

Compilation of DNA sequences of *Escherichia coli* (update 1991)

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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 third listing replacing and increasing the former listing roughly by one fifth. However, in order to save space this printed version contains DNA sequence information only. The complete compilation is now available in machine readable form from the EMBL data library (ECD release 6). After deletion of all detected overlaps a total of 1 492 282 individual bp is found to be determined till the beginning of 1991. This corresponds to a total of 31.62% of the entire *E.coli* chromosome consisting of about 4,720 kbp. This number may actually be higher by some extra 2.5% derived from lysogenic bacteriophage lambda and various DNA sequences already received for statistical purposes only.

INTRODUCTION

Within this sequence supplement issue we were able to publish a compilation of DNA sequences of *Escherichia coli* both in 1989 and 1990 and asked our colleagues from all over the world for additions and corrections [1,2]. Ever since the number of newly published *E.coli* sequence data increased substantially (see Table 1). Thus we were able to add and correct a number of entries. According to our data a total of 1 492 282 bp is sequenced till January 1991. At least one third of the nucleotides is published twice. The data presented here may serve as a basis for encouragement to our colleagues to either send us their unpublished, mostly flanking material or to determine additionally the sometimes very small gaps towards known neighbouring sequences.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 complete form quarterly from EMBL data library together with their current release on tape (ECD). It may also be received 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 [3]. These data were recently updated and we tried to follow this update as much as possible. Three other groups [4–8] started a program to fit the DNA sequence data directly onto the physical map compiled by Y.Kohara et al. [9]. We preferred the genetic map positions rather than the physical map coordinates, since we try to include genetic data as well. 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 [10,11]. In order to be prepared for merging our data with those regarding the Kohara map data directly [4–8] we have compared our data and paid attention to all of these collection as far as possible. Only the unpublished material (about 68 000 bp) available exclusively to us, to K.Rudd or to B.Baum (both Bethesda, MD) is not included into the collection presented here, but may be available on personal request. Additions and corrections of several colleagues are indicated in the main list within the comment column (see Table 1 for abbreviations).

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 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 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 used B.Bachmann’s genetic map data 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

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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 [4–8], we preferred to use their assignment including the respective orientation.

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
>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. 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 third edition of ECD contains a major increase of information by adding the exact coordinates for the performed overlaps. In order to make the calculations transparent, we preferred to keep all references with contributions to the respective area. In future issues we may only be able to quote one reference per data bank entry. However, the full set of information will always be provided on the electronic ECD version. Structural information besides the DNA sequence data and some other functional data, e.g. restriction map data, functional analysis data, sequence corrections or sequenced mutations are now also only in the electronic ECD version. Most tRNA sequences are compiled together with their respective anticodon sequence. For crossreferences to the tRNA collection [12] 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 [13,14]. A future issue of this collection may contain this information 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 (orf 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 here.

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.

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 the 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 now 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.

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 January 1991 is 1 492 282 bp = 31.6%

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.

DATA DISTRIBUTION IN MACHINE READABLE FORM

This compilation is available as a flat file (ECD) from the EMBL data library 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, but this version is also available on disk on request from Gießen. Both versions including the service program are available from the EMBL file server [15]. Using this 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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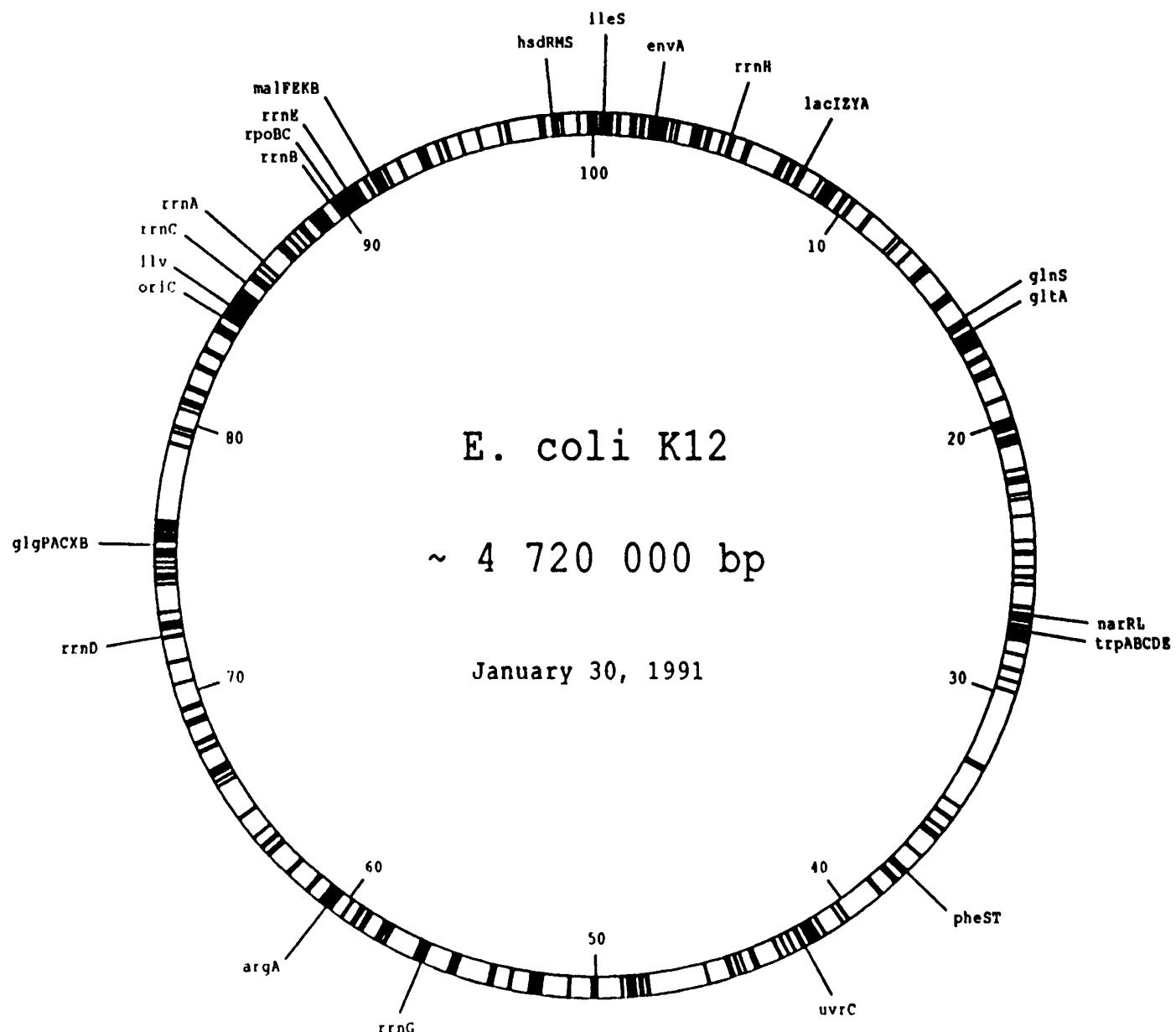


Fig.1 The sequenced areas within the circular chromosome of *Escherichia coli* K12. The sequenced areas are calculated in percent of the total chromosome according to the main list. All sequences exceeding 2000 bp are shown as in scale black bars at the respective genetic map position. Some prominent markers are included as well.

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).
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
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 the database

Table 2. Annual growing of the *E.coli* DNA-sequence information. This table represents all included sequence information. The final number for total information exceeds the actual number of sequenced nucleotides (1 492 282 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	21	81	6670	12445
1979	41	122	20077	32522
1980	55	177	36222	68744
1981	75	252	115712	184456
1982	93	345	81382	265838
1983	125	470	131753	397591
1984	137	607	178844	576435
1985	155	762	159183	735618
1986	170	932	246432	982050
1987	148	1080	203457	1185507
1988	179	1259	248349	1433856
1989	194	1453	285993	1719849
1990	229	1682	326875	2046724
1991	11	1693	26507	2073231

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
AnMi	Annales of Microbiology
ANYA	Annales of New York Academy of Science
BBA	Biochemical Biophysica Acta
BBRC	Biochemical Biophysical Research Communications
BChF	Biochimie (France)
BiCh	Biochemistry (USA)
BInt	Biochemistry International
BiRp	Bioscience Report
BJ	Biochemical Journal (UK)
Bioo	Bioorganic Chemistry (UdSSR)
CJMi	Canadian Journal of Microbiology
CRC	Carlsberg Research Communication
CSHQ	Cold Spring Harbour Symposium of Quantitative Biology
Cell	Cell
DANs	Doklady Akademii Nauk (UdSSR)
DNA	DNA
EJB	European Journal of Biochemistry
EMBO	EMBO Journal
FEBS	FEBS Letters
FedP	Federation Proceedings
FEMS	FEMS Microbiological Letters
G	Genetics
GANt	Gene Analysis Techniques
Gene	Gene
JBCh	Journal of Biological Chemistry
JBac	Journal of Bacteriology
JBio	Journal of Biochemistry (Japan)
JCBc	Journal of Cellular Biochemistry
JGMi	Journal of General Microbiology
JMAG	Journal of Molecular and Applied Genetics
JMB	Journal of Molecular Biology
MBE	Molecular Biology and Evolution
MGG	Molecular General Genetics
MiRV	Microbiological Reviews
MoMB	Molecular Microbiology
N	Nature
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 Sequences and Data Analysis
Scie	Science
Unpub.	unpublished material quoted in the databanks
ZNfC	Zeitschrift für Naturforschung Part C (Biological Sciences)

