M23240	ECOTYRPA
42.20 tyrP	890 T	890	285	1	JBac 170	1985	X03239	ECOGLYWG
42.30 leuZ, glyW	955 C	955	157	1	BChf 67	1986	M12299	ECOPGSA
42.33 pgsA	955 C	4549	1	1	JBCh 261	1983	X00189	ECOUVRC
42.35 uvrC, orf & pgsA	120 C	4549	561	1	EMBO 2	1983	X17440	ECOHAG48
42.60 flbC, hag48	2526 T	2526	2384	1	MGG 216	1982	M85240	ECOFLGPRO
42.63 flhDST	2400 C	101	1588	1	JGM1 138	1992	ECFTAA L01642	ECOFTAA
42.64 flhT, anyA	5160 C	69	5123	1	Unpubl.	1993	ECAMYAP L13279	-
42.65 anyA, flhE	1086 T	545	1	1	JBac 174	1992	ECFLIE M84992	ECOFLIE
42.66 flhE, flhF	1763 T	1	1086	1	Unpubl.	1993	ECFLIG L13243	-
42.70 flhG	499 C	52	1763	1	JBac 166	1986	ECFLAA M12784	ECOFLAA
42.74 flhAI	3655 T	1	3655	1	JBac 171	1989	M26294	ECOFLAA
42.90 dcm, orf	934 T	1	934	1	NAR 17	1989	ECDCM X13330	ECODCM
43.00 rcsA	1803 T	1	1803	1	Unpub.	1991	ECRCSA M58003	ECORCSA
43.20 asnT	200 T	1	200	1	BCh 28	1989	ECAMN M30469	ECOAMN
43.21 serU	150 T	0	287	0	BCh 212	1990	ECSTRAN X52790	ECOTRAN
43.22 supD	284 T	1	284	1	Unpub.	1987	ECGSSD M10746	ECOTGSSD
43.30 aspV	200 T	1	200	1	JBac 161	1985	ECGSSD M10746	ECOTGSSD
43.40 asnU	302 T	1	302	1	Unpub.	1985	ECGSSD M10746	ECOTGSSD
43.45 asnV	1927 T	1	1927	1	JMB 212	1990	ECSTRAN2 X52791	ECOTRAN2
43.60 attP2H	708 T	1	714	1	JMB 212	1990	ECSTRAN3 X52792	ECOTRAN3
43.70 sbcB	1927 T	1	1927	1	JBac 174	1992	ECBP2ASA Z11491	ECOBP2ASA
43.90 hlsG	708 T	1	714	1	NAR 9	1987	ECSCBC J02641	ECOSBCB
						1981	ECHIS1 V00284	ECOHIS1

50.91 dsdAC	-	1000 C	281	1989	0	JBAC 154	1508	1983	ECSDSA	J01603	ECODSDA
50.93 dsdA	corr	1445 C	0	0	0	JBCh 263	16926	1988	ECSDSA	J01603	ECODSDA
51.10 lycB	& gltX,orf294,62,105,16	1880 T	1	1369	1369 Unpub.	825	825	1990	ECGLTXVA	X55757	-
52.00 lysV, valU	reading frame only	1514 C	4	1413	0 JBCh 261	10610	10610	1986	ECGLTX	M13687	ECOGLTXU
52.04 gltX	& alaW, orf167	1862 C	1	1862	0 JMB 214	825	825	1990	ECGLTXVA	X63977	ECOGLTXU
52.05 orf62,105	& trNA Lys & trNA Val 17 bp differ.	542 T	1	542	0 JMB 212	579	579	1990	ECRNNAVX	X52796	ECOTRNNAVX
52.10 lig	-	3195 T	1	3195	3195 Unpub.	3150	3150	1989	ECLIG	M24278	ECOLIG
52.20 cysK	& ptsHI, crf	2596 T	1	2597	4861 JBAC 170	3827	3827	1988	ECXSPTS	M21451	ECOCISPTS
52.21 orf, cysK & ptsHI, crf	-	3144 C	881	3144	0 JBAC 170	3358	3358	1990	ECPHOSYS	M21994	ECOPHOSYS
52.30 cysP	& cysTWAM	1291 T	1	5736	5736 JBAC 172	367	367	1991	ECBENT111	M32101	ECOCYS
52.60 bent 111	no neighboring gene	361 T	1	361	361 MGG 226	2270	2270	1992	ECBENT111	M63986	ECOBENT111
53.00 dape	-	2270 T	1	1069	0 JBAC 174	5265	5265	1992	ECDAPE	X57403	ECODAPE
53.20 purC,dapX	2D:purC B026.3	2060 T	1	2060	0 JBAC 172	6035	6035	1990	ECPURCA	M33928	ECOPURCA
53.21 nlPB -dapX	-	1366 C	1070	1366	0 JBAC 173	5523	5523	1991	ECNLB34	X57402	ECONLB34
53.22 dapa	-	1171 C	1131	1171	0 JBAC 166	297	297	1986	ECDAPA	M12844	ECODAPA
53.23 orf, bcp	53.3 min region; M37689	1001 T	1	275	0 JBAC 172	361	361	1991	ECORF123	M63654	ECORF123
53.70 upp	-	2043 C	1	2899	6776 EJB 204	51	51	1992	ECURPUPT	X57104	ECOURPUPT
53.71 purMN	-	2255 C	462	2255	0 JBCh 261	10632	10632	1986	ECPURMN	M13747	ECOPURMN
53.73 ppk	polyphosphate kinase	1884 C	36	1884	0 JBCh 267	22556	22556	1992	ECOKINASL03719	-	ECOKINAS
53.74 ppk	exopolyphosphatase	1847 T	3531	323	4825 NAR 13	1303	1303	1985	ECGUABA	M10101	ECOGUABA
53.90 guaAB	overlay gua-xse HD	1616 C	1	1616	0 JBCh 261	14929	14929	1986	ECXSEA	J02599	ECOXSEA
53.93 xseA	-	1673 T	1673	1673	3239 JBCh 260	10063	10063	1985	ECHISS	M11843	ECOHISS
54.10 hiss	-	1697 C	1697	107	0 Unpub.	31	31	1992	ECGCPD	X64451	S113083
54.12 gcPE	J.Parker	724 T	1	724	724 Gene 105	31	31	1991	--NDK	0005MK	-
54.20 ndk	within crypt. phage 428	1017 T	1	1017	1017 JBAC 172	2124	2124	1990	ECURHBA	M34828	ECOSUHBA
54.60 subB	-	1725 T	1725	146	3634 NAR 11	2065	2065	1983	ECGLYA	V00283	ECOGLYA
54.90 glyA, hmp & ginB	J01620 in Gb	2054 C	1	2054	0 MGG 226	49	49	1991	ECHMPLNBX	55872	ECOHMPLNB
54.94 hmp, ginB	4 differences	5865 T	1	5865	5865 B1Ch 28	2459	2459	1989	ECPUKLA	J02848	ECOPUKLA
55.20 purL	orf178 & 190; x61396 ?	3000 T	1	3000	3000 MOMB 6	900	900	1992	--GEF	0002MK	-
55.40 orf360 & J	new BB	1466 T	1307	151	6915 JBAC 174	1554	1554	1992	ECPDJDPJM	74526	ECOPDJDPJ
55.50 djP, pdxJ	-	1588 C	1590	844	0 JBAC 171	3641	3641	1989	ECRECO	M27251	ECORECO
55.52 reco, era	-	1020 C	1020	185	0 PNAS 83	8849	8849	1986	ECERA	M14658	ECORA
55.55 era	-	1076 C	1076	185	0 NAR 13	4677	4677	1985	ECRNC1	X02673	ECORNC1
55.58 rnc	-	2220 T	3099	1	0 JBCh 260	7206	7206	1985	ECLP	K00426	ECOLEP
55.61 lepA	put. RNA helicase	10272 T	1	10272	10272 Unpub.	221	221	1988	ECRBAB	D13169	-
55.80 nadB, rbaB	new BB	1724 C	0	0	0 EJB 175	221	221	1988	ECNADB	X12714	ECONADB
55.81 nadB	-	1532 C	0	0	0 JBCh 263	7776	7776	1988	ECUNGO1	J03725	ECOUNG
55.83 ung	-	1977 T	1	1925	0 JBCh 266	5323	5323	1991	ECPSS	M58699	ECOPSS
56.20 pss, kgtP	& rrrG, gltW, rsl, clpB	94 C	60	1	0 PNAS 88	3802	3802	1991	--WITA	0015MK	-
56.22 kgtP -wita	60 bp missing X53027?	1560 C	1560	1	0 JBAC 172	4745	4745	1990	ECWITAG	X53027	ECOWITAG
56.23 wita	loc. betw. pss & rrrG	480 C	287	1	0 JBAC 172	3056	3056	1990	ECRRFG	X52363	ECORRFG
56.25 rrrG, wita	distal end of rrrG	600 C	120	35	0 NAR 18	735	735	1967	ECRN10	X00414	-
56.32 spacer	analogue rrrf ECRNA8	2904 C	6403	3500	0 N 215	107	107	1981	ECRRNBZ	V00348	ECORGNB
56.33 rrlG	RNA analog J01695 in Gb	431 C	431	1	0 JMB 148	1235	1235	1988	ECTGC	M20397	ECOTGC
56.34 gltW, rsl	rel, trNA Glu2	1541 C	3059	2194	0 JBAC 170	107	107	1981	ECRRNBZ	V00348	ECORGNB
56.35 rrrf, 16S	RNA analog J01695 in Gb	5684 C	4248	1	0 JMB 148	107	107	1981	ECRRNBZ	V00348	ECORGNB
56.37 clpB, rrrG	last 1438 bp ?	3503 C	1165	2	0 Unpub.	4247	4247	1991	ECCLPB	X57620	-
56.38 clpB	only 564 bp in paper	800 T	1	800	800 JBCh 173	11120	11120	1992	ECFDX	M8654	ECOFDX
56.45 fdx	[2F8-28] ferredoxin	4509 T	1	4509	4509 JMB 180	1023	1023	1984	ECTYRA	X02137	ECOTYRA
56.60 tyrA & L19	put. RNA helicase	5378 T	1	5378	4586 EMBO 2	899	899	1983	ECTRMD	X01818	ECOTRMD
57.40 mprA	-	742 T	1	742	742 JBAC 173	3924	3924	1991	ECMPRA	X54151	ECOMPR
57.60 gabTPD	& trNA Ser3	1200 T	1	1200	5378 Unpub.	579	579	1990	ECSEDEHMB8334	ECOSUSEDEH	-
57.90 argV, serV	similar to HNS	978 T	1	978	1200 JMB 212	6735	6735	1992	ECSTPA	X65210	-
57.95 stpA	new BB	280 T	1	240	978 NAR 20	205	205	1991	--ALAS	0001MK	-
58.00 alas mRNA	-	500 C	1	500	3010 JBCh 256	6531	6531	1980	ECALAS1	J01581	ECOALAS
58.01 alas	-	2767 C	498	2767	0 PNAS 77	1497	1497	1981	ECALAS1	V00254	ECOALAS
58.02 alas	J01581 in Gb	1320 T	1	1391	0 Scle 213	313	313	1980	ECRECA	V00328	ECORECE
58.10 recA	J01672 in Gb	1374 C	0	1391	1391 PNAS 77	2611	2611	1980	ECRECA	V00328	ECORECE
58.11 recA	J01672 in Gb	1374 C	0	0	0 PNAS 77	2611	2611	1980	ECRECA	V00328	ECORECE