map name	comment	bp *	offset	from	to	total	journal	vol	page	year	EMBL	AccNr	GenBank
0.01 thrA	operator	new	BB	349	P	1	1	123	6045	JBCh	257	3896	-
0.02 thrBC	-	208	C	124		1	1	5922	0	PNAS	76	1706	1979 ECTHR
0.25 dnaKJ	Promoter	corr	BB	182	T	1	1	179	3541	PNAS	82	2679	1985 ECODNAKA
0.26 dnaK	Corr	BB	1920	C	180	1	1	1917	0	PNAS	81	848	1984 ECODNAK
0.27 dnaKJ	mut	corr	BB	1623	C	2097	179	1623	0	JBCh	261	1778	1986 ECODNAJK
0.31 gef	cell killing	new	KR	780	P	1	1	780	780	MOMB	1463	1989 X17311	ECANTAP A
0.34 ant_rpsT & illeS	rpst & illeS, lspA,dapB,carAB	KR	1349	P	1	1	1349	17033	JBCh	263	10408	1988 ECANTAP A	
0.35 rpsT	-	2881	C	1350		2631	1	1349	0	NAR	114	6965	1986 ECORPSTB
0.37 illeS_rpsT	also ECORPSTB	part. aa-sequence only	1806	C	3424	1	1806	0	JBCh	260	5616	1985 ECORPSTA	
0.38 illeTs	part. aa-sequence only	2169	F	5230		2169	0	Scie	1315	1984	-		
0.41 lspA	Corr	BB	1138	C	7399	1	912	0	FEBS	173	264	1984 ECLIPEP	
0.46 lsp,orf	orf	149, 316, 304, dapB	2696	C	8311	1	2559	0	NAR	119	180	1991 ECLSPDAP	
0.47 dapB	-	1281	C	10870		10870	1	938	0	JBCh	259	14829	1984 ECDAFB
0.50 carA	carA	5227	C	11808	0	1	5227	0	PNAS	81	4139	1984 ECOCARAB	
0.90 colA,apagh & ksgA,pdxa,surA	J01609	1200	P	0	1	971	4465	NAR	8	2255	1980 ECFOFX		
0.93 apagh,ksgA	-	2396	C	972	2396	1	0	MGG	205	515	1986 ECOPAH		
0.95 pdxA,surA	-	1469	F	3369	1081	1	0	JBac	171	4767	1989 -		
1.40 aracBAD	Corr BB	1172	B	1172	1	1	9016	JMB	154	649	1982 ECARAK		
1.41 aracC	E.coli B	J01641 in Gb	1162	B	1173	105	1	0	NAR	8	5267	1980 ECARAK	
1.42 arAB	-	254	C	0	0	0	0	0	JBCh	253	6931	1978 ECARABOB	
1.44 araC	E.coli B	J01641 in Gb	180	C	0	0	0	0	PNAS	77	3346	1980 -	
1.45 aradAB	E.coli B	4478	B	1278	67	0	0	PNAS	78	752	1981 ECARACZ		
1.49 aradAB	= dina	4475	B	1345	118	3154	0	Gene	47	231	1986 ECARAABD		
1.53 polB	-	4666	C	4381	31	4666	0	NAR	18	7185	1990 ECOPOLBDA		
1.77 leuAP	overlap HD, BB	855	T	269	855	282	0	JBac	149	579	1981 ECLEUEA		
1.78 leuO	analog to lysR	960	C	842	842	956	0	PNAS	85	1113	1986 ECLEYSR		
1.79 leuO	-	389	C	1797	1	302	0	JBac	163	186	1985 ECILVIHP		
1.80 llyVHI	-	2323	C	2099	1	2323	0	NAR	11	5299	1983 ECILVIIH		
1.81 llyVH	next to orfB, Hind3 Id?	1820	C	4422	159	1228	0	JBac	172	4696	1990 ECISHL		
1.82 shl	& ppBP, mur, ftsA, ddl, envA	1500	P	1	1	22099	0	NAR	18	2813	1990 ECOPPBRR		
2.10 orfB	= ftsI	2759	C	1229	1	2759	0	MGG	191	1	202063 -		
2.11 ppBP	= murF	1656	F	3988	485	1551	0	CJMI	335	1051	1983 ECOPPB		
2.13 murE, ftsI	-	1491	C	5053	1	1242	0	NAR	17	5379	1989 ECISHL		
2.14 murF	-	2608	C	6295	1	968	0	NAR	18	1058	1990 ECIMURYO		
2.17 orfy, murD	-	1629	C	7263	1	1629	0	NAR	18	183	1990 ECIMURD		
2.18 murD, ftsBW	corr in ECIMURD	1497	C	8892	279	1351	0	JBac	171	6375	1989 ECFTSW		
2.19 ftsBW	-	2745	C	9964	1	2476	0	NAR	18	4014	1990 ECIMURGC		
2.21 murGC,ddl	ftsBW, murGC, ddl	2132	C	12440	1	844	0	JBac	167	809	1986 ECDDLFITS		
2.22 ftsQAZ	ftsQAZ,envA,secA,murT	1152	C	13284	1	2000	0	JBCh	184	399	1985 ECFTSOA		
2.24 ftsQAZ	-	1870	C	15284	1	1500	0	Gene	36	241	1985 ECFTSOAZ		
2.25 ftsQAZ	or sulB;	corr BB	2048	C	1984	1299	1	11343	MOMB	3	1091	1989 ECAMPDE	
2.30 envA,secA	-	3811	C	16784	3283	508	1	0	JBac	169	653	1990 ECAROPA	
2.31 secA	-	3811	C	17809	1	3423	0	EJB	133	3404	1987 ECSECA		
2.32 mutT, secA	wrong BB	867	C	2132	1	867	0	EJB	133	155	1983 ECACEX		
2.41 quac	new BB	1991	T	1	1	1991	1991	BJ	255	35	1988 EGUAC		
2.50 ampe, arop & aceEF, lpd	-	1983	T	1	1	1983	0	EJB	135	519	1983 ECACEX		
2.52 arop	-	1440	C	1984	1299	1	2792	JBac	171	4457	1989 ECACEX		
2.53 arop	corr BB	585	C	3283	508	1	0	JBCh	262	16037	1987 ECSPDPE		
2.54 aceE,orf	-	3780	C	3791	188	7740	0	EJB	133	1542	1982 ECOPCNB		
2.55 aceEF	-	2040	C	3791	0	0	0	EJB	133	2635	1989 ECGLDE		
2.56 lpd	from	corr BB	2100	C	0	0	0	EJB	135	1273	1990 ECDSKSA		
2.90 SPEED	bad ref Em	corr BB	1882	C	0	0	0	JBCh	262	16037	1987 ECSPDPE		
2.91 SPEED	bad ref Em	bad ref Gb	1542	T	1	1	1542	JBac	171	1254	1989 ECOPCNB		
3.00 pcnB	glucose dehydrogenase	-	2635	T	1	1	1	JBac	172	6308	1990 ECGLDE		
3.10 gcb	-	1273	C	1273	1	1	1	JBac	172	1273	1990 ECDSKSA		
3.60 mcrB	& ponB)	fhuADCB	1273	C	1273	1	1	1	JBac	172	9195	1985 ECPCNBS	
3.69 mcrB	& ponB)	fhuADCB	2758	T	1	1	1	JBac	172	437	1985 ECPCNBS		

9.60 pgpa	length BB	704	T	1	7	711	T	1	7	704	JBac	170	5110	1988	M23546	
9.72 boLA	morphogene	1597	P	1	1	899	3482	EMBAC	8	3923	1989	ECBOLA	X17642	X17642		
9.74 trigger	fa	1809	F	1	1	1346	0	JBAC	172	5555	1990	-	-	-		
9.75 clpP	ctor	1236	C	2246	1	1236	0	JBCh	265	12536	1990	ECCLPAA	M31045	ECCLPAA		
9.80 lon	conflict with 9.83	2812	T	1	1	6	3334	B100	14	408	1988	ECLONA	M38347	ECLONA		
9.82 lon	-	3002	C	7	1	3002	0	JBCh	263	11718	1988	ECLON	J03896	ECLO		
9.84 HU-1(hupB)	-	460	C	134	460	0	MGG	201	360	1985	ECHUPB	X16540	X16540			
10.10 cycABCDE	-	5813	T	1	1	5813	5813	JBCh	265	11185	1990	ECCYOA	J05492	ECCYOA		
10.20 ffs	= 4.5 S RNA	764	T	1	1	764	764	JMB	178	509	1984	ECRNA45	X01074	ECOSGK		
10.41 nusB	-	683	T	1	1	683	NAR	12	498	1984	ECNUSB	X00681	ECONUSB			
10.87 apt,dnaX & orf12,reCR,hptG,adk	-	6820	T	1	1	6820	6820	JBAC	172	6042	1990	ECAPPTADK	M38777	ECAPPTADK		
10.90 dnaZX	-	2218	C	0	0	0	0	NAR	14	6541	1986	ECAPTA	M38777	ECAPTA		
10.91 dnaZX	-	2775	C	0	0	0	0	NAR	14	8091	1986	ECAPTA	M38777	ECAPTA		
10.92 reCR,orf12	-	1329	C	0	0	0	0	NAR	17	6781	1989	ECAPTA	M38777	ECAPTA		
10.93 hptG	-	2235	C	0	0	0	0	PNAS	84	5177	1987	ECAPTA	M38777	ECAPTA		
10.94 adk	-	1055	C	0	0	0	0	NAR	13	7139	1985	ECAPTA	M38777	ECAPTA		
11.35 ushA	-	1819	T	1	1	1819	1819	NAR	14	4325	1986	ECUSHA	X03895	ECUSHA		
11.70 rhdB	start region	400	T	1	1	400	400	JBAC	171	636	1989	ECRHSD1	M21764	ECRHSD1		
11.71 rhdB	core region	140	T	1	1	140	140	JBAC	171	636	1989	ECRHSD2	M21768	ECRHSD2		
11.72 rhdB	-	589	T	1	1	589	589	JBAC	172	446	1990	ECRHSD	M29719	ECRHSD		
12.14 purK	-	2449	T	1	1	2449	2449	JBAC	171	198	1989	ECPURE01	M19657	ECPUREK		
12.34 dnaX orf	cryptic prophage qbr'	2520	T	0	1	1	968	3237	MGG	220	325	1990	K16622	-		
12.38 argU,IS3	cr.phage = M27155 in Gb	2269	C	0	1	1	2269	0	JBAC	171	6197	1989	ECINTDLP	M31074	ECINTDLP	
12.45 cyBS	-	2194	T	1	1	2194	2194	NAR	19	265	1991	ECYSSG	X56234	ECYSSG		
12.60 rmpC	-	1303	T	1	1	1611	1611	JBCh	261	12723	1986	ECEPNMPC	M13457	ECOEPNMPC		
12.61 rmpC	-	1608	C	0	0	0	0	Unpub.	1	3323	1987	ECOEPNC	M13457	ECOEPNC		
12.85 M5 protein	ompT;E.coli JM83	753	T	0	0	0	0	JBAC	171	3924	1987	ECOM5	Y00138	ECOM5		
12.86 apy = M5	-	1874	C	1	1	1291	1291	0	0	JBAC	171	1683	1989	ECAPPYAA	M24530	ECAPPYAA
12.87 ompT	poor overlay	2035	C	1292	2032	1	1	NAR	16	1209	1988	ECONOPT1	X06903	ECONOPT1		
12.98 envY	next to ompT	945	T	1	1	945	945	0	0	JBAC	171	800	1989	ECENVY	X13548	ECENVY
13.60 entD	& fepA,fes,entF	943	T	1	1	941	941	MoMB	3	757	1989	X17426	-	-		
13.62 fepA	-	2624	C	942	2470	271	0	JBCh	261	10797	1986	ECFEPAA	M13748	ECFEPAA		
13.63 fepA,fes & entF, prom	1997	3142	C	1997	3142	1997	0	JBCh	263	18857	1988	ECFEE6	J04216	ECFEE6		
13.69 orf,repB & entCBA,p15,orf	-	2177	T	1	1	2177	1	7743	1	7743	1989	ECFEPB	M29730	ECFEPB		
13.70 entC	-	1400	C	2178	419	1655	0	JBAC	171	775	1989	M24142	M24142	M24142		
13.72 entCE	-	1655	C	3415	1655	1655	0	FEMS	59	15	1989	M27490	M27490	M27490		
13.73 entEBA	& p15,orf5	3249	C	4952	458	3249	0	JBAC	171	791	1989	M24148	M24148	M24148		
14.01 rnsA	ribonuclease I	1206	T	1	1	1206	1206	Gene	95	1	1990	ECNAG134	M55687	-		
14.90 pbpa	=mrda	2936	T	1	1	2936	2936	EJB	160	231	1986	ECOPBPB	X04516	ECOPBPB		
14.91 roda	=mrdb	1260	C	2937	89	1260	0	JBAC	171	558	1989	ECRODA	M22857	ECRODA		
14.92 r1PA	-	1408	C	4109	111	1408	0	JBAC	169	5692	1987	ECRLPA	M18276	ECRLPA		
14.93 dacA	& r1PA,roda,pbpA;	5407	C	5407	362	1597	0	FEBS	165	165	1984	ECDACAG	M18277	ECODACA		
15.10 r1PA	-	938	T	1	1	285	285	3902	0	JBAC	169	5692	1987	ECRLPB	M18278	ECRLPB
15.11 leuS	-	3618	C	1	1	286	3618	NAR	15	10199	1987	ECLEUS	Y00869	ECLEUS		
15.50 tRNA met & leu	gln1 gln2	1100	T	1	1	1100	1100	Cell1	23	239	1981	ECTGTOP	J01713	ECTGTOP		
15.54 asnB	-	3080	C	1101	2861	1	0	JBCh	265	12895	1990	ECASNB	J05554	ECASNB		
15.58 nagDCAEB & glnS	new BB	3619	C	3962	2628	3391	1	MoMB	3	505	1989	ECNAGACD	X14135	X14135		
15.60 glnS	see 15.65	M10187	in Gb	3391	6590	226	1	Gene	62	197	1988	ECNAGBE	M19284	ECNAGBE		
15.64 glnS	filling the gap	BB	2306	9755	190	2306	0	JBCh	257	11639	1982	ECGLNS	V01575	ECGLNS		
15.65 glnS	see 15.60	M10187	in Gb	11871	1	1	688	MGG	200	110	1985	ECFUR	X02589	ECFUR		
15.80 fur (iron)	loc BB	868	T	1	1	280	0	JBCh	257	11639	1982	-	-	-		
16.00 kdPDE	-	3600	T	1	1	65	65	Unpub.	1	4933	1984	-	-	-		
16.01 kdPABC	-	4933	C	2978	1	1	868	MGG	200	0	PNAS	81	4746	1984		
16.10 rhSC	start region	400	T	1	1	400	400	JBAC	171	636	1989	ECRHPABC	K02670	ECRHPABC		
16.11 rhSC	3'-end	535	T	1	1	535	535	JBAC	172	446	1990	ECRHSC	M21763	ECRHSC		
16.21 phr	-	2039	T	1	1	2039	2039	JBCh	259	6033	1984	ECPHRORF	K01299	ECPHRORF		
16.47 gltA,cyba,	-	3264	T	1	1	13063	13063	B1ch	22	5243	1983	ECGLTA	J01619	ECGLTA		
16.53 gltA,cyba, & sdhDAB	corr	3614	C	0	0	0	0	BJ	222	519	1984	ECSDHACD	X00980	ECOSDHACD		

16.55	sdhB	iron binding	J01619	in Gb	961	0	0	X01070	ECOSDHB
16.56	sucAB, sdhB		J01619	in Gb	3180	0	0	X00661	ECOGLTAA
16.57	sucAB		J01619	in Gb	1500	0	0	X00664	ECOGLTAA
16.61	succD	-			2451	0	0	6245	1985 -
16.62	succD	-	new BB		13064	818	1	730	JMB 177
16.63	tRNA	lyst & valT	mut	corr BB	2901	1	1	3845	3845 JBC 263
16.70	cys	map unclear			1855	1	1	1885	5037 JBac 169
16.80	tolQRA	& tolAB			2900	1856	200	2668	0 JBac 171
16.81	tolAB	-	lipoprotein	map acc KR	713	4325	201	713	0 EJP 163
16.82	pal	-	new BB		1470	1	1	1470	EJB 175
16.90	nada	-	summ HD, BB		2107	1	1	2107	NAR 10
16.95	argC	-	J01612	in Gb	139	0	0	3646	Cell 12
17.01	galletK	mut			148	0	1	122	0 Gene 21
17.05	galletK	-	length BB		2070	123	1	2070	0 NAR 14
17.08	galte	-	new BB		1634	2193	169	1622	0 NAR 13
17.10	galk	-	new BB		1609	1	1	1609	JBac 169
17.23	child	bloABFCd, uvrB	summ BB		260	1	1	8633	Scie 197
17.44	atbb	lam & bloABFCd	summ BB		5793	261	1	5793	0 JBch 263
17.45	bloABFCd	-	J01722	in Gb	2605	5966	48	2605	0 NAR 14
17.48	uvrb	-			2400	8524	2291	2400	0 NAR 14
17.49	uvrb	-	(mut?)	x01583 in Gb ?	3120	0	1	3436	MGG 205
18.00	qinNHPQ	-	From		268	0	0	0	NAR 15
18.01	qinNHPQ	-			2492	0	1	2492	JBac 170
18.20	chlen	-			1147	0	1	1147	Gene 43
18.50	grx	-			986	0	1	986	NAR 13
18.71	deor	-			1974	1	1	1974	NAR 14
18.94	doxB	-			729	1	1	501	Prot 1
19.00	livR	-			1559	1	1	1559	MGG 217
19.05	rimK	-			3380	1	1	3380	JBch 265
19.10	c1PA	-			1392	1	1	1431	JBac 171
19.90	orf, pf1	-			3592	1432	140	3592	0 EJP 177
19.91	pf1	-			1854	1	1	1854	7578 NAR 15
20.00	serS	-	map approx.	20 HD, Gb	6492	1855	679	679	0 MOMB 2
20.01	dmsABC	-			328	1	1	328	328 NAR 15
20.10	infA	-			300	1	1	300	JMB 212
20.15	tRNA Ser5	new tRNA Ser5	locus		1517	0	1	1490	2983 BJ 234
20.24	serC, aroA	-	new BB		1284	1491	1	1284	0 FEBS 170
20.25	aroA	-			1760	2775	1552	1760	0 BJ 234
20.26	aroA	-			1202	0	1	1202	1202 JBch 263
20.40	trxB	-	28 bp difference	MK	977	1	1	977	3031 MGG 196
20.50	rpsA	-	J01682	in Gb	2412	978	708	2287	0 NAR 10
20.52	rpsA	-			597	2556	1	475	0 JMB 183
20.53	hip (himD)	-	asnS, pconB, pepB	BB	1415	1	1	9110	BJ 234
20.65	aspC, ompF	6	GbNew	BB	1807	1416	1531	1	1531 0 Gene 84
20.69	ompF	-	new Tp		2040	2947	1968	1205	1 JMB 265
20.73	asnS	-			1490	4915	1205	1	1205 0 Gene 84
20.74	pncB	-			870	6120	296	342	0 EJP 155
20.75	pepN	-			2945	6166	1	2945	0 Gene 48
20.76	pepN	-	corr		1357	1	1	1357	EJP 151
21.25	pyrd	-	only 726 bp	acc.BB	979	1	1	979	979 JBch 263
21.65	faba	-	mut	J01654 in Gb	2271	1	1	2271	NAR 8
21.71	ompA, sulA	helicase V	loc acc KR		2821	1	1	2821	JBch 264
22.00	hyABCDEF	= dive	ser tRNA		6023	1	1	6023	6023 JBac 172
22.10	serT	Glucose-1-phosphatase			1336	1	1	1336	1336 EMBO 3
22.20	agp	Glucose-1-phosphatase			1675	1	1	1674	1675 JBac 172
22.50	appA	Glucose-1-phosphatase			700	1	1	802	802 ECAGPA
22.61	appA	correction of 22.60			1881	1	1	696	2056 BChF 69
22.79	putACP	also ECPUTC M35174			730	1	1	515	515 1797 ECOPUTP
22.80	putACP				1	1	1	644	2212 0 MGG 210

1845	C	-	putP	22.80	new tRNA Ser5 locus	-	ECOPUTP	X05653	ECOPUTP			
123.00	tRNA	Ser5	2. new tRNA Ser5 locus	1000	T	1000	JMB	212	70 1987			
23.00	near pyrc	D00002	in Gb	22	F	22	JBac	173	579 1990 X52787			
23.40	pyrc	2046	T	1	1	2046	EJB	160	391 1991 -			
23.44	rpmf L32	1191	T	1	1	1191	JBac	171	77 1986 ECOPYRC			
23.50	rlnJ	1220	T	1	1	1220	MGG	209	5707 1989 ECORPMFA			
24.05	mopa	3178	T	1	1	595	JBac	161	M06118 ECORIMJ			
24.30	rne	1523	T	1	1	3178	NAR	19	M11294 ECAMS			
24.44	rpmf	1522	C	1	1	1523	4124	261	M54309 ECORNE			
24.50	ptSG	new BB	BB	1	1	1522	1	0	J02618 ECOPTSG			
24.72	fhue	re recep	M16186 Gb	KR	2057	T	2057	EJBJ	116	X04469 ECOPYRC		
24.80	ndc	J01653	In Gb; loc acc	KR	1248	T	1	1568	1568	M29698 ECORPMFA		
25.23	icd	-	att e14	K03521	in Gb	2614	T	2614	EMBO	4	481 1987 ECRIMJ	
25.27	pnl1	-	att e14	K03521	in Gb	1772	T	1772	JBac	170	446 1985 ECAMS	
25.35	lit	-	-	M19689	in Gb?	1439	T	1439	JBac	170	125 1991 ECORNE	
25.40	att e14R	(minCDE)	loc?	2400	T	1	2400	2400	Cell	56	16398 1986 ECPTSG	
25.60	minB	2454	T	1	1	2454	2454	PNAS	82	X17615 ECOPFHUE		
25.65	umucD	224 bp	lambda in Em	BB	1070	T	1	1070	NAR	16	V00306 ECONDB	
25.70	fadR	2538	T	1	1	2538	2538	MGG	217	J02799 ECOICD		
25.90	treA	* osmA	next to hema	acc KR	1785	T	1	1785	JBch	261	X01805 ECOPINP	
26.69	pro	-	-	2925	T	1	2271	3711	Gene	82	M19683 ECOTATE	
26.70	hema, pfra	1440	C	2272	T	1	1440	1504	PNAS	82	M19683 ECOTATE	
26.73	prfa (RF1)	1504	T	1	1	3211	0	13023	NAR	17	M03153 ECOMINB	
26.77	kdsA	-	-	945	T	0	0	0	NAR	17	M10107 ECOUNMUD	
26.98	narrL	new BB	BB	3211	C	1	3211	599	FEBS	177	X05552 ECOKDSA	
27.00	narrXL	-	-	2482	C	1	5096	5096	FEBS	177	-	
27.01	narr(X(R))KG	-	-	5400	C	1	5471	447	MGG	207	4336 1985 ECUMUCD	
27.02	narrG	-	-	1890	C	1	10425	595	1890	0	X058087 ECFAADR	
27.05	narrGHJ	-	-	1545	C	1	11721	1	10303	0	X15868 ECFTREA	
27.07	narrHJI	-	-	2759	T	1	1	2759	JMB	155	M13174 ECOPRS	
27.24	tyrTV, tpr	K01197	in Gb	GbNew	1380	T	1	1380	MGG	209	M30785 ECOHEMA	
27.40	alcohol DH	-	-	1920	T	1	1920	1920	JBch	265	X15159 ECORF1X	
27.46	osmE	drdx	oligopeptide binding	??	350	T	1	350	350	FEBS	177	X05552 ECOKDSA
27.50	oppa	overlap 27.58	overlap 27.55?	summ KR	1291	T	1	1697	13540	PNAS	80	-
27.55	att phi80	-	-	653	C	0	0	0	Cell	41	436 1985 ECNARG1	
27.57	tonB	overlap 27.55?	summ KR	3779	C	1	3641	1	0	120	X13360 ECNARXL	
27.59	tonA, P14	-	-	140	C	1	140	5339	7134	0	X15996 ECNARXL	
27.60	trpB - tonB	intergenic region	-	7017	C	1	7017	0	0	NAR	17	X15996 ECNARXL
27.61	trpe	-	-	1202	C	1	12473	1068	1	B100	10	X16181 ECNARGHJ
27.79	trpABCDE	-	-	4071	T	1	4071	4071	JMB	191	M20147 ECNARI	
27.87	trp 5' end	-	-	1840	C	1	4072	668	1840	577	X04168 ECOTRY1	
27.90	topA	-	-	1113	T	1	1113	1113	JBac	170	X33504 ECODADHEX	
27.91	cysB	-	-	652	T	1	1	652	JBac	170	X07688 ECOPNS	
28.10	pgPB	osmotic. ind.	lipoprot.	within pyrF	487	T	1	1	488	1549	X05433 ECOPPA	
28.30	terC1	-	-	1549	C	1	489	364	1549	M04475 ECOTRTPZ		
28.31	pyrF	-	-	1964	T	1	1	1964	JBch	262	X02768 ECOTOPA	
28.77	tyrR	-	-	3853	T	1	1	3853	EMBO	9	X13583 X13583	
29.00	prBCD	-	-	1641	T	1	1641	341	2019	X02784 ECOTRTOI		
29.43	fnr (nirR)	-	-	1301	T	1	1301	1	0	J01714 ECOTGP		
29.44	ogt, fnr	summ BB	-	1668	T	1	1668	1	0	X010431 ECOTONB		
29.60	dbpA	second nar operon	map acc.	KR	2475	T	1	2475	2475	X00431 ECOTONB		
29.80	racCC, recE	new KR	map operon	-	1439	T	1	1439	1439	X00431 ECOTONB		
31.08	cysB	-	-	1722	T	1	1722	1722	PNAS	81	X07569 ECOTYRR	
31.10	trgI	-	-	1248	T	1	1248	1248	MGG	217	X02073 ECOTRG	
32.60	rlnJ	-	-	7080	T	1	7080	7080	MGG	222	X15860 ECORELB	
32.70	narZYWW	-	-	1765	T	1	1765	1765	G	X17110 ECORELB		
33.30	bfcA	-	-	454	T	1	454	454	CeII	55	X02405 ECORELB	
33.90	terC3	-	-	2142	T	1	2142	2142	EMBO	4	X02405 ECORELB	