Listing 1: (continued)

Accession	Gene/Feature	Map/Location	Size (bp)	Orientation	Other	Accession	Gene/Feature	Map/Location	Size (bp)	Orientation	Other
58.20	recN	-	2224	T		1	2224	NAR	15	1987	ECRECN
58.22	ampAB	map, overlap unclear	611	T		1	611	JBac	173	1991	ECSPROT
58.24	smpB	-	2216	T		1	2216	Unpub.		1992	ECSPROT
58.30	pru(VWX)	2D:prov	4361	T	G033.5	1	4361	Unpub.	171	1989	ECSPRAL
58.34	bent 105	next to prov	280	T		1	280	MGG	226	1991	ECBENT105
58.40	gshI	mut	2098	B		0	4393	NAR	14	1986	ECGSHI
58.50	gutABD	= srlABD	3523	T		0	4770	JBCh	262	1987	ECGUT
58.54	gutC	-	935	C		252	935	DNAS	1	1990	ECGUTQ
58.60	ascG	B.Hall/L.Xu	4286	C		1	4286	MBE	9	1992	ascGeco
58.61	hydNA	overlap to ascG unclear	4075	C		310	4075	Unpub.		1993	ECHYDA
58.80	hevA	CDERF & hevH	7650	T		0	16907	MOMB	4	1990	ECHEVOP
58.81	hevOP	-	211	C		0	0	MOMB	4	1990	ECHEVOP
58.83	hypABCD	hydrogenase isoenzyme	3793	C		1	3720	MOMB	5	1991	ECHYP
58.84	flhA	flhB at 95.4 div.seq.	2443	C		210	3327	JBac	172	1990	ECFHILA
58.87	mutS	fdv	3327	T	E093.0	44	1642	Unpub.		1991	ECMUTS
59.00	rpos	new sigma 38 factor	1642	T		1	1642	Unpub.		1992	ECSIGMA38D1548
59.04	katF	correction	1029	C		0	0	Unpub.		1992	ECATFWT Z14969
59.10	pcm	protein carboxyl methyl	1145	T		0	1145	JBCh	266	1991	ECPCM
59.20	cysCND, iap	-	3821	T		3821	336	JBCh	267	1992	ECYSDNC
59.24	iap	conflict last bp = C	1664	C		332	1664	JBCh	169	1987	ECIAP
59.25	iap	14 times 29 bp repeat	1465	C		1	1168	JBac	171	1989	M27059
59.32	cysIH	cysI, PAPS-reductase	2866	T		1	2866	Unpub.		1991	ECYSH
59.32	cysJ	Y07525 in Gb	355	T		1	355	Gene	122	1992	ECYSJ
59.33	cysJI	E.coli B	2089	T		1	2089	JBac	171	1989	ECYSJ01
59.35	cysJIH	E.coli B	3876	B		27	3876	JBCh	264	1989	ECYSJIH
59.75	pyzC	to 6 times 29 bp repeat	1531	T		1	1531	JBac	171	1989	M27060
59.80	pyzG	acc. K.Rudd	2442	T		1	2442	JBCh	261	1986	ECPYRG
59.81	mag	G.Glaser/M.Cashel	1059	C		1	1059	Unpub.		1991	mageco
59.83	relA	map	2858	C		1	2858	JBCh	263	1988	ECRELA
59.84	relA	G.Glaser/M.Cashel	1011	C		1	1004	Unpub.		1991	relAeco
59.84	barA	-	3060	T		1	3060	MOMB	6	1992	ECBARA
60.20	metZ	tRNA met	344	T		1	344	Gene	67	1988	ECTGM12
60.30	fucO	-	1690	T		0	0	JBac	171	1989	ECFUOCO
60.32	fucAPIKR	-	8901	C		0	8901	NAR	17	1989	ECFUOCSE
60.60	argA	-	1575	T		1	1571	NAR	15	1986	ECARGA
60.62	recD	-	3960	C		2160	361	NAR	14	1986	ECRECD
60.63	recB	-	3120	C		3120	1094	NAR	14	1986	ECRECB
60.64	ptr	-	3120	C		3120	191	NAR	14	1986	ECPTR
60.65	ptr	-	1171	C		1171	191	Gene	54	1987	ECPTR31
60.66	thyA, recC	& ptr, recDC, argA	6000	C	G095.0	5992	756	NAR	14	1983	ECOTHYA
60.67	thyA	16 bp linker deleted	1147	C	G095.0	1155	8	PNAS	80	1987	ECMUTH
61.05	mutH	-	790	T		1	790	NAR	15	1987	ECMUTH
61.15	aaa	next to mutH	316	T		1	316	MGG	226	1991	ECBENT107X63984
61.35	galR	-	3186	T		1	3186	Unpub.		1993	ECMAAS
61.36	lysR, orfX	J01614 in Gb	1150	T		1	1150	PNAS	79	1982	ECGALR
61.37	lysA	-	1854	C		1151	3231	Unpub.		1983	ECGALLY
61.38	araE	-	2346	C		0	0	JMB	168	1983	ECGALLY
62.00	glyU	Gly-tRNA	2866	C		2866	1	JBCh	263	1988	ECARARA
62.00	glyU	-	464	T		1	464	AMP	35	1986	ECTGG1
62.20	herC	-	1832	T		1	1832	PNAS	85	1988	ECHEHC
62.23	prfB	-	1440	C		1181	1	PNAS	82	1988	ECRF2X
62.25	recJ	map; last 16 bp artifical	3772	C	D058.5	3266	1	JBac	173	1991	ECREJXP
62.60	gcvT	T-protein	1823	T		1	1620	Unpub.		1992	ECGCVH
62.61	gcvH	H-protein	516	C		1	516	Unpub.		1991	ECGCVH
62.80	sbm, iclA	second sbm gene ?	6055	T		1	299	JBac	174	1982	ECSEARAICIX66836
62.82	serA	-	1233	C		457	1	JBac	173	1986	ECSEARA
62.83	serA	-	545	C		1	954	JBac	161	1991	ECSSR
62.90	ser	-	954	T		1	954	JBac	174	1982	ECPUTV
63.00	visBC, pep2	includes flanking seq.	4948	T		1	4948	MOMB	3	1989	ECFDAPGK
63.40	fda, pgk &	new BB	8029	T		1	8029	Unpub.		1992	ECTKT
63.55	tkk	transketolase	2441	T		2441	1	Unpub.		1992	ECTKT