34.50 uxAB	& dicAC	new BB	286 T	1	1	1	286	JGMI	132	1986	ECUXAB	M15737	
34.90 dicB	-	-	4440 T	0	0	0	4440	NAR	14	6821	ECDICABC	X04395	
34.91 dicB	-	-	1720 C	0	0	0	0	NAR	16	6327	ECDICABC	X07465	
34.92 dic operon	iss2 insertion site corr	-	968 T	0	0	0	0	NAR	16	10388	1988	ECDICABC	X07465
35.40 pntAB	-	-	2129 C	0	0	0	3240	PNAS	158	647	ECPTNTAB	X04195	
35.69 tus	terC2 & fumCA, manA	-	3240 T	1	1	1	6179	PNAS	86	1593	ECTAU	D90037	
35.74 fumCA	-	-	2416 T	1	1	1	0	BJ	237	547	ECFTUMC	X04065	
35.75 fumA	-	-	2250 C	1	1	1	430	0	0	3631	1986	ECFTUMC	X05222
35.76 manA	-	-	2250 T	1	1	1	550	NAR	12	3631	1984	ECFTUMA	X05222
35.82 uidA	-	-	2408 C	1	1	1	0	Gene	32	41	1984	ECMANAA	M15380
35.83 uidA	-	-	1604 C	0	0	0	0	MGG	199	101	1985	ECUIDAAI	X02395
35.95 tyrs	-	-	460 T	0	0	0	2439	PNAS	83	8447	1986	ECUIDAA	M14641
36.00 mali	-	-	2439 C	1	1	1	970	PNAS	150	419	1982	ECTYRS	J01719
36.20 tRNA	Vall2	new tRNA Val2A,B locus map	1275 T	1	1	1	1275	FEBS	150	4888	1989	ECMLIXA	M28539
36.50 nth	-	-	1925 T	1	1	1	1925	JBac	171	579	1990	ECMLIXA	M28539
36.65 sodB	-	-	1604 T	1	1	1	300	PNAS	75	2190	1978	-	-
36.69 purR	correction for J04212	loc: 1555 kbp map	460 T	0	0	0	300	JMB	212	579	1988	ECMLIXA	X52788
36.70 purR	loc: 1555 kbp map	-	2439 C	1	1	1	780	BioCh	28	4444	1989	ECMLIXA	X02857
36.72 lpp	-	-	1604 T	0	0	0	970	JBCh	263	1555	1988	ECMLIXA	X03511
36.73 lpp	J01645 in Gb	-	1604 T	1	1	1	2041	EJB	187	373	1990	ECMLIXA	X51368
36.85 aroD	loc BB	-	1604 T	1	1	1	0	JBCh	263	19653	1988	ECMLIXA	X04212
36.95 aroH	J01592 in Gb	-	1604 T	1	1	1	0	PNAS	75	2190	1978	-	-
36.98 aroH	-	-	1604 T	1	1	1	814	Cell	18	1109	1979	ECLPPX	X03032
37.43 btuDE, himA & phoST, lnfC, thrs, rpmI	himA -	-	1604 T	1	1	1	1798	BJ	238	475	1986	ECAROD	X04306
37.47 himA	-	-	1604 T	1	1	1	1798	JBac	163	47	1981	ECAROH	V00261
37.48 phoST, himA also M10430	-	-	1604 T	1	1	1	1798	JMB	145	239	1989	ECAROH	J04221
37.50 lnfC, thrs	-	-	1604 T	1	1	1	1924	Unpub.	0	285	1983	ECAROH	K01128
37.51 lnfC, rpmI	-	-	1604 T	1	1	1	3169	JBac	167	928	1986	ECBTUCED	M14031
37.70 pfkB	-	-	1604 T	1	1	1	3169	PNAS	75	237	1984	ECBTUCED	K02500
37.71 pfkB	-	-	1604 T	1	1	1	3169	Unpub.	0	337	1984	ECBTUCED	K02844
37.90 katE	catalase HPII	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X03032
38.00 celABCD	cryptic cel operon	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.31 xthA	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.50 gdhA	map	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.65 topB, selD	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.66 selD	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.70 sppA	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.75 ansA	& orf1, 2	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.87 ntr-like	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
38.35 gapDH	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
39.60 rnd	E.coli D	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
39.80 pabB	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
40.20 ptsPPL	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
40.45 args	length BB	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.20 ruvBA	new BB	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.46 cheZYBZ	& tap, tar, cheWA, MotBA, fla	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.47 cheZYBZ	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.49 tap, tar & cheW	J01705 in Gb	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.50 cheWA	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.51 cheA, motB & cheW	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.52 motB	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.53 motA	2005 bp EMBL ?	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.54 fbbB, fbaI	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.80 arafGH	Corr	map BB	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
41.82 arafGH	promoter char.	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
42.00 tyRP	length BB	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
42.07 uvrC, orf & pagA	X03691 in Gb	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
42.08 uvrC	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306
42.09 uvrC	-	-	1604 T	1	1	1	3169	Unpub.	0	5784	1985	ECBTUCED	X04306

42.11	glyW, pgSA	-	insertion	M14391 in Gb	955	C	4550	157	955	0	JBCh	261	1329	1986	ECGLYWA	M12299	ECOGLYWA
42.12	glyW, is1	= flbC, fliCD			890	C	5349	285	890	0	BChF	67	1053	1985	ECGLYWG	X03239	ECOGLYGA
42.45	hag, rfs				351	T	0	0	0	0	2526	JBac	155	74	ECHAGFLG	J01607	ECOAGFLG
42.46	hag				1667	C	0	0	0	0	JBac	168	1479	1986	ECHAG	M14358	ECOAG
42.47	flbC, hag48	hag48 = wt			2526	F	1	1	2526	0	MGG	216	44	1989	-	-	-
42.73	flaA1 & flaAII, motD (fliM)				1763	T	1	1	1763	2213	JBac	166	1007	1986	ECFLA	M12784	ECOFLAA
42.74	motD	-			1764	C	499	52	499	0	JBac	171	2728	1989	M26294	M26294	M26294
43.00	dcm, orf				3655	T	1	1	3655	3655	NAR	17	5844	1989	ECDCM	X13330	ECDCM
43.09	asnT	trNA Asn near tRNA Ser2			200	T	1	1	200	200	JMB	212	579	1990	X52790	-	X52790
43.10	serU	mut tRNA ser2			150	T	0	0	287	287	JBac	161	207	1985	ECTGSSD	M10746	ECOTGSSD
43.11	supD	tRNA ser2			287	C	1	1	287	0	Unpub.		1985	ECTGSSD	M10746	ECOTGSSD	
43.20	aspV	tRNA Asp[1]			284	T	1	1	284	284	MGG	206	356	1987	ECASPV	X14007	ECASPV
43.26	alkA	loc 44.7 BB ?			1942	T	1	1	1942	1942	BCh	259	13730	1984	ECALKA	K02498	ECALKA
43.30	amn	AMP nucleosidase			1803	T	1	1	1803	1803	BCh	228	8726	1989	ECAMN	M30469	ECAMN
43.35	tRNA Asn	2. locus for tRNA Asn			200	T	1	1	200	200	JMB	212	579	1990	X52791	-	X52791
43.40	tRNA Asn	3. locus for tRNA Asn			200	T	1	1	200	200	JMB	212	579	1990	X52792	-	X52792
43.60	sbcB	-			1927	T	1	1	1927	1927	JBCB	262	455	1987	ECSCBC	J02641	ECOSBCB
43.90	hisG	corr J01627 in Gb			708	T	1	1	714	7779	NAR	9	2075	1981	ECHIS1	V00284	ECOHISOPA
43.91	hisGDC	& hisBBFIE corr BB			7390	C	715	316	7390	0	JMB	203	585	1988	ECHISOP	X13462	ECOHISOPA
44.41	gnd	-			1887	T	1	1	1887	1887	Gene	27	253	1984	ECGNND	K02072	ECGNND
44.43	gnd	iss5 insertion			1013	C	1	1	1013	1013	MGG	5	691	1988	ECGNND	M23181	ECGNND
44.60	mrp, metG	-			1506	T	1	1	1094	3712	MGG	223	121	1990	-	-	-
44.61	metG ST	45.6 Bachmann map			1986	C	1095	1	2346	0	EJB	127	449	1982	ECMETG	J01649	ECOMETG
44.63	metG	-			451	C	0	0	0	0	JBac	160	1115	1984	ECMETG	K02671	ECOMETG
44.63	5' end metG	-			347	C	3441	76	347	0	MGG	223	121	1990	-	-	-
44.85	cld	-			2340	T	1	1	2340	2340	EJB	144	367	1984	ECLD	X01067	ECOLLD
44.90	mrp, metG	-			1384	T	1	1	1384	1384	MGG	208	247	1987	ECMGLB1	X05646	ECOMGLB1
44.96	cld	-			641	T	1	1	641	2499	JBac	169	5343	1987	ECOCIRIR	M19295	ECOCIRIR
44.97	cld	-			2240	C	642	382	2239	0	JBac	171	1041	1989	ECCIR	J04229	ECOCIR
45.05	nfo	ptsF, orf3			1020	T	1	1	1020	1020	JBac	170	5141	1988	ECNFO	M22591	ECONFO
45.80	ptsF, orf3	ptsF = fruA new locus for tRNA Pro2			2600	T	1	1	2600	2600	JGMI	134	2757	1988	M23196	M23196	M23196
46.00	tRNA Pro2	cAMP regul. promoter			300	T	1	1	300	300	JMB	212	579	1990	X52793	-	X52793
46.40	cdd	-			485	T	1	1	485	485	MOMB	3	315	1989	ECCDDP	X16419	X16419
47.60	ada	-			267	T	1	1	267	1997	JBac	15	315	1986	ECADAPA	M13155	ECADADA
47.61	ada	-			1324	C	268	189	1324	0	JBCh	260	7281	1985	ECADADA	M10211	ECADADA
47.63	alkB	-			959	C	1404	366	959	0	JBCh	261	15772	1986	ECADAB	J02607	ECADAB
47.70	ompCR, mlcF	-			240	T	1	1	1713	1713	FEBS	151	159	1983	ECCOMP	K00541	ECOCMP
48.00	rcsBC	including unpubl. data			5246	T	1	1	5246	5246	JBac	172	659	1990	ECRCSCB	M28242	ECORCSBC
48.24	gyrA	= hisW			3327	T	1	1	3327	3327	JMB	197	729	1987	ECCYRAJ	X06373	ECGYRAJ
48.26	gyrA, orf	-			4729	T	1	1	4729	4729	MOMB	1	259	1987	ECCYRAAM	Y00544	ECGYRAAM
48.50	ndrAB	-			8554	T	1	1	8561	8561	PNAS	81	4294	1984	ECNRDA	K02672	ECNRDA
48.70	91PT	new HD			1560	T	0	1560	120	6180	MOMB	1	251	1987	ECCGLPT	M20938	ECOGLPT
48.71	91PABC	-			4739	C	1441	1	4739	0	JBac	170	2448	1988	ECCGLPT	M20938	ECOGLPT
49.00	menD	-			2345	T	1	1	2345	2345	JBac	171	4349	1989	ECMEND	M21787	ECOMEND
49.91	hisMP	-			1332	T	1	1	1332	1332	NAR	15	8568	1987	ECHISMP	Y00455	ECOHISMP
49.94	argT, dedF	& purF, dedEDCBa, hist			6172	T	1	1	6172	4728	10775	262	1209	1987	ECHISPUR	J02800	ECOHISPUR
49.95	purF	J01666 in Gb			2478	C	1445	2321	911	0	JBCh	257	3525	1982	ECPURF	V00322	ECOPURF
49.96	argT, dedF	2. Part of divided sequ			6172	C	2855	4729	161	0	JMB	148	107	1981	ECCRNBZ	J02800	ECOCCRNBZ
50.03	usg, hist	-			2323	C	7423	2323	470	0	NAR	13	5297	1985	ECHIST1	X02743	ECOHIST1
50.05	pdxB, usg1	div, pdxB = usg2			1500	C	9276	1500	1748	1748	CRC	53	6084	1989	ECFDXB	M29962	ECOFDXB
50.25	fadb	-			1748	T	1	1	1748	1758	JBac	171	357	1988	ECFABB	M24427	ECOFABB
50.37	ackA	loc 49.8 BB ?			1758	T	1	1	1758	1758	JBac	171	577	1989	ECACKA	M22956	ECOACKA
50.40	arcC	new BB			1690	T	1	1	1690	1690	BJ	251	313	1988	ECAROCX	M33021	ECOAROCX
50.45	medA	-			1765	T	1	1	1690	1765	MOMB	4	209	1990	ECREPMR	X16909	ECREPMR
50.61	fadL	-			1899	T	1	1	1899	1899	MOMB	2	363	1988	ECFADL	Y00552	ECOFADL
50.96	dsdC	contains M13 sequence			1633	T	1	1	1633	1342	JBac	170	330	1988	ECDSDA	M19035	ECODSDAA
50.97	dsdAC	-			1000	C	1634	281	1899	0	JBac	154	1508	1983	ECDSDA	J01603	ECODSDA
50.99	dsdA	corr			1445	C	0	0	0	0	JBCh	263	1692	1988	ECDSDA	J01603	ECODSDA
51.05	tRNA Arg5	new locus for tRNA Arg5			300	T	1	1	300	300	JMB	212	579	1990	X52794	-	X52794

51.95	tRNA Lys & tRNA Val	17 bp differ.	X52796
52.00	lysV, valU	& gltX, orf294, 62,105,16	X55757
52.04	gltX	reading frame only	X55757
52.05	orf62,105	& alaW, orf167	M13687 ECOGLTX
52.10	l19	-	V00348 -
52.15	cysK	& ptsHI, crr	542 JMB 212 579
52.16	orf cysK	& ptsHI, crr	542 JMB 214 825
52.35	cystWAM	& cystWAM	542 JMB 261 10610
52.36	cystWAM	last 18 bp Mu	542 JMB 148 107
53.15	dapa	-	3291 1 3195 Unpub.
53.16	purC	-	3291 1 2597 4861
53.80	purN	-	2598 881 3144 0
53.81	guarAB	-	1291 1 5736 0
53.90	xsea	-	4446 0 0 0
53.93	xsea	-	1171 0 0 0
54.10	hisS	-	2060 C 1132 1 2060 1
54.60	suhB	-	2043 T 1 2899 1
54.77	ginB (PII)	map	2043 T 0 0 0
54.90	glyBX	-	1149 C 3531 1 323 0
54.91	glyA	-	1847 T 3209 1 1616 0
55.20	purl	& rnc, era	1616 C 1673 T 1 1673 1
55.40	lePA	-	2089 T 1017 1 1017 1
55.43	rnc	-	3132 1 474 1
55.46	era	-	1076 C 378 T 1 1 1
55.48	reco, era	-	1725 C 379 202 1 1 1
56.00	ung	-	1588 C 4176 185 0 1 1
56.30	nadB	-	1588 C 5012 844 0 1 1
56.44	wta	new BB	1532 T 1532 1 1 1
56.45	rrfG	length BB	1724 T 1 1 1 1
56.53	spacer	distal end of rrfG	1560 C 1560 1 1 1
56.54	rrfG	analog rrnF	1480 C 1561 1 1 1
56.55	rrfG	23S RNA analog	1848 128 33 0 0
56.56	rrfG	J01695 in Gb	2904 C 1941 6403 3500 0 0
56.57	rrnG	space rsl, tRNA Glu2	440 F 4844 440 1 0 0
56.58	rrfG	16S RNA analog	1541 C 5324 2959 2194 0 0
56.62	c1PB, rrnG	last 1438 bp?	6089 4248 1 0 0
56.63	pheA	& tyra, aroF	M10431 in Gb 4509 T 1 1 1
56.76	trmD	& rplS, rpSP	4586 T 1 1 1
57.60	trmD	-	1612 P 1 1 1
57.79	gshI	E.coli B	mut 2098 B 0 0 0
57.90	hydHG	-	1744 T 1 1 1
57.95	mpRA	-	742 T 1 1 1
58.00	proU (VWX)	-	4362 T 1 1 1
58.01	proU	corr delete G39	1 C 0 0 0 0 0
58.10	tRNA Arg2	& tRNA Ser3	1200 T 1 1 1 1 1
58.15	orf	61 aa small protein	611 T 1 1 1 1 1
58.20	mRNA	new BB	280 P 1 1 1 1 1
58.21	alas	-	500 C 244 1 1 1 1
58.22	alas	-	2767 C 744 498 1 1 1
58.25	recA	J01581 in Gb	1320 T 1 1 1 1 1
58.26	recA	J01672 in Gb	1374 C 0 1 1 1 1
58.28	recN	J01672 in Gb	2224 T 1 1 1 1 1
58.30	gutABD	= srlABD	3523 T 1 1 1 1 1
58.32	srlDMRQ	-	1800 C 3524 554 4771 252 935 0 0 0 0 0
58.33	gutQ	-	935 C 4771 252 935 0 0 0 0 0
58.46	ssrA	-	648 T 1 1 1 1 1
58.90	katF	-	1483 T 1 1 1 1 1
58.95	hevABCDFG	& hevH	7650 T 1 1 1 1 1
58.96	hevOP	fhlB at 95.4 + 60bp 3'	59.03 fhlA = orfe
59.03	fhlA	-	2443 P 2193 C 2193 0 0 0 0 0
59.04	orfe	-	211 C 0 0 0 0 0
59.05	orfe	-	1319 1990 X52227 210 0 0 0 0 0

59.25	cysD	cysD promoter	492	T	1	1	492	Gene	87	127	1990	ECCYSD	M35098		
59.30	cysUJ	E.coli B prom	324	B	1	1	2089	PNAS	80	130	1989	ECCYSJ01	M23008		
59.31	cysUJ	E.coli B	1825	B	0	0	5939	JBac	171	15796	1989	ECCYSJ01	M23008		
59.32	cysUJH	E.coli B	3876	B	2090	27	3876	0	JBac	264	15726	1989	ECCYSJ01	J05009	
59.40	lap	conflict last bp = C	1664	T	1664	21	1664	2832	JBac	169	5429	1987	ECAIP	M18270	
59.41	lap	14 times 29 bp repeat	1465	C	1665	1	1168	0	JBac	171	3553	1989	M27059	M27059	
59.75	pyrg	next to 6 times 29 bp repeat	1531	T	1	1	1531	1531	JBac	171	3553	1989	M27060	M27060	
59.80	pyrg	-	2442	T	1	1	2442	2442	JBCH	261	5568	1986	ECPYRG	M12843	
59.82	relA	map	2858	T	1	1	2858	2858	JBCH	263	15699	1988	ECRELA	J04039	
60.30	fucO	-	1690	T	0	0	8901	JBac	171	3754	1989	M27177	M27177		
60.32	fucAPIKR	-	6901	C	1	1	8901	0	NAR	17	4883	1989	ECPUCOSE	X15025	
60.51	thyA	ptr,recDC,argA	1147	T	1	1	1163	16371	PNAS	80	4914	1983	ECTHYA	J01710	
60.52	thyA	recc	6000	C	1164	766	5992	0	NAR	14	4437	1986	ECRECC	X03966	
60.53	ptr	-	1171	C	6391	189	1171	0	Gene	54	185	1987	ECPTR31	M17095	
60.54	ptr	-	3120	C	7374	1094	3120	0	NAR	14	7695	1986	ECPTR	X06227	
60.55	rscB	-	3960	C	9401	361	3960	0	NAR	14	8573	1986	ECRECB	X04581	
60.56	recD	-	2160	C	13001	361	2160	0	NAR	14	8583	1986	ECRECD	X04582	
60.58	argA	&	1575	C	14801	1571	1	790	NAR	15	10586	1987	ECARGA	Y00492	
61.11	mutH	-	790	T	1	1	1832	1	344	Gene	67	49	1988	ECTGM12	M21680
61.25	metZ	tRNA met	344	T	1	1	1832	1	344	Gene	67	49	1988	ECGALR	V00280
61.35	galR	-	1150	T	1151	1	1150	6097	PNAS	79	2427	1982	ECGALLYS	-	
61.36	lysR,orfX	-	1854	F	1151	1	1151	3231	0	JMB	168	333	1983	ECGALLYS	J01614
61.37	galR,lysR	-	2346	C	3232	0	0	0	JMB	168	321	1983	ECGALLYS	J01614	
61.38	araE	& galR,lysRAS	2866	C	3232	2866	1	0	JBCH	263	8003	1988	ECARAEEA	J03732	
62.00	glyU	tRNA Gly1	300	T	300	1	300	300	JMB	212	579	1990	X52798	-	
62.29	herC,prfB	& recF	1832	P	1832	1	1832	1	6279	PNAS	85	5620	1988	ECHERC	J03795
62.32	prfB (RF2)	partial map	1440	C	1833	1	1833	1	0	PNAS	82	3616	1985	ECRF2X	M11520
62.34	recJ	-	3772	F	3014	3266	1	1233	1233	JBCH	261	353	1991	-	-
62.80	serA	-	1233	T	3011	1	1	954	954	JBac	161	1162	1985	ECSSR	N00029
62.84	ssr	-	954	T	8029	1	8029	8029	MonB	3	723	1989	ECFDAPGK	X14436	
63.28	fda,	pgk & gapB	8029	T	1090	1	2458	1	6529	Unpub	1990	ECSPPEAA	M32363		
63.65	speB	additional sequences near speA,metK	1090	T	1090	1	1090	0	JBac	173	12179	1986	ECSSERA	M32363	
63.66	speB	-	1371	C	0	0	0	0	JBac	172	538	1990	ECSPPEAA	-	
63.67	speBA,metK	-	3236	C	2459	2887	0	0	JBac	172	4631	1985	ECSPPEAA	M32363	
63.68	metK	-	1462	C	5346	278	1462	1	0	JBac	259	14505	1984	ECMETS	K02129
63.71	gshII	E.coli B	1474	B	1	1	1474	0	NAR	12	9299	1984	ECGSIII	X01666	
63.80	ansB	-	1643	T	1	1	1643	1643	Gene	91	101	1990	ECANSBA	M34234	
63.81	ansB	ansA maps at 39.10 adenine glycosylase	1522	T	1	1	1522	1522	JBac	172	1491	1990	ECALSNII	M12277	
63.90	mutY	-	1231	T	1	1	1231	1231	NAR	18	3841	1990	ECMUTY	X52391	
64.00	pheV	-	487	T	1	1	487	487	NAR	13	3699	1985	ECPHEV	X02480	
64.11	nupG	regulatory region	111	T	111	1	111	23	1509	EJB	190	547	1990	X55813	-
64.12	nupG	-	1486	C	24	1	1486	1486	EJB	168	385	1987	ECNUPG	X06174	
64.15	spec,crp	crp on 2.strand ?	2330	T	2330	1	2330	2330	Unpub.	0	1990	ECSPPEC	M33766		
65.00	metC	-	1880	T	1880	1	1880	1	3246	PNAS	83	867	1986	ECMETC	M12858
65.01	exBD	overlay met-exb HD X00016 in Gb	2195	C	1881	830	2195	0	JBac	171	5117	1989	ECEXBB	M28819	
66.40	toIC	-	173	T	0	0	0	0	FEBS	156	307	1983	ECTOL	V01505	
66.43	toIC	corr M37832	2096	C	1	1	2096	0	NAR	18	5547	1990	ECTOLCMP	V54049	
66.55	pare	-	1869	T	1	1	1869	1869	Cell	63	393	1990	ECPARC	M58408	
66.60	parC	-	2284	T	1	1	2284	2284	Cell	63	393	1990	ECPARC	M58409	
66.80	cca	-	2257	T	1	1	2257	2257	JBCH	261	6444	1986	ECCCA	M12788	
66.91	rpsU	-	255	T	1	1	3930	8989	MCG	195	391	1984	ECRPSU01	M16194	
66.92	rpsU	& orfXYZ	4644	C	0	0	0	0	Gene	51	149	1987	ECRPSU01	M16194	
66.93	rpsU	& dnaG, rpoD	2600	C	3931	1	5059	0	NAR	9	2889	1981	-	J01687	
66.94	rpsU	J01687 in Gb	1283	C	0	0	0	0	MGG	189	48	1983	ECRPSU	V00346	
66.95	dnaG	J01687 in Gb	2000	C	0	0	0	0	PNAS	79	4550	1982	ECRPSRPO	V00274	
67.05	tRNA Ile2	new locus for tRNA Ile2	200	T	1	1	200	200	JMB	212	579	1990	X52B00	-	
67.79	egrABC	flanking seq	4983	T	1	1	4983	4983	G	123	635	1989	ECEBG	X52031	
67.92	uxaC	exut	318	T	1	1	318	318	FEMS	33	205	1986	ECUXEX	M35280	
68.10	tdCRABC	& orfX	3294	T	0	0	6294	6294	MGG	201	308	1985	ECIDC	M21312	