Listing 1: (continued)

70.30 nana	= npl new BB D00067 in Gb	1	1243	1243	2155	1986	ECNANAA	M20207	ECNANA
70.50 rpaI, rplM	length BB	26	1184	1159	279	1985	ECRPSI	X02130	ECORPS1
70.70 mdh, argR	-	0	1046	3028	4993	1987	ECMDH1	Y00129	ECOMDH1
70.72 mdh argR	new BB	2470	369	0	36	1987	M24777	M24777	M24777
70.73 argR	new BB	1	926	0	4389	1988	ECXERA	X13968	ECOXERA
70.80 rplC	= xera	1	2672	2672	5881	1992	ECPRLC	M93984	ECOPRLC
71.00 mrd, orfEF	orfZ, orfF	1	310	5590	135	1991	ECMRED	X57166	S65051
71.02 mrcD	bad name in Gb	2314	1	0	6511	1989	ECMRBCD	M31792	ECOMRBCD
71.03 mrcB & mrcD; mreB = envB	bad name in Gb	1965	1	0	4619	1988	ECMRBB	M22055	ECOMRBB
71.10 fabE	= fabG in M83198	1621	1	0	855	1992	ECACOAC	M80458	ECACOAC
71.15 fabG	bad name fabG (24.40)	1	4180	6084	9730	1991	ECFABG	M79446	ECOFABG
71.16 panF	bad name panF	0	1904	0	3842	1990	ECPANF	M30953	ECOPANF
71.60 fls, orf2, 3	pantothen permease	1	2467	2467	8043	1992	ECFISORFSM95784	ECOFISORFS	
71.70 bending	site 10/49 bp misplaced	1	173	173	6827	1987	ECBENT10	X05963	ECOBENT10
71.81 rrlD, rrfD, thrV, rrfD	J01693 in Gb	667	471	5761	3793	1980	ECRNAG	V00334	ECORNA6
71.82 RNA 7 S	-	0	0	0	2952	1984	ECAP	K02180	ECORRAP
71.83 rrfD, thrV GGU	-	302	1	1	4089	1992	EC5RTRH	D12500	EC05SRTRH
71.84 rrlD, rrfD	-	169	134	0	3793	1980	ECRNAG	V00334	ECORNA6
71.85 rrlD 23S RNA analog J01695 in Gb	-	6403	3500	0	107	1981	ECRRNBZ	V00348	ECORNBZ
71.87 rrd tRNA ile ala tRNA:A250	-	437	1	0	3264	1979	ECRGNX2	K00763	ECORGNX2
71.88 rrd 16S RNA analog J01695 in Gb	-	2959	1512	0	107	1981	ECRRNBZ	V00348	ECORNBZ
71.92 rrd 16S operon J01692 in Gb	-	424	7	0	225	1979	ECRGNX1	J01700	ECORGNDS1
71.93 rrd upstream sequence	-	19	1	0	1992	ECRRNDUS	X67682	ECORNDUS	
72.00 aroE	-	1	819	819	319	1988	ECAROE1	Y00710	ECAROE1
72.05 aroE, rplQ	intergenic M11148 in Gb	1	242	242	5813	1984	ECAROE	X00767	ECARO1
72.10 fms, fnt	-	1	2256	2256	4294	1992	ECFMT	X63666	ECOFMT
72.15 trkA, orf KR	-	1	1788	1788	1991	ECRTRKAG	X52114	ECOTRKG	
72.40 rplQ, Ll1	= neaA	3154	329	14392	3891	1985	ECRPA	X02543	ECORPA
72.46 rpsM, S13	-	759	654	0	4653	1980	ECRPLP2	M12432	ECORPLP2
72.51 rplO, L15	-	5922	224	0	2599	1983	ECSPC	X01563	ECORPLS10
72.66 rpsC, L29	901 bp not det, here BB	5421	902	0	4521	1985	ECRPOS10	X02613	ECORPOS10
72.75 rpsJ, S10	J01680 in Gb	1241	1	0	205	1981	ECRPSL	V00344	ECORPSL
72.95 bfr, gp24'	ca.100 bp gap	1	1350	1350	3940	1989	ECBFR	M27176	ECOBFR
73.00 tufA	-	200	1	0	25	1980	ECSTR4	J01691	ECOSTR4
73.05 tufA	-	1374	70	4769	25	1980	ECSTR3	J01690	ECOSTR3
73.07 fusa	length BB	2145	310	0	2181	1984	ECFUSG	X00415	ECOSTR3
73.08 rpsG, S7	J01689 in Gb	405	1	0	4660	1980	ECSTR2	V00356	ECOSTR2
73.10 rpsG, S7	-	281	201	0	93	1992	ECRPSG	X64592	-
73.12 rpsL, S12	-	1016	1	0	215	1978	ECSTR11	J01688	ECOSTR1
73.50 crp, orf	-	783	196	1880	109	1991	ECRPPDDNAX61919	ECORPPDDNA	
73.51 crp	-	7	1127	0	1363	1982	ECRCP	J01598	ECORCP
73.53 crp	-	99	269	0	654	1987	ECRCP3B	M15200	ECORCP3B
73.80 envCD (dtu)	-	1	6792	5792	230	1991	ECENVCD	X57948	ECOENVCD
74.00 argD (dtu)	-	1	1	3923	69	1990	ECARGD	M32796	ECOARGD
74.01 pabA & orf, utu, dtu	-	1221	1	0	397	1990	ECPABAA	M32354	ECOPABAA
74.04 fic & orf190, orf77	-	2008	1	0	4525	1989	ECFIC1	M28363	ECOFIC1
74.20 nirBDEC & cysG, orf	entire operon sequence	694	5596	5596	315	1990	ECNIRBC	X14202	ECONIRBC
74.23 cysG, orf	entire operon sequence	1	5280	5280	325	1991	ECYSAA	M64606	STYCISAA
74.30 trps, dam	J01716 in Gb	2664	1	0	1993	ECAMOPRAZ19601	-	-	
74.32 trps	length BB	8297	0	0	6132	1982	ECSTRPSZ	V00371	ECOTRPSZ
74.35 dam, orf	76 bp artificial subtr.	0	0	0	837	1983	ECADM	J01600	ECODAM
74.36 dam, orf & aroB	first 8 bp artificial	0	0	0	85	1989	ECURF743	X15162	ECOURF743
74.37 aroB	incl. dam promoter	0	0	0	11	1986	ECAROB	X03867	ECAROB
74.38 aroK	identical BgIII ?	0	0	0	525	1992	ECAROK	M76389	ECAROK
74.60 mrcA	severe differences	1	2764	2764	437	1985	ECPCKA	X02164	ECOPCKA
74.80 pckA	corr BB	1511	1	0	7151	1990	ECPCKA	M59823	ECOPCKA
74.83 envZ	corr BB	1100	2	0	13692	1982	ECENVZ	J01606	ECOENVZ
74.85 cmpR, envZ	corr BB	1	2614	2614	13685	1982	ECOMP	J01656	ECOMP
75.01 bioH	-	1	8703	8703	473	1988	ECBIOH	X15587	ECOBIOH
75.15 malQP	corr BB	2866	1	0	394	1987	ECMALQP	M32793	ECOMALQP
75.16 malPT, zhg	X02003 in Gb	1900	1	0	394	1987	ECMALP2	X06791	ECOMALP2