68.11	tdcB	-	990	C	PNAS	84
68.12	tdcC, orfx	-	2122	C	0	0
68.14	tdc	flanking sequences	2044	C	0	0
68.41	prfF	-	927	T	0	0
68.80	mtr	near rnp, rps	1868	F	1	1
68.84	pnp, rpso & infB, nusA, metY	corr BB	3030	T	1	1
68.89	p15B, p35	-	2753	T	1	1
68.90	nusA, infB	Gene and mRNA	1861	C	0	0
68.91	nusA	corr BB	903	C	0	0
68.92	nusA, infB	trnA:X250	4140	C	0	0
68.98	nusY	flank 3' flanking sequence	2427	C	0	0
69.03	argG	-	3203	C	0	0
69.08	leuU	trnA Leu2	800	C	9352	0
69.11	gltB-	psiQ-	48	T	1	1
69.12	gltB-	psiQ -	39	T	1	1
69.13	gltB-	psiQ -	52	T	1	1
69.35	nana	= npl new BB D00067 in Gb	1243	T	1	1
69.40	gltB	= aspB; gltB ?	6292	T	1	1
69.44	asp	-	1616	T	1	1
69.51	arcB	-	2390	T	1	1
69.94	rnpB	-	799	P	1	1
69.96	rnpB	preM1 RNA	600	C	800	0
70.24	rpsL, rplM	new BB	773	F	805	1
70.40	mdh	length BB	1159	T	1	1
70.42	argR	-	1046	T	0	0
70.42	mdh	argR	2470	C	2102	1
70.43	argR	= xerA	2470	C	2102	1
70.76	sohA	supp. htrA	928	F	1	1
71.10	panP	-	1904	T	1	1
71.18	mreB	& mreCD; mreB = envB	2101	T	1	1
71.20	mreCD	bad name in Em, Gb	1966	C	1622	1
71.40	fabE	-	1229	T	1	1
71.50	fas	-	536	T	1	1
71.51	fas	new BB	473	C	537	427
72.07	rrnD	operon J01692 in Gb	472	T	0	0
72.11	rrnD	16S RNA analog J01695 in Gb	1541	C	426	1519
72.12	rrnD	tRNA 16S ala tRNA: A250	1545	C	1866	2959
72.14	rrnD	23S RNA analog J01695 in Gb	2903	C	2303	3501
72.15	rrnD, rrfd	thrV, rrFD J01693 in Gb	667	C	5205	134
72.26	aroE	new BB	819	T	1	1
72.29	aroE, rplQ	intergenic M11148 in Gb	242	T	1	1
72.40	alpha, spc	spc & S10 operons	3154	T	1	1
72.43	rplII	(secY, rpmJ, rpsM)	759	C	2826	0
72.44	rplN L14 & rpsQ S17, spc	5922	C	2932	5922	
72.46	rpsJ S10	901 bp not det. here	4520	C	8631	5421
72.48	rplC L3	BB	1241	C	1315	1241
72.95	bif,	J01680 in Gb	1350	T	1	1
73.00	strA	map	365	T	0	0
73.02	rpSL S12	J01688 in Gb	405	C	1	1
73.05	strA, rpsL	fusa, tufA	73	T	0	0
73.06	fusa	length BB	2076	C	406	310
73.07	strA, rpsL	= S12 (fusa, tufA)	1374	C	2242	70
73.20	strA, rpsL	= S12 (tufA)	200	T	1	1
73.53	crr	-	1127	T	1	1
74.00	argD	-	269	C	1128	99
74.01	pabA, fic	orf, utu, dtu	1224	C	1221	3923
74.03	pabA, fic	orf190, orf77	2059	C	1225	2008
74.20	nirDEC	cysG, last 18 bp artf MK	2496	C	3233	694
74.23	cysG, orf	-	5618	F	5281	1
74.40	ecnrBC	-	5799	F	5281	1
74.42	ecnrBC	-	325	F	325	1

74.28 trps	figure 5	J01716 in Gb	length BB	160 T	BB	1005 C	127	1	1	1132 JBac	148	941 1981 ECTRPS
74.29 trps		76 bp artificial subtr.		1058 T		1134 77	1005 0	JBac	257	6132 1982 ECTRPSZ	V00370	-
74.35 dam,orf				1058 T		3852 NAR	11			837 1983 ECDAM	V00371	ECOTRPS
74.36 dam,orf	&			1560 C		1059 1	1265 1	MGG	217	85 1989 ECURF743	X01600	ECODAM
74.37 aroB				1636 C		2324 1	1528 1			85 1989 ECURF743	X15162	ECOTRPS
74.37 aroB	last 7 bp	artificial ?		2764 T		2764 1	2764 1	FEBS	200	11 1986 ECAROB	X03867	ECOTRPS
74.60 mrlA	-			1861 P		1861 1	1861 1	EJB	147	437 1985 ECOPNA	X02164	ECOPNA
74.76 pckA	-	corr BB		1288 T		1286 1	1286 1	JBac	172	7151 1990 -	-	-
74.80 ompR,envZ	=	ompB		1603 C		1287 1	187 1	JBac	257	13685 1982 ECOMPB	J01606	ECOMPB
74.81 envZ	-	corr BB		2614 T		1600 1	2614 1	Unpub.		13692 1982 ECENVZ	X015587	ECOMPB
75.01 bioH	-			2866 T		2866 1	8728 MOMB		2	1989 ECBIOH	X15587	ECOMBP
75.15 malQ	-	corr BB	x02003 in Gb	2437 C	2867	1926 1	1926 1	ZNFC	42	473 1988 -	M32793	ECOMALQP
75.16 malPT,zhg			length BB	1901 C	2437	1926 1	1926 1	N		313 1985 ECMALP2	X06791	ECOMALP
75.17 malP				4793 C	2437	639 1	639 1	Gene	42	500 1985 ECMALP1	X02003	ECOMALP
75.20 malT	-			5432 C	2437	5432 1	5432 1	NAR	16	313 1986 ECMALT	M13585	ECOMALT
75.56 glpRGED		x07520 in Gb	flavoenzyme	2913 T		2913 1	2913 1	Gene	42	201 1986 EGLPRG	M54940	ECOGLPREG
75.58 glpDP		flavoenzyme	asd, 21 bp difference	2838 C	2838	2838 1	2838 1	AgrB	53	7732 1988 ECOGLPDA	D00425	ECOGLPDA
75.60 g19PACXB & asd,				2580 C	2838	2580 1	2580 1	ECGLGPA	263	1135 1989 ECOGLGPA	J03966	ECOGLGPA
75.63 g19GA	-			1601 C	5419	1505 1	1505 1	JBac	261	16256 1986 ECOGLGAA	J02616	ECOGLGAA
75.64 g19C	-			1328 C	6924	1182 1	1182 1	JBac	258	5084 1983 ECOGLG	V00281	ECOGLG
75.67 g19X	-			2047 F	8106	2026 1	2026 1	Gene	70	363 1988 ECOGLG	J01616	ECOGLG
75.68 g19B	-			2559 C	10132	2352 1	2352 1	ECGLGBA	261	8738 1986 ECOGLGBA	M13751	ECOGLGBA
75.69 asd	-			1674 C	12226	1674 1	1674 1	EMBO	1	379 1982 ECASDX	V00262	ECOASD
75.70 upBAEC	-	map	counterclockwise	2148 T	8119	2148 1	2148 1	JBac	171	5169 1989 M28722	M28722	M28722
76.01 upVHKJ	-			4717 C	820	8119 1	8119 1	NAR	17	2854 1989 ECUGPQ	X14437	ECUGPQ
76.03 livVHKJ		ATGA overlaps		1087 T		4558 0	4558 0	MOMB	2	767 1988 ECUGP	X13141	ECUGP
76.09 liv Operon	-			7586 C	5053	0 0	0 0	JBac	166	565 1986 ECOLIVHMG	M13166	ECOLIVHMG
76.10 htpR		correction and summary		1222 C	8703	155 0	155 0	JBac	265	11436 1990 ECOLIVHMG	J05516	ECOLIVHMG
76.15 ftsKEY	-			4480 C	13600	0 0	0 0	Unpub.		1990 ECOLIVHMG	J05516	ECOLIVHMG
76.20 gor	-			1500 T	4480	1 1	1 1	MGG	205	134 1986 ECFTSYEX	X04398	ECFTSYEX
77.40 rbsB	-	start core		400 T	1500	1 1	1 1	Bich	25	2736 1986 EGOR	M13141	EGOR
77.41 rbsB	-			140 T	400	1 1	1 1	JBac	171	636 1986 ECRHSB	M21762	ECRHSB
77.42 rbsB	-			577 T	140	140 1	140 1	JBac	171	636 1989 ECRHSB3	M21766	ECRHSB3
78.00 tRNA Prol		new locus for tRNA Prol		184 T		184 1	184 1	JBac	172	446 1990 ECRHSB4	M29717	ECRHSB4
79.00 cspA		cold shock prot.A		1205 T		1205 1	1205 1	JMB	212	579 1990 X52802	X52802	-
79.10 tag,bisc	-			869 T		869 1	869 1	PNAS	87	283 1990 ECCSPA	M30139	ECOSCPAA
79.12 bisC	-	overlay KR		3337 C		870 1	3024 1	JBac	261	15761 1986 ECTAG3M	J02606	ECOTAG
79.40 dppA = fpp		dipeptide transport pr.		1950 T		1950 1	1950 1	JBac	172	2194 1990 ECIBISCAS	M34827	ECIBISCAS
79.51 glyS	-			240 T		0 0	0 0	JBac	173	234 1990 ECOPPP	M35045	ECOPPP
79.52 glyS	-			3153 C		1 1	1 1	JBac	173	12503 1982 ECGLYNS	J01623	ECGLYNS
79.71 xyLAB	-	K01996 in Gb		4175 C		4175 1	4175 1	JBac	258	10637 1983 ECGLYS	J01622	ECGLYS
80.30 avtA		map BB		1752 T		1752 1	1752 1	NAR	15	9461 1987 ECXYLIK	X04691	ECXYLIK
80.40 selB	-			2000 T		1 1	1 1	2000 N	342	453 1989 ECSELB	X16644	X16644
80.60 rbsA	-	corrected by 80.71		9234 T		1 1	1 1	JBac	172	446 1990 ECRHS4	M29716	ECRHS4
80.70 mtLOP		K00051 in Gb		300 C		300 1	299 1	MOMB	2	405 1988 ECMTL0P	X06793	ECMTL0P
80.72 mtLA		corrected by 80.74		2164 C		2403 1	2162 1	JBac	258	10761 1983 ECMTL0A	V01503	ECMTL0A
80.73 mtLDA				1407 C		172 1	1407 1	MOMB	2	405 1988 ECMTL0D	X06794	ECMTL0D
80.95 cySE	-			1135 T		1 1	1 1	JBac	172	1398 1987 ECYSE	M15745	ECYCSE
80.96 cyXE		overlap on 2. strand		1396 C		3 1	1 1	BBRC	167	948 1990 ECYSE	M34333	ECYCSE
81.05 secB		revers overlap of gene		593 T		1 1	1 1	Gene	75	167 1989 ECSECB	M24489	ECSECB
81.15 kbl,tdh		length BB		1694 T		1 1	1 1	NAR	16	3586 1988 ECKBLTDH	X06690	ECKBLTDH
81.16 tdh	-	length BB		1872 C		0 0	0 0	JBac	264	5226 1989 ECKBLTDH	M33577	ECRFDADA
81.25 rfdA	-			2037 C		1 1	1 1	JBac	172	4652 1990 ECRFDADA	J01677	ECRPMBG
81.80 rfbC fpg	-			764 T		1 1	1 1	MGG	184	218 1981 ECRPMBG	X06036	ECRPMBG
81.81 fpg	-			1093 C		621 1	1093 1	EMBO	6	3177 1987 ECFFG	X06036	ECFFG
81.95 dut,orf	&	pyrE, atte X01714 in Gb		1613 T		1 1	1 1	JBac	2568 5352	967 1983 ECDUTPYR	V01578	ECOPYREA
81.97 pyrE	-			1113 C		2569 657	351 1	EMBO	135 135	223 1983 ECOPYRE	X00781	ECOPYRE
81.98 pyrE	-			1177 C		0 0	0 0	EMBO	3 3	1783 1984 ECOPYRE	X00781	ECOPYRE
81.99 orxy		in paper X14235 new BB		2375 F		2875 1	2375 1	MOMB	3	393 1989 -	-	-