Listing 1: (continued)

Accession	Gene/Feature	Map	Start	End	Strand	Length	Year	Author
83.25	lbpAB		2886	T	1	2886	1992	
83.42	gzcB		1498	T	1	6389	1984	
83.52	dnaW		3278	C	1	159	1984	
83.55	rnpA		1069	C	1	85	1985	
83.70	thdP		1925	T	1	6018	1991	
83.71	tnaA	corr	623	C	1	731	1985	
83.75	tnaAC	G046.5	2044	C	1	787	1981	
83.76	tnaB		1688	C	1	3231	1991	
84.00	bgIR		473	T	1	6827	1987	
84.05	phou		5270	T	1	2579	1985	
84.15	gid,unc & glms,phos		3730	C	1	189	1985	
84.41	gidA,oric & fvd,asnCA		14106	C	1	799	1984	
84.46	trkD,rbsD		4012	C	1	265	1993	
84.50	rbsBACK		2367	T	1	5820	1991	
84.54	rbsR		377	T	1	377	1991	
84.66	kdsB		1308	T	1	15831	1986	
84.69	rnc		682	T	1	5073	1985	
84.70	rnc		1541	C	1	107	1981	
84.71	glu		354	C	1	1235	1988	
84.72	rlic		2903	C	1	107	1981	
84.75	rzc,aspt, trpt		500	C	1	12725	1979	
84.79	84.5-86.5		91400	C	7	771	1991	
84.80	orfI, II		4900	C	0	21	1991	
84.86	llyGMEDAYC		574	C	0	2289	1979	
85.10	hel		2671	C	0	465	1987	
85.12	gppA		1748	C	0	886	1991	
85.13	rhlR		1535	C	0	945	1986	
85.17	trxA		1493	C	0	3531	1983	
85.20	rho		1800	C	0	746	1992	
85.45	rfe,orf		2543	C	0	813	1991	
85.70	argX		187	C	0	934	1984	
85.71	hlsR		646	C	0	K.Rudd	1991	
85.73	prom		4260	C	0	9871	1988	
85.74	hemy		4310	C	0	10367	1988	
85.84	cyfA,cya		1308	C	0	6973	1990	
85.85	dapF		2500	C	0	1579	1986	
85.86	orf,xerc		2846	C	0	6827	1987	
85.90	uvrD		426	C	0	1993	1993	
85.96	bending		4722	C	0	1655	1984	
86.01	rard,corA		1232	C	0	298	1986	
86.02	corA		1319	C	0	1017	1985	
86.15	pldA,recQ		2695	C	0	4407	1989	
86.17	recQ		1576	C	0	7076	1990	
86.25	pldB		254	C	0	6741	1989	
86.31	metE,metH		1013	C	0	1003	1992	
86.33	metR		2479	C	0	3673	1991	
86.40	udp		894	C	0	10424	1990	
86.70	rfaH(sfrB)		3591	C	0	4937	1990	
87.10	fze		4151	C	0	6439	1990	
87.22	fadA		426	C	0	201	1979	
87.23	pepQ,orf		1541	C	0	107	1981	
87.24	rnaA		241	C	0	3593	1978	
87.26	rnaA		545	C	0	3264	1979	
87.31	alaUV		2903	C	0	107	1981	
87.32	rriA		247	C	0	393	1980	
87.33	intergenic		120	C	0	2453	1979	
87.35	5S rRNA		675	T	1	581	1991	
87.40	dbaA = dsf							

Listing 1: (continued)

108.03 hole	theta subunit DNA polym	507 T	1	8	649 Unpub.	1992	ECODNAPOLY	ECODNAPOLY
108.04 hole	theta subunit DNA polym	641 C	1	641	0 Unpub.	1992	ECOHOLETTA	ECOHOLETTA
113.01 MBP16-1	maltose binding protein	87 T	1	87	87 JBac 171	1989	ECMPB161	M29860
113.02 mdl	related to P-glycoprote	3690 T	1	3690	Unpub.	1993	ECMDL	L08627
113.03 methionine	S-adenosinemeth.synthet	2847 T	1	2847	Bich 31	1992	ECMDMS	M87625
113.04 metX	reverse transcriptase ?	1152 T	1	1152	Unpub.	1992	ECMETX	M98266
113.05 mit	chromosome partitioning	1743 T	1	1743	JBac 174	1992	ECMLT	M87660
113.06 mar,msd	phosphoenolpyruvate tr.	1330 A	1	1300	MOMB 0	1991	ECRNEC107	ECORNEC107
113.07 mukB	meth.sulfoxide reductas	5353 T	1	5353	Unpub.	1991	ECMUKB	M63930
113.08 murA	-	2147 T	1	2147	Unpub.	1992	ECMURA	M96355
113.09 peptide	-	1270 T	1	1270	JBCh 267	1992	ECMNSR	M89992
114.01 narQ	-	1710 T	1	9	Unpub.	1992	ECNARQ	X65714
114.02 narQ	-	1719 C	1	1729	0 Unpub.	1992	ECNARQB	M94724
114.03 neuC	E.coli K1	1283 T	1	1283	JBCh 264	1989	ECNEUA	J05023
116.01 prmoter	E.coli K1	1676 C	155	1676	0 JBac 174	1992	ECNEUC	M84026
116.02 ppx	strong promoter search	201 T	1	201	JJGe 66	1991	ECPPX	D01031
116.03 ppx	exopolyphosphatase	1884 T	1	1884	Unpub.	1992	ECPPX	L05129
116.04 ppfA	aminopeptidase P	1850 T	1	1850	EMBO 11	1989	ECAPP2	D00398
116.05 ppa	phosphatase folding	2192 T	1	2192	EMBO 11	1992	ECPPFA	X63186
116.06 paiK	pyrophosphatase	1195 T	1	1195	JBac 170	1988	M23550	M23550
116.07 paiR	-	86 T	1	86	JBac 172	1990	ECALPHOP	M33738
116.08 paiJ	-	37 T	1	37	JBac 172	1990	ECALPHOS	M33741
116.10 heat shock	promoter 10,92 BB ?	96 T	1	96	PNAS 82	1991	ECPT2	D10976
116.11 prfII	protease II	2339 T	1	2339	Unpub.	1991	ECPT2	D10976
118.01 rarB,rhlE	regulation DNA replicat	8355 T	1	8355	Unpub.	1993	ECRHEA	L02123
118.02 regX	to heterologous protein	256 T	1	256	Unpub.	1992	ECRHEA	L02123
118.03 response	-	2885 T	1	2885	Unpub.	1992	ECRPROTS	M94104
118.04 rpsV	-	2605 T	1	2605	Unpub.	1992	ECRPSV	D13179
119.01 sdaA	-	2785 T	1	2785	Unpub.	1989	ECSDAB	M28695
119.02 sdaB	-	1967 T	1	1973	N 336	1992	ECSDAB	L07763
119.03 srmB	-	2804 T	1	2804	Unpub.	1988	ECSRMB	X14152
119.04 sseAB	enhance of serine sense	977 T	1	977	Unpub.	1993	ECSSERAB	D10496
119.05 slyDX	phage infect cell lysis	1168 T	1	1168	Unpub.	1993	ECSTESA	L06182
120.01 teaA	thioesterase I	363 T	1	363	NAR 14	1992	ECUSPA	X67639
121.01 uspA	universal stress protei	768 I	1	768	MGG 169	1986	ECYLUP1	X04387
200.01 ls1	gene for xylose-uptake	1331 I	1	1331	Gene 59	1979	IS1ECLAC	J01729
200.02 ls2	6 common copies	1258 I	1	1258	NAR 13	1987	IS1ECLAC	V00279
200.03 ls3	7 copies M18426 in Gb	1426 I	1	1426	MGG 181	1985	ECIS3	X02311
200.04 ls4	1 common copies	1195 I	1	1195	N 297	1981	IS4ECO	J01733
200.05 ls5	1 common copy	160 I	1	160	JBac 164	1982	IS5LAM	J01735
200.10 ls10	length MK	160 I	1	160	JBac 164	1985	EC00UT2	K03315
200.10 ls10	IS10-R	1221 I	1	1221	EMBO 3	1985	EC00UT1	M14410
200.30 ls30	3 common copies	1829 T	1	1829	JBac 174	1992	ECIS30	X00792
200.91 ts91	1 common copy	1443 I	1	1443	NAR 16	1984	ECIS91TP	X17114
201.50 ls150	4 copies	1341 I	1	1341	FEBS 192	1988	ECIS150	X07037
304.03 tRNA asp & trp	length MK	236 T	1	382	NAR 10	1982	IS186	K01858
313.04 leu tRNA1	trp	146 T	1	146	Cell 30	1982	ECTGLGKP	K01687
313.06 leu tRNA3	CTC single gene	300 T	1	300	Gene 81	1989	ECTGLJ3A	M29082
401.00 6S RNA	-	492 T	1	492	NAR 14	1986	ECPHEW	X04126
402.00 spot 42RNA	-	184 T	1	184	NB 229	1971	ECRRN6S	X01238
	-	109 T	1	109	JMB 131	1979	EC42RNA	X01895

Listing 2: Partial main list sorted on genetic names

name	min.	name	min.	name	min.	name	min.
aas	61.16	aroC	50.42	cbt	16.25	ddl	2.16
aat	19.15	aroDH	37.00	cca	66.81	ddla	8.60
aat*	54.50	aroE	72.00	cdd	46.10	deaD	68.82
abc	101.00	aroF	56.63	cdh	88.28	dedA	1.60
abpS	60.40	aroG	16.85	cds	4.35	dedB	50.03
abs	94.65	aroI	83.90	cdsS	69.25	dedF	49.90
acca	4.49	aroK	74.38	celABCDEF	37.92	degP	3.86
accD	50.02	aroLM	8.90	cet	99.77	del	61.50
acd	62.40	aroP	2.71	cfa	36.65	deoABCDR	99.40
aceBAK	90.65	aroT	27.53	cheABRWYZ	41.51	dfp	81.80
aceEF	2.95	artIQMJ	19.30	chlAM	17.71	dga	89.72
aceK	90.70	artP	18.95	chlB	86.80	dgd	69.75
ackA	49.50	ascG	58.60	chlC (nar)	26.94	dgkA	91.80
ackB	38.90	asd	75.64	chLDJ	17.30	dgkR	93.75
acn	28.34	aslAB	85.92	chLEN	18.20	dgoADKRT	83.00
acpP	24.41	asnAC	84.42	chlG	0.45	dgsA	35.20
acpS	43.15	asnB	15.15	chm	103.00	dgt	3.81
acrA	10.60	asnS	20.74	cir	46.40	DH1	104.00
acrC	4.60	asnT	43.20	cita	17.60	dicB*	90.18
act	20.12	asnUV	43.40	clpA	19.11	dicBACF	34.90
ada	47.60	aspA	94.12	clpB	56.36	dinA	1.47
add	35.83	aspC	20.66	clpPX	9.93	dinF	91.86
adhE	27.42	aspS	41.14	cls	26.85	dinG	17.80
adhR	71.45	aspT	84.75	cmlA ?	19.50	dinH	19.42
adi	93.40	aspU	5.18	cmtAB	63.57	divE	22.31
adk	10.89	aspV	5.20	coaA	89.89	djp	55.50
ads	11.90	aspV*	43.30	codAB	7.60	dksA	3.54
agp	22.60	asu	33.20	colicin A	46.50	dld	46.20
aidBC	95.30	atoCDAB	47.95	corA	86.00	dmsABC	20.01
air	92.80	atp	59.21	corB	96.30	dnaAN	83.48
alaS	58.01	atpBX	84.18	cpdB	95.70	dnaB	91.90
alaUV	87.31	att e14R	25.20	cpsABCDE	44.50	dnaE	4.48
alaV*	5.15	att phi80	27.56	cpsF	90.20	dnaG	66.94
alaW	52.03	att186	57.10	cpxA	88.21	dnaI	39.50
ald	32.10	att253	6.10	cpxB	40.30	dnaJK	0.27
ALDH	29.50	attb lam	17.44	crg	28.65	dnaL	28.70
alkA	44.80	attHK139	43.65	cri	5.81	dnaQ	5.34
alkB	47.63	attHK22	22.40	crp	73.54	dnaTC	98.76
alr	91.92	attP1,P7	66.70	crp*	64.12	dnaX	10.80
als	93.02	attP2 II	87.60	crr	52.23	dnaY	12.30
alsB	19.40	attP2 III	32.20	cscB	51.10	dnaZX	10.83
alu	79.02	attP22	5.86	csgA	23.15	dniR	104.00
alx	67.50	attP2H	43.60	csi	59.00	dpj	55.51
amiA	51.50	attP4	97.05	cspa	78.80	dpp	13.90
amn	43.10	attPA-2	51.00	cstA	13.61	dppA	79.01
ampC	94.41	avtA	80.31	cup	97.60	dps	18.00
ampDE	2.90	azaA	43.55	cutE	14.70	drdX	27.37
ams	24.13	azaB	69.85	cvpA	50.10	drpA	4.80
amtA	95.72	azl	55.30	cxm	6.40	dsbA	87.40
amyA	42.64	baCA	102.00	cyaAF	85.81	dsbB	26.20
ana	27.28	baeSR	102.00	cybA	16.31	dsdAC	50.90
anr	37.94	baIF	0.76	cybB	31.00	dsf	87.40
ansA	38.80	barA	59.84	cybC	103.00	dtu	74.00
ansB	63.80	basRS	102.00	cycA	95.60	dut	81.90
ant	0.46	bax	80.30	cydAB	16.60	dvl	7.40
antizyme	101.00	bcp	53.23	cydCD	18.90	dye	99.78
apaGH	1.10	betABI	7.53	cynRSTX	7.85	ebqRABC	67.80
apeA	101.00	betT	7.50	cyoABCDE	9.80	ecfA	64.80
aphCF	14.20	betT*	0.80	cyr	91.77	ecfB	87.98
appACB	22.50	bfm	85.55	cysB	28.32	eci	49.40
appII	116.03	bfr	72.95	cysCHIJK*NP	59.31	ecos1	34.60
appR	59.05	bglBCRST	84.01	cysEX	80.81	ecos2	12.75
appY = M5	12.81	bglY	27.36	cysG	74.22	eda	40.80
apt	10.82	bioABFCD	17.45	cysQ	95.73	edd	40.80
araABCD	1.49	bioH	75.02	cysS	12.23	efg	38.10
araE	61.38	bioP	86.45	cysT*	42.31	endA	63.70
araFGH	41.80	biotin	17.47	cysAKMTW	52.31	endB	19.60
araJ	9.00	birA	89.86	cytR	88.80	eno	59.60
arcA	99.80	bisC	79.30	dacA	14.43	entABCD	13.59
arcB	69.71	bolA	9.91	dacB	69.11	envA	2.02
arcA	60.60	brnQR	8.40	dacC	18.60	envB	70.90
argBCEH	89.34	brnS	1.40	dadAX	26.00	envCD	73.80
argD	74.00	brnT	62.15	dadB	1.77	envM	28.90
argF	6.51	btuB	89.70	dadQ	98.65	envN	3.95
argG	68.98	btuCDE	37.45	dadR	26.05	envP	90.40
argI	96.62	btuR	28.20	dam	74.30	envQ	57.80
argM	88.70	bymA	92.90	dapAE	53.01	envT	14.10
argP	63.30	cadABC	94.00	dapB	0.62	envY	12.90
argR	70.70	cadR	46.55	dapCD	4.25	envZ	74.83
argS	41.30	caiABCDET	0.78	dapF	85.85	era	55.52
argT	49.90	calA	95.20	dapX	53.20	esp	17.40
argU	12.34	calC	15.50	dbpA	29.90	ethidium	105.00
argV	57.90	calD	9.35	dcd	45.60	evgAS	105.00
argX	85.70	can	63.35	dcm	42.90	exbBD	65.00
aroA	20.24	capR	9.96	dcp	30.95	exbC	58.95
aroB	74.37	carAB	0.64	dctA	79.40	excC	16.73