82.05	rpoZ, spot	-	orf	M24503 in Gb	1	278	3451	Gene	33	1986	ECCOMEGA	M15266		
82.07	rpoZ, spot	-	orf	M24503 in Gb	1	3171	0	JBCh	264	15074	ECSPO	J04976		
82.40	solC	&	Soleno tRNA		1	233	233	N	723	1987	ECSPO	X17419		
82.60	uhPTCBa	&	11vBN		1	5403	1	JBac	169	3556	ECSPLC1	X17419		
82.63	11vBN	-			1	2462	C	NAR	13	3995	ECSPLC1	X17419		
82.66	11vB	-			1	5401	2240	0	NAR	12	ECLVBN	M17102		
83.42	gyrB, recF	&	dnaNA, rpmH, rnpA		1	7641	7	0	NAR	12	ECLVBN	X02541		
83.44	gyrB	corr			1	1498	T	0	8716	12	ECLVBN	X01131		
83.46	recF	-			1	3752	C	0	NAR	12	ECLVBF	X04341		
83.48	bglBCS	&	photS, unc, ori, assNA		1	1325	C	3753	1314	1	ECLVBF	X04341		
83.51	dnaAN, rpmH	-			1	3278	C	5067	2681	0	PNAS	81		
83.54	rnpA	-			1	1069	C	7648	101	0	Gene	28		
83.71	tnaA	corr	antitermination site		1	623	T	1	1069	0	Gene	38		
83.75	tnAAC	-			1	1994	C	18	1	2011	0	Gene	85	
84.02	rglMS	&	glmS, phos		1	5270	T	1	1994	0	JBac	164		
84.06	photU, pstB	-			1	3860	C	4684	3860	0	JBac	164		
84.07	phot	&	pstBAC		1	3730	C	4894	3730	1	JBac	161		
84.09	phot	-			1	1497	C	86624	1302	295	JBac	157		
84.19	gid, unc	&	glmS, phos		1	14106	C	9633	14526	1	BJ	224		
84.34	uncBL, gldB	-			1	1150	C	0	0	0	MGG	193		
84.45	gida, oric	&	fvd, assNA		1	4012	C	24159	995	4012	0	Gene	24	
84.50	rbsBAC	-			1	5820	T	1	5820	Unpub.	0	Gene	265	
84.60	rrnC	16S	ribosomal operon C		1	682	T	1	664	6048	PNAS	82		
84.61	rrnC	16S	RNA analog J01695 in Gb		1	1541	C	665	1519	3054	0	JBac	148	
84.62	91tU	trNA	glu2, relA1		1	354	C	2200	1	6495	0	JBac	170	
84.63	rrnC	23S	RNA analog J01695 in Gb		1	2903	C	2554	3501	0	JBac	148		
84.66	rrfC, aspt,	-	trPT		1	500	C	5548	1	500	0	JBCH	254	
84.75	kdsB	-			1	1308	T	1	1308	1308	0	JBCH	261	
84.81	11vg	-			1	300	T	1	1	43	PNAS	77		
84.84	ilvGEDA	-	E.coli B		1	304	B	0	0	0	JBac	164		
84.88	11vgAE	mut	M10313 in Gb		1	2343	C	44	1	317	0	PNAS	78	
84.93	11vgMEDA	mut	Corr BB		1	361	C	361	1	6742	0	NAR	15	
84.94	11vYC		length BB		1	7201	C	7201	213	3009	0	JBCH	261	
85.05	rep, hel	-			1	7102	C	7102	1	2671	2671	NAR	15	
85.20	trxA	-			1	657	T	1	1	33	2349	JBac	163	
85.21	trxA, rho	-			1	842	T	0	0	0	0	Gene	32	
85.22	trxA, rho	-			1	1493	C	34	1	436	0	JBac	166	
85.24	rho	-			1	1800	C	470	1	1880	0	NAR	11	
85.60	tRNA arg	&	his leu1 pro		1	646	T	1	1	646	646	JBac	158	
85.70	hemCDXY	&			1	4260	T	0	4260	1	7573	NAR	16	
85.76	cyaA	-			1	3697	C	4261	387	3699	0	NAR	12	
85.83	dapF	-			1	1308	P	0	1	1010	5870	NAR	16	
85.84	orf, xerC	-			1	2500	F	1011	1	2500	0	JBac	172	
85.88	uvrD	corr			1	2849	C	2501	483	2846	0	JBio	99	
86.15	p1da, recQ	-			1	1319	T	1	1	809	3504	JBio	96	
86.17	recQ	-			1	2695	C	810	1	2695	0	MGG	205	
86.25	p1dB	-			1	1576	T	1	1	1576	1576	JBCH	98	
86.30	metR	E.coli B	operator		1	360	B	0	0	0	0	PNAS	86	
86.31	metEH	operator			1	285	T	0	285	50	1013	0	PNAS	87
86.33	metR	-			1	1013	C	286	286	50	1013	0	PNAS	87
86.40	udp	including unpub. seq.	map		1	2479	T	1	1594	1367	2479	2479	NAR	17
87.22	fadaB	-			1	1594	T	1	1594	1367	13217	13217	ECMTR	M37630
87.23	fadaB	-			1	3679	C	228	4950	1368	0	NAR	18	
87.24	pepO, orf	-			1	4151	C	3809	1	4041	0	NAR	18	
87.25	rRNA ribos	operator A	J01694 in Gb		1	426	C	7850	1	376	0	Cell	17	
87.26	rRNA	RNA analog J01695 in Gb			1	1541	C	8227	1519	2959	0	JMB	148	
87.31	alaUV	& 1leuV tRNAs analogs			1	545	C	9667	1	438	0	JBCH	254	
87.32	rrLA	23S RNA analog J01695 in Gb			1	2903	C	10105	3501	6403	0	JMB	148	
87.33	intergenic region rrLA	-			1	247	C	13007	129	247	0	Cell	19	
87.35	5S RNA	-			1	120	C	13125	28	120	0	NAR	6	