Listing 2: (continued)

expA	22.20	gada	77.60	H-NS	27.32	katG	89.07
exuTR	68.00	gadB	33.70	hag(48)	42.60	kba	69.80
fabA	21.67	gadSR	81.60	hap2 ??	108.00	kbl	81.11
fabB	50.20	galETK	17.01	hdhA	35.80	kch	27.55
fabDG*	24.40	galP	63.85	hel	85.10	kdgK	78.00
fabEG	71.14	galR	61.35	held	22.00	kdgR	40.20
fabH	24.17	galS	46.33	hemAM	26.65	kdGT	87.96
fadAB	87.20	galU	27.30	hemB	8.21	kdpABCDE	15.61
fadD	39.90	gapB	63.44	hemCDXY	85.75	kdsA	26.70
fadE	4.95	gapDH	39.35	hemE	90.30	kdsB	84.66
fadI	106.00	garA	15.55	hemF	17.25	kdtA	81.27
fadL	50.60	garB	3.40	hemG	86.90	kefB	73.40
fadR	25.90	gatCAD	45.50	hemH	11.10	kefC	0.96
fam	75.96	gcd	3.10	herC	62.20	kgtP	56.20
fatA	69.15	gcl	11.60	het	84.44	kpsDMT	64.31
fabA	63.41	gcpE	54.12	hevABCDEFG	58.80	ksgA	1.12
fbp	95.95	gcvHT	62.60	hevOP	58.81	ksgB	36.75
fcsA	87.00	gdhA	38.44	hflB	69.20	ksgC	12.10
fdA	63.41	gef	0.31	hflCKX	94.93	ksgD	30.70
fdhDE	88.15	gen-165	42.00	hfq	94.88	kpsS	64.37
fdhF	92.60	geneX	2.33	hga	40.81	lacAIOPYZ	7.89
fdnGHI	33.40	genF	93.51	himAB	37.46	lamB	91.63
fdv	58.86	ggt	75.80	himD	20.43	lepA(B)	55.60
fdx	56.45	gidAB	84.30	hip	33.90	leuABCDOP	1.80
fecEDCBARI	97.20	glc*	52.25	hip (himD)	20.43	leuJ	13.70
feeB	15.14	glc	64.60	hisABCDEGHI	43.91	leuR	78.20
feo	38.70	glgABCPSXY	75.54	hisJMPT	49.75	leuS	14.63
fepABCDEG	13.43	glgS*	107.00	hisS	54.11	leuT	85.72
fes	13.45	glk	51.80	hisW	48.24	leuU	69.00
fexB	86.50	glmS	84.11	hlpA	4.40	leuVX	99.15
ffs	10.20	glnALG	87.70	hmp	54.90	leuW	15.11
fhlA	58.84	glnB (PII)	54.94	hnr	27.26	leuX*	15.14
fhuABCD	3.61	glnD	4.12	hns	27.33	leuY	9.70
fhuE	24.72	glnHPQ	18.01	hola	14.60	leuZ	42.30
fhuF	98.90	glnR	23.80	holBE	108.00	lev	8.95
flc	74.04	glnSTUV	15.21	holC	96.74	lexA	91.82
flmABCDEFGH	97.82	glpABCTQ	48.70	hold	99.11	lig	52.11
firA	4.42	glpKFX	88.40	hpt	3.25	linB	29.25
fis	71.60	glpRGED	75.50	hpdRMS	98.45	lipAB	14.40
fiu	17.90	glTA	16.30	htgA	0.22	lit	25.50
fixABCX	0.84	glTBDEF	70.01	htpG	10.88	livHJK	75.85
flaA (I,II)	42.74	glTE	80.75	htpR	75.93	livR	19.90
flaGHI	41.35	glTH	21.35	htpX	40.40	lon	9.97
flbB	41.57	glTM	42.45	htrA	3.83	lpcA	5.60
flbC	42.60	glTN	76.70	htrB	23.41	lpcB	65.50
fldA	15.41	glTP	107.00	htrC	90.12	lpd	27.55
flgABCDEFG	23.90	glTR	92.30	htrD	19.21	lpd*	2.97
flgHIJKL	23.91	glTSTU	84.71	htrM	81.22	lpp	36.80
flhABCD	41.40	glTV	90.58	htrP	66.65	lpxAB	4.45
fliADSTFEFGH	42.50	glTW	56.25	HU-1	10.01	lrp	19.40
fliIJKLM	42.72	glTX	52.04	HU-2	90.30	lrs	2.65
flinOPQR	42.80	glyAX	54.91	hupAB*	90.31	lsp(A)	0.57
flpB	85.95	glyB	79.51	hupB (lon)	9.99	luxH	66.64
flpC	72.30	glyT	89.94	hyaABCDEFG	22.10	lysAR	61.37
flrD	87.12	glyU	62.01	hyc	58.88	lysC	91.20
flu	43.50	glyV	94.75	hydCD	77.30	lysP	46.20
fms	72.10	glyW	42.30	hydGH	90.51	lysS	62.22
fnt	72.10	gnd	44.41	hydL	64.70	lytS	16.50
fnr	29.80	gntR	75.70	hyp	58.88	lysU	93.01
foIA	0.98	gntS	95.40	hypABCDEFN	58.61	lysV	52.02
foIC	49.97	gntT	75.10	iap	59.20	lysX	60.45
foID	11.90	gntV	96.90	ibpAB	83.25	lytA	57.85
foIE	45.00	gor	77.20	icd	25.41	M5 protein	12.80
foIK	3.50	gp24'	72.95	icIA	62.80	mac	10.10
foIP	69.01	gppA	85.12	icIR	90.73	mafB	1.90
fpg	81.29	gppB	85.92	ict	80.70	malA	0.93
fpp	79.00	gprAB	0.20	ihb	19.46	malBEFGKM	91.49
fpr	88.44	gpsA	80.95	ileR	99.90	malIXY	35.81
frdABCD	94.44	gpt	5.76	ileS	0.55	malPQT	75.21
frdR	26.50	greA	69.10	ileV	5.15	malS	80.30
fre	87.10	groELS	94.16	ilvACDEGMY	84.84	malZ	9.10
frr	4.21	gronB	10.41	ilvHI	1.87	manA	35.67
fruABFK	46.80	grpD	71.50	ilvBN	82.63	manC	87.90
fruR	1.97	grpE	57.00	ilvF	54.30	manYZ	40.12
fts36	2.00	grx	18.50	ilvJ	1.42	map	4.15
ftsAILMQWZ	2.02	GSA	3.65	ilvR	99.95	marAR	33.60
ftsESYX	75.97	gshA	57.75	ilvU	7.10	mazG	59.81
ftsJH	69.30	gshI	58.40	inaA	48.54	MBP16-1	113.00
ftsN	106.00	gshII	63.75	infA	19.12	mcrA	25.81
fucOAPIKR	60.30	gsk	13.10	infB	68.87	mcrBCD	98.30
fumB	93.50	guaAB	53.91	infC	37.50	mdh	70.71
fumCA	35.66	guac	2.70	inm	78.50	mdl	113.00
fur	15.40	gurb	73.70	intX	58.24	mdoA	23.05
fusa	73.07	gurC	17.85	ior	45.30	mdoB	99.00
fusb	14.90	gurD	68.05	ispA	9.50	mdrA	19.15
g20.3	23.60	gutABDQ	58.50	katC	6.70	melABR	93.41
g30k	24.15	gyrA	48.21	katE	37.90	menA	88.60

gabTPD	57.60	gyrB	83.43	katF	59.01	menBCDE	48.95
mepA	50.40	neuAC	114.00	pgi	91.22	psaF	8.82
met	84.82	neuES	64.37	pgk	63.40	psiH	23.72
meta	90.62	nfnA	80.20	pgl	17.35	psiJKR	116.00
metBFJL	89.00	nfnB	13.20	pgm	15.05	psiQ	70.02
metC	65.01	nfo	46.60	pgpA	9.55	pspABCDE	29.10
metD	4.70	nfsA	21.40	pgpB	28.50	psa	56.21
metEH*R	86.30	nfsB	11.40	pgsA	42.33	psrR	84.62
metG	45.92	nhaAR	0.47	pheA	56.61	pstBAC	84.07
metH	90.74	nhaB	25.91	pheP	13.00	psu	1.65
metK	63.62	nirBDEC	74.20	pheRU	93.86	pth	26.40
metT	15.10	nirR	29.80	pheST	37.48	ptr	60.65
metX	113.00	nlp	69.50	pheV	64.00	ptrII	116.00
metYZ	68.97	nlpA	82.50	pheW	316.00	ptsF	45.80
metZ*	60.20	nlpB	53.21	phnA-Q	93.31	ptsG	24.70
mfd	25.30	nmpC	12.61	phoA	8.70	ptsHI	52.24
mglABCD	46.31	non	44.60	phoBR	9.05	ptsMPL	40.10
mgt	92.50	npl	70.31	phoZ	5.82	pufXY	48.20
miaA	94.85	nrdAB	48.51	phoH	23.70	purA	95.00
micA	63.90	nrdB*	88.04	phoM	99.76	purB	25.62
micF	47.82	nrdD	96.20	phoPQ	25.60	purC	53.20
minBCDE	26.10	nth	36.40	phoSTU	84.04	purDH	90.54
mioc	84.39	ntr-like	37.95	phr	15.70	purEK	12.00
mlt	113.00	ntrA	69.60	phrA	17.20	purF	49.91
mnrA	85.14	ntrC	87.81	phxB	16.90	purL	55.20
mng	38.95	nuo	49.20	pilA	97.85	purMN	53.71
moaABCDE	17.70	nupC	51.60	pinI	25.70	purP	83.84
modABCD	17.32	nupG	64.11	pit	76.50	purR	36.61
mola	91.66	nur	59.08	pldAB	86.16	pus	19.80
molR	65.30	nusA	68.94	plsB	91.79	putACP	22.80
momR	89.63	nusB	10.40	plsC	66.40	pykA	40.85
mopA*	24.00	nusG	89.98	plsX	24.17	pykF	36.70
mopBA	94.15	nuvA	9.30	pmbA	96.10	pyrBI	96.50
mor	89.60	nuvC	43.05	pmi	15.05	pyrC	23.50
motAB	41.55	ogr	87.62	pncA	38.75	pyrD	21.20
motD	42.76	ogt	29.82	pncB	20.76	pyrE	81.92
mprA	57.40	ompA	21.75	pnp	68.83	pyrF	28.81
mraBRY	1.98	ompBCR	47.80	pntAB	35.41	pyrG	59.80
mrbaABC	90.22	ompF	20.65	poaR	63.10	pyrH	4.65
mrcA	74.60	ompH	4.40	pog	70.10	pyrS	80.90
mrcB	3.60	ompR*	74.82	polA	87.50	qmeA	28.95
mrdaB	14.47	ompT	12.83	polB	1.45	qmeC	74.10
mrreBCD	71.00	oppABCD	27.51	polC	4.48	qmeD	61.60
mrp	45.90	oppE	98.60	popC	3.65	qmeE	36.90
mrr	98.46	oppI	19.46	popD	0.15	qor	91.90
msbA	20.50	opr	18.70	potABCD	15.00	queA	9.12
msbB	40.96	ops	63.50	potE	15.60	racC	30.21
msgB	53.01	optA	3.85	potFHGI	19.00	radA	99.55
msd	113.00	oriC	84.38	poxA	94.60	radC	81.33
msr	113.00	oriJ	30.40	poxB	18.81	ranA	55.82
msyA	27.31	osmB	28.83	ppa	116.00	rap	26.40
msyB	23.10	osmC	32.40	ppc	89.22	rarB	118.00
mtIACD	80.62	osmY	99.25	ppfa	116.00	rarD	86.01
mtLOP	80.60	osmZ	27.34	ppiA	74.05	ras	9.75
mtr	68.80	otsBA	41.60	ppiB	12.20	rbaB	55.80
mukA	66.10	oxyR	89.61	ppk	53.73	rbsABCDKR	84.52
mukB	20.60	pabA	74.01	ppsA	37.11	rcaA	43.00
mul	82.80	pabB	39.80	ppx	116.00	rcaCB	48.10
mureine	12.65	pabC	25.00	prc	40.41	rcaF	4.90
murA	113.00	pac	90.13	prfa (RF1)	26.68	rdgA	16.15
murB	89.85	pal	16.72	prfb (RF2)	62.24	rdgB	64.20
murCDEFG	2.05	panBCD	3.30	priA	88.82	recAN	58.10
murH	99.05	panF	71.12	priB	95.51	recBD	60.63
murZ	69.45	papABDEHFG	84.16	pric	10.70	recC	60.66
mutD	5.30	parC	66.41	priA	72.49	recE	30.20
mutH	61.05	parE	66.50	priB	84.64	recF	83.45
mutL	94.86	pbpA	14.48	priC	70.80	recG	82.15
mutM	81.70	pbpB	2.04	priD	2.60	recJ	62.25
mutS	58.87	pckA	74.81	priF	68.41	recO	55.54
mutT	2.31	pcm	59.10	prmA	71.40	recQ	86.15
mutY	63.91	pcnB	3.51	prmb	50.50	recR	10.87
mvrA	88.43	pcsA	81.75	proAB	5.83	regX	118.00
mvrB	28.45	pdxA	1.13	proC	8.86	relA	59.82
mvrC	12.37	pdxB	50.01	proK	79.21	relBEF	34.70
NAD(P)H	0.95	pdxH	36.01	proL	46.00	relX	59.90
nadA	16.80	pdxJ	55.50	prom	85.73	rep	85.11
nadB	55.81	pel	40.14	prop	92.70	rer	89.55
nadC	2.80	pep2	63.00	pros	4.80	rfaBCDFGIJ	81.20
nagABCDE	15.18	pepD	5.73	proT	83.60	rfaH	86.70
nalB	57.70	pepN	20.77	protein E	21.66	rfaLKPOYZ	81.20
nalD	89.15	pepP	116.00	proU (VWX)	58.30	rfaBCKM	44.40
nanA	70.30	pepQ	87.23	prp	97.50	rfe	85.45
nargHJKLRX	27.02	pfa	49.65	prpBCD	29.30	rffDE	85.50
narQ	114.00	pfkA	88.26	prs	26.60	rfs	42.61
narZYWV	33.10	pfkB	37.71	psd	94.70	rglB	98.42
ndh	24.80	pfl	20.10	psi51	48.73	rhaABCDRST	88.00
ndk	54.20	pfra	26.64	psiC	75.84	rh1B	85.13
neab	73.90	pfs	3.80	psid	93.32	rh1E	118.00
nek	72.35	pga	90.16	psie	91.48	rho	85.19
rhaA	80.52	rpsI	70.50	srmb	119.00	trkG	30.50