87.40	pola, spf	J01663 in Gb	3190 T	0	0	4127 JBCh	257	1958	ECPOLA
87.41	glnALG	J01618 in Gb	1076 F	1	1	4127 0 JBac	152	1211	-
87.70	glnALG	= ntrBC	814 T	1	1	659 4972 MGG	190	1983	ECGLNA
87.71	glnALG	new BB	4311 C	660	1	4311 0 NAR	15	171	ECGLNA
88.00	rhasR		2201 T	1	1	2201 0 JMB	196	2757	ECRHAC
88.05	fdHE	-	1200 T	1	1	1200 Unpub.		1987	ECRHAC
88.11	sod(nrdB)	-	1053 T	1	1	1053 NAR	14	4777	ECOSOD
88.14	cpxA	new BB	1841 T	1	1	1841 JMB	203	1986	ECCPXA01
88.26	pflA, sfp & cdh, tpiA		3304 T	1	1	3306 4267 EJB	149	467 1988	ECCPXA01
88.28	tpi	-	1338 C	3307	1	961 0 MGG	195	363 1985	ECPFKA
88.40	g1PKF	incl. unpubl. material	1170 T	1	1	1170 NAR	17	X00617	ECOTPIA
88.42	g1PK	site 6	1171 C	129	0	2028 0 NAR	0	X02519	ECOTPIA
88.42	bending	-	195 C	0	0	2299 0 PNAS	87	X05961	ECOBENT6
88.78	priA, cytR	Ac Nr D00616	2907 T	0	1	1384 0 NAR	14	M33881	ECPRIAY
88.80	cytR	-	1384 C	2300	1	1384 0 NAR	14	X03683	ECOCYTR
88.97	metJBLF	corr BB	729 T	1	1	729 8542 JBCh	259	X01282	ECMETJLA
89.00	metLB	-	1411 C	240	1	1411 0 JBCh	258	X01282	ECMETJLB1
89.01	metL	J01651 in Gb	1902 C	16	1	1902 0 JBCh	258	X01282	ECMETJLB1
89.05	metL	direct continuity	240 C	4316	1	240 0 JBCh	258	X01282	ECMETJLB2
89.09	metF, katG	direct continuity	1238 C	4555	1	1182 0 NAR	11	X01502	ECOMETF
89.10	katG, rpme	-	2805 C	5737	1	2805 0 JBAC	170	M21516	ECOKATGA
89.22	ppc	ppc 59, ppc 67	3106 T	1	1	3106 3106 JBio	95	X05903	ECOPPCG
89.30	argE	-	440 T	1	1	440 1 NAR	10	X01587	ECARGOP1
89.34	argCBH	-	2117 C	331	1	2117 0 Gene	68	M21446	ECARGCBH
89.40	mor = oxyR	= momR	1500 T	1	1	1500 1500 JGMi	136	X00305	ECOMOR
89.75	btUB, rrnB	& birA, rtB, tufB, sec, nus	2220 T	1	1	1511 30222 JBAC	161	X01547	ECOMETLB2
89.77	rrnB	5'-flanking region corr	1821 C	1512	1	1512 7578 BBA	161	X01547	ECOMETLB2
89.82	rrsB rrlB	rrrfB corr	7258 C	2083	1	7258 7508 JMB	148	X01695	ECRGNB
89.82	birA	length BB	2491 C	9316	1	9316 893 2491 Gene	35	M10123	ECOBIR
89.91	rtS	-	1407 C	10914	1	10914 1133 158 Gene	74	M36321	ECORTSA
89.94	tufB	& tRNA thr tyr gly J01717	1973 C	11989	1	11989 1973 0 Gene	12	X057091	ECOTGTUFFB
89.99	secE, nusG	-	1380 C	13862	1	13862 79 1380 0 Gene	12	M30610	ECOSECE
90.01	rpoBC, rplK	J01678 in Gb	3072 C	15163	2	15163 224 12337 0 PNAS	76	X00339	ECOPRLRPO
90.02	rpoBC	J01678 in Gb	1089 C	0	0	0 0 BioO	5	V00339	ECOPRLRPO
90.05	rpoB	mut	4714 C	0	0	0 0 EJB	116	X00340	ECOPRLRPO
90.08	rpoC	-	5321 C	0	0	0 0 NAR	110	J01678	ECOPACK
90.15	pac	penicillin acylase	2593 C	27227	7	2593 0 NAR	14	X04114	ECOPACK
90.16	pac	penicillin acylase	360 C	29864	324	360 0 JMag	3	M12373	ECOPA2
90.17	pga	83 bp diff p.acylase G	3158 C	29900	2836	3158 0 Gene	56	X01760	ECOPGA
90.30	hupB	promoter regulation	288 T	0	0	0 584 0 Gene	56	X01760	ECOPGA
90.31	hupA	HU-2 comparison	0 C	1	27	42 0 JMB	213	X01760	ECOPGA
90.32	HU-2	-	568 C	17	1	568 0 MG	209	M22975	regul
90.38	purHD, rrnE	& meta, aceBAK	3535 T	1	3535 1 16036 JBCh	264	X05994	ECOHU2	
90.41	rrnE	ribos operon E J01697 in Gb	410 C	3536	59	370 0 Cell	1	J05126	ECPURHD
90.43	rrnE	16S RNA analog	1541 C	3908	1519	3054 0 JMB	148	V00335	ECORGNE
90.44	g1tv	-	354 C	5442	1	354 0 JBAC	170	J01695	ECORGNB
90.45	rrnE	23S RNA analog	2903 C	5802	3500	6403 0 JMB	148	M20398	ECORGNB
90.46	rrnE/A	Intergenic region	247 C	6699	129	220 0 Cell	1	X00766	ECRGND3
90.47	rrnE	-	1444 C	8791	1	1197 0 NAR	13	M31761	ECICLR
90.49	meta	-	973 C	9988	1	662 0 NAR	17	X14501	ECMETAG
90.51	aceB	publ. also NAR 16 9342	13280 C	10650	1	2280 0 NAR	16	X12431	ECACEB
90.52	aceA	-	1344 C	12930	163	970 0 NAR	16	X07543	ECACEA
90.54	aceK	-	2358 C	13737	1	2358 0 JBAC	170	M20714	ECIDHKPA
90.80	lacR	repressor	1166 T	1	1166 1 4989 JBAC	172	X02800	ECORRNE1	
90.81	meth	100 bp deleted	4098 C	1167	276	4098 0 Gene	87	X16584	ECMETAG
91.21	lysC	-	1587 T	1	1587 1 4154 JBCh	261	M11812	ECLYSCA3	
91.30	pgi	-	2573 C	1588	7	2573 0 MG	217	X15196	ECPGI
91.47	xyle	& malFEKB, lamB	2842 T	0	0	10803 JBCh	262	J02812	ECXYLE
91.48	xyIE	-	984 C	1	2842 1	0 NAR	16	X06663	ECMALG3

91.50	malG	-	1103	C	2843	1	1013	0	EMBO	4	2287	1985	ECMALG	X02871		
91.51	malE	nut			3856	169	6545	0	N	285	78	1980	ECMALB	JO1648		
91.55	lamB	, malM	J01648	in Gb	2183	0	0	0	Cell	27	507	1981	ECLAMBA			
91.58	malX	-			1292	C	0	0	NAR	10	7449	1982	ECMALB	X00298		
91.60	male	-	K02117	in Gb?	1191	C	0	0	JBCH	259	10606	1984	ECMALB	JO1648		
91.62	malM	corr			1744	C	0	0	JBCH	259	10896	1984	ECMALB	JO1648		
91.66	malM				1023	C	743	0	JBCH	191	303	1986	ECMALM	X04477		
91.78	pISB, dgkA	-			1313	C	0	0	PNAS	78	4274	1981	ECPLSB	K00127		
91.81	lexA	-			3865	T	1	1	JBCH	258	10856	1983	ECPLSB	K01643		
91.90	dnaB	-			951	T	1	1	951	Cell	23	689	1981	ECOLEXA		
91.95	tyrB	-			1661	T	1	1	1661	JBCH	259	97	1984	ECDNAB	K01174	
92.01	ssb	-			1733	T	1	1	1733	BBRC	133	134	1985	ECTYRBA	M12047	
92.05	uvrA, ssb	-			764	T	1	1	3850	PNAS	78	4274	1981	ECOSSB	K01704	
92.60	fdhF	-			3205	C	765	120	3205	0	JBCH	261	4895	1986	ECUVRAA	M13495
92.61	fdhF	-			2273	T	1	1	2971	PNAS	83	4650	1986	ECFDHF	M13563	
93.00	lysU	comp to lysS			784	C	0	0	0	ACMB	148	44	1987	ECFDHF		
93.20	leuV	tRNA leu	J01712	in Gb	1518	T	1	1	1578	NAR	18	305	1990	ECLYSUG	X16542	
93.31	phn-Q	alkylphosph.			699	T	1	1	699	NAR	9	2121	1981	ECTRNA	V00363	
93.32	psd	= phn			15611	B	0	0	0	JBCH	265	4461	1990	ECPHNAQ	J05260	
93.33	psd	= phn			203	T	1	1	203	JBAC	172	3191	1990	ECALPHO	M32730	
93.39	meIRAB	& aspa			52	T	1	1	52	JBAC	172	3191	1990	ECALPHOF	M33728	
93.41	mELA	-			1628	T	1	1	1628	Gene	59	253	1987	ECMELOPA	M18425	
93.43	mELB	-			1835	C	1629	139	139	0	NAR	15	2213	1987	ECMELA	X04894
93.48	fumB, genF	map			1575	C	3171	1	294	JBCH	259	4320	1984	ECMELB	K01991	
93.65	lysU	-			3162	T	1	1	3162	JBAC	171	3494	1989	ECFUMB	M27058	
93.75	pheU	152 bp id. K00969			3034	T	1	1	3034	PNAS	83	3237	1990	ECFLYSU	M30630	
93.80	pheU	2.locus for ph <u>e</u> U			312	T	1	1	312	NAR	11	4379	1983	ECTRNAP	X00912	
94.11	aspa	-			200	T	1	1	200	JMB	212	579	1990	X53235		
94.12	aspa	-			2921	T	1	1	2921	BJ	237	547	1986	ECASPAG	X04066	
94.15	mopBA	= groESL			2901	W	2459	2901	2901	NAR	13	2063	1985	ECASPAG	X02307	
94.39	frdD	terminator			2267	T	1	1	2267	JBAC	172	333	1988	ECGROESL	X07850	
94.42	frdD	,ampC			2105	T	1	1	5482	JBAC	164	1100	1985	ECAMPCF2	M11979	
94.43	frdA	-			1536	C	0	0	0	PNAS	78	4897	1981	ECAMPCFR	J01611	
94.44	frdBCD	& ampC			2640	C	0	0	0	EJB	122	479	1982	ECAMPCFR	J01611	
94.45	frdBC	-			2922	T	1	1	2922	PNAS	79	1111	1982	ECFRDB	V00277	
94.70	psd	-			2267	T	1	1	2267	EJB	126	211	1982	ECAMPCFR	J01611	
94.80	mIAA	quoted in 519.00			1350	T	1	1	1350	JBCH	263	11516	1988	ECPSD	J03916	
95.00	glyV	tRNA Gly3			2225	P	1	1	2225	-	-	-	-	-	-	
95.50	rpsF,R,rplI	-			423	T	1	1	2726	JBCH	263	19147	1988	ECPURAA		
95.69	cpdB	operator and orf			1979	T	1	1	1979	MGG	204	5759	1990	X53236	X53236	
95.95	fdp	-			543	T	1	1	333	2531	222	161	1990	X54008	X54008	
96.00	pmbA	-			2198	C	334	1	2198	JMB	165	1002	1986	ECOPSFRI	X04022	
96.50	pyrB1	-			1611	C	1	1	1611	NAR	16	8707	1988	ECOPDB	M13464	
96.55	pyrB1	-			1682	T	1	1	1682	MONB	4	1921	1990	ECOPB	X54152	
96.57	pyrB1	-			758	T	1	1	1581	2038	JBAC	163	991	1985	ECOPYRBIB	M10743
96.60	argI	-			990	C	0	0	0	PNAS	80	2462	1983	ECOPYRBIB	V00323	
96.62	argI	-			1582	C	334	1	1611	0	0	1115	1984	ECOPYRBIA	K01472	
96.76	valS	-			1085	C	301	1	1085	EMBO	1	853	1982	ECARGIPR	M24186	
96.79	valS	-			57	T	1	1	3011	0	NAR	11	8509	1983	ECARGI	X00210
96.84	xerB	= pepA & urf13			3291	C	3012	1	3293	0	NAR	15	9081	1987	ECOSYNTGV	J03497
96.85	urf13	-			1692	T	1	1	2038	EMBO	8	1623	1989	ECOVALS	X05891	
96.95	leuX	flanking regions new BB			446	C	0	0	0	Unpub.	-	-	-	-	-	
97.10	is4	function			new	BB	300	1	1	1101	T	1	1100	1981	ECOXERB	X15130
97.80	uxuA	-			1450	C	3051	1	1450	EJB	143	1389	1986	ECOXERB	J01733	
98.03	fimA	10kb map of fimBEACDFGH			1450	T	3051	1	612	3050	EMBO	5	1395	1984	ECOFIMBE	X03923
98.10	fimD	-			2718	T	1	1	2718	4728	MGG	220	334	1990	ECOFIMA1	X51655