Listing 2: (continued)

rhsB		77.41	rpsJ	S10	72.75	srnA		9.45	trmA		89.69
rhsC		15.67	rpsK	S11	72.45	ssaD		9.25	trmB		7.20
rhsD		11.51	rpsL	S12	73.12	ssaE		50.30	trmC		50.45
rheE		31.90	rpsM	S13	72.46	ssaG		41.20	trmD		56.81
ribA		28.34	rpsN	S14	72.61	ssaH		94.55	trmEF		83.80
ribB		66.00	rpsO	S15	68.85	ssb		92.15	trnA		59.50
ribC		40.00	rpsQ	S17	72.65	sseAB		119.00	trpABCDEG		27.72
ridA		71.30	rpsR	S18	95.50	sspAB		70.15	trpP		83.82
ridB		85.30	rpsS	S19	72.70	ssr		62.90	trpR		99.70
rimB		37.80	rpsT	S20	0.52	ssrA		58.25	trpS		74.31
rimC		26.75	rpsU	S21	66.93	ssyA		54.40	trpT		84.77
rimD		87.93	rpsV	S22	118.00	ssyB		9.40	trxA		85.16
rimE		72.25	RRF		4.21	ssyD		3.20	trxB		19.20
rimFG		0.70	rrnA		87.26	stpA		57.95	ts8		63.42
rimH		13.80	rrnB		89.73	strM		76.20	tsf		4.17
rimI		99.10	rrnC		84.69	stsA		83.88	tsp		40.42
rimJ		23.61	rrnD		71.92	sucABCD		16.39	tsr		98.95
rimK		19.05	rrnE		90.56	sufI		66.40	tsx		9.18
rimL		32.60	rrnG		56.36	sugE		94.20	tufa		73.06
rit		89.10	rrnH		5.11	suhA		76.90	tufB		89.96
rlpAB		14.45	rsl		56.34	suhB		54.60	tus		35.64
rmf		21.65	rts		89.88	sula		21.71	tyna		26.80
rna		14.30	ruvABC		41.10	sulB		2.28	tyrA		56.60
RNA 7 S		71.82	sad		34.30	supD		43.22	tyrB		91.95
RNAse 10Sb		68.23	sbaA		96.40	supQ		12.70	tyrP		42.21
rnb		28.75	sbcB		43.70	surA		1.14	tyrR		29.20
rnc		55.56	sbcC		9.03	tabC		86.05	tyrS		36.00
rnd		39.60	sbm		62.80	tag		79.31	tyrTV		27.15
rne		24.11	sbmA		8.50	tap		41.49	tyrU		89.93
rnhA		5.35	sbp		88.27	tar		41.50	ubiAC		91.76
rnhB		4.47	sdaAB		119.00	tau		35.61	ubiB		87.11
rnpA		83.55	sdhAB		16.36	tcp		23.35	ubiDE		86.60
rnpB		68.19	sec63		1.20	tdcABCR		68.12	ubiF		14.95
rnsA		14.30	secA		2.30	tdh		81.10	ubiG		48.25
rnt		36.11	secB		81.00	tdi		4.00	ubiH		63.01
rob		99.75	secC		68.50	tdk		27.38	ubiX		49.85
rod		44.20	secDF		9.15	terC1		28.82	udhA		89.68
roda		14.46	secE		89.98	terC2		35.60	udk		44.65
rph		81.96	secY		72.50	terC3		34.40	udp		86.40
rplA		63.25	sefA		4.30	terC4		27.06	ugpABCEQ		75.83
rplA L1		90.00	seg		0.29	terE		23.00	uhpABCT		82.61
rplB L2		72.71	selABC		80.40	terF		48.12	uidAR		35.70
rplC L3		72.74	seld		38.55	tesA		120.00	umuCD		25.93
rplD L4		72.73	semA		39.70	tesB		10.30	uncABDEFI		84.12
rplE L5		72.62	serA		62.82	tet1		0.12	ung (1)		55.83
rplF L6		72.59	serB		99.50	tet2		0.89	upp		53.70
rplI L9		95.50	serC		20.24	tgt		9.13	ups		25.45
rplJ L10		90.01	serR		1.94	thdA		10.55	urfA		37.20
rplK L11		89.99	serS		20.00	thdC		94.80	usg (1,2)		49.99
rplL L12		90.02	serT		22.30	thdD		99.65	ushA		11.30
rplM L13		70.50	serU		43.24	thdF		83.70	uspa		121.00
rplN L14		72.64	serV		57.90	thiABC		90.44	uup		21.45
rplO L15		72.51	serW		19.12	thiD		45.20	uvrA		92.10
rplP L16		72.67	serX		23.20	thiK		24.90	uvrB		17.51
rplQ L17		72.40	sfaA EC536		119.00	thiL		9.60	uvrC		42.37
rplR L18		72.58	sfcA		33.50	thrABC		0.03	uvrD		85.87
rplS L19		56.80	sfiB		2.28	thrS		37.57	uxaA		67.90
rplU L21		69.40	sfiC		26.35	thrTU		89.95	uxaB		34.50
rplV L22		72.69	sfrB		86.70	thrV		71.83	uxaC		67.91
rplW L23		72.72	sfrC		7.00	thrv		5.85	uxuABR		98.20
rplX L24		72.63	sfs1		3.55	thyA		60.67	vals		96.73
rplY L25		47.70	sfuABC		1.70	tig		9.92	valU		52.00
rpmA L27		69.41	shiA		43.35	tkt		63.56	valV		36.20
rpmB L28		81.31	shl		1.88	tknA		10.50	valW		36.20
rpmC L29		72.66	sipCD		82.45	tls		41.15	visA		10.90
rpmD L30		72.56	sKp		4.44	tmk		24.60	visBC		63.00
rpmE L31		89.08	sloB		73.60	tnaABC		83.74	vsr		42.91
rpmF L32		24.16	slt		99.71	tnm		92.00	wseA		66.75
rpmG L33		81.32	slyDX		119.00	toc		66.85	witA		56.22
rpmH L34		83.54	smbA		4.18	tolABQR		16.71	x96		96.00
rpmI A		37.52	smp		99.51	tolC		66.61	xapAR		52.40
rpmJ X		72.48	smpAB		58.22	tolDE		22.90	xerB		96.77
rpoA		72.41	sms		99.60	tolIJ		0.11	xerC		85.86
rpoBC		90.04	sodA		88.03	tolM		72.20	xseA		53.93
rpoD		66.96	sodB		36.50	tolZ		77.70	xseB		9.65
rpoH		75.98	sohA		68.40	tonA		27.59	xthA		38.31
rpoN		69.60	sohB		28.30	tonB		27.57	xylAB		79.70
rpoS		59.00	soxQ		33.80	topA		28.30	xyle		91.46
rpoZ		82.12	soxRS		92.23	topB		38.55	xylose		124.01
rpsA S1		20.40	speABC		63.61	torA		28.10	xylRF		79.75
rpsB S2		4.16	speDE		3.01	tpi		88.29	zhg		75.16
rpsC S3		72.68	speF		15.60	tpr		27.15	zwf		40.82
rpsD S4		72.44	spf		87.52	treA		26.30			
rpsE S5		72.57	sportU		82.10	trg		31.10			
rpsF S6		95.50	spov		14.46	trkA		72.15			
rpsG S7		73.08	sppA		38.59	trkD		84.46			
rpsH S8		72.60	srlDMRQ		58.53	trkE		29.00			