Table 4. The number of GroES pattern matches found in GroEL substrate proteins from *E. coli* (1).

				GroES repeats		
No.	Swiss-Prot ID	Protein	Seq. length	6	5	4
1	ATDA_ECOLI	Spermidine N(1)−acetyltransferase (EC 2.3.1.57) (Diamine acetyltransferase) (SAT)	185	1	2	2
2	EFTU_ECOLI	Elongation factor Tu (EF-Tu) (P-43)	393	0	4	7
3	FABZ_ECOLI	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-) ((3R)-hydroxymyristoyl ACP dehydrase) (17 kDa actomyosin component)	151	1	3	7
4	FUR_ECOLI	Ferric uptake regulation protein (Ferric uptake regulator)	148	1	1	2
5	GLMS_ECOLI	Glucosamine–fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase)	608	4	10	19
6	HDFR_ECOLI	HTH-type transcriptional regulator hdfR (H-NS-depdendent flhDC regulator)	279	1	2	3
7	HFQ_ECOLI	Hfq protein (Host factor-I protein) (HF-I) (HF-1)	101	1	2	3
8	MPL_ECOLI	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) (Murein peptide ligase)	457	2	4	11
9	PURU_ECOLI	Formyltetrahydrofolate deformylase (EC 3.5.1.10) (Formyl-FH(4) hydrolase)	280	2	3	9
10	RL1_ECOLI	50S ribosomal protein L1	233	0	0	1
11	RL11_ECOLI	50S ribosomal protein L11	141	0	0	1

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
12	RL14_ECOLI	50S ribosomal protein L14	123	0	1	1
13	RL15_ECOLI	50S ribosomal protein L15	144	0	0	0
14	RL17_ECOLI	50S ribosomal protein L17	127	0	0	2
15	RL2_ECOLI	50S ribosomal protein L2	272	0	0	1
16	RL28_ECOLI	50S ribosomal protein L28	77	0	1	1
17	RL32_ECOLI	50S ribosomal protein L32	56	0	0	0
18	RL9_ECOLI	50S ribosomal protein L9	149	0	0	2
19	RS1_ECOLI	30S ribosomal protein S1	557	0	1	7
20	RS12_ECOLI	30S ribosomal protein S12	123	0	1	1
21	RS15_ECOLI	30S ribosomal protein S15	88	0	0	1
22	RS19_ECOLI	30S ribosomal protein S19	91	0	0	0
23	RS2_ECOLI	30S ribosomal protein S2	240	0	1	5
24	RS20_ECOLI	30S ribosomal protein S20	86	0	0	0
25	RS3_ECOLI	30S ribosomal protein S3	232	0	2	4
26	RS4_ECOLI	30S ribosomal protein S4	205	1	2	3
27	RS5_ECOLI	30S ribosomal protein S5	166	1	2	4
28	RS7_ECOLI	30S ribosomal protein S7	178	0	1	4
29	RS9_ECOLI	30S ribosomal protein S9	129	0	1	2
30	RSUA_ECOLI	Ribosomal small subunit pseudouridine synthase A (EC 5.4.99.-) (16S pseudouridylate 516 synthase) (16S pseudouridine 516 synthase) (rRNA-uridine isomerase A) (rRNA pseudouridylate synthase A)	231	0	4	6
31	SLYD_ECOLI	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	196	1	1	1

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	 5	 4
32	YBHA_ECOLI	Phosphatase ybhA (EC 3.1.3.-)	272	2	5	9
33	THIO2_ECOLI	Thioredoxin 2 (EC 1.8.1.8) (Protein-disulfide reductase) (Disulfide reductase) (Trx2)	139	0	1	1
34	TPX_ECOLI	Thiol peroxidase (EC 1.11.1.-) (Scavengase P20)	167	1	3	3
35	PTGA_ECOLI	Glucose-specific phosphotransferase enzyme IIA component (EC 2.7.1.-) (PTS system glucose-specific EIIA component) (EIIA-Glc) (EIII-Glc)	168	0	1	3
36	FABA_ECOLI	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) (Beta-hydroxydecanoyl thioester dehydrase)	171	1	2	4
37	IPYR_ECOLI	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase)	175	0	1	2
38	AHPC_ECOLI	Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15) (Peroxiredoxin) (Thioredoxin peroxidase) (Alkyl hydroperoxide reductase protein C22) (SCRP-23) (Sulfate starvation-induced protein 8) (SSI8)	186	0	1	1
39	RRF_ECOLI	Ribosome recycling factor (Ribosome releasing factor) (RRF)	185	0	0	1
40	GRPE_ECOLI	GrpE protein (HSP-70 cofactor) (Heat shock protein B25.3) (HSP24)	197	0	0	2
41	DEOD_ECOLI	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP)	238	0	0	1
42	THIG_ECOLI	Thiazole biosynthesis protein thiG	256	2	3	7

TABLE 4: (continued)

				GroES repeats		
No.	Swiss-Prot ID	Protein	Seq. length	6	5	4
43	DEOC_ECOLI	Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA)	259	0	0	5
44	PANB_ECOLI	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase)	264	2	4	9
45	GPMA_ECOLI	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (PGAM) (BPG-dependent PGAM) (dPGM)	249	0	0	1
46	EFTS_ECOLI	Elongation factor Ts (EF-Ts)	282	1	2	5
47	RBSB_ECOLI	D-ribose-binding periplasmic protein precursor (EC 3.6.3.17)	296	2	6	10
48	BLAT_ECOLI	Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3) (TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6) (IRT-4) (Penicillinase)	286	0	2	5
49	G3P1_ECOLI	Glyceraldehyde-3-phosphate dehydrogenase A (EC 1.2.1.12) (GAPDH-A)	330	0	2	6
50	RPOA_ECOLI	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)	329	0	0	3
51	OMPA_ECOLI	Outer membrane protein A precursor (Outer membrane protein II*)	346	1	3	7
52	YNCE_ECOLI	Hypothetical protein yncE precursor	353	3	7	14

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	 5	 4
53	OMPC_ECOLI	Outer membrane protein C precursor (Porin ompC) (Outer membrane protein 1B)	367	1	5	6
54	PGK_ECOLI	Phosphoglycerate kinase (EC 2.7.2.3)	386	0	2	8
55	FABB_ECOLI	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41) (Beta- ketoacyl-ACP synthase I) (KAS I)	406	1	7	12
56	ACKA_ECOLI	Acetate kinase (EC 2.7.2.1) (Acetokinase)	400	2	4	10
57	SERA_ECOLI	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (PGDH)	409	1	3	7
58	GLYA_ECOLI	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase) (SHMT)	417	0	3	8
59	ENO_ECOLI	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D- glycerate hydro-lyase)	431	2	4	7
60	PURA_ECOLI	Adenylosuccinate synthetase (EC 6.3.4.4) (IMP–aspartate ligase) (AdSS) (AMPSase)	431	2	4	11
61	TIG_ECOLI	Trigger factor (TF)	432	1	1	2
62	KPYK1_ECOLI	Pyruvate kinase I (EC 2.7.1.40) (PK-1)	470	2	7	15
63	6PGD_ECOLI	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	468	0	3	10
64	SYN_ECOLI	Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine–tRNA ligase) (AsnRS)	465	3	5	8
65	OPPA_ECOLI	Periplasmic oligopeptide-binding protein precursor	543	0	2	7

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
66	ODP2_ECOLI	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex)	629	0	2	14
67	CIRA_ECOLI	Colicin I receptor precursor	663	0	1	6
68	PNP_ECOLI	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	711	1	6	15
69	EFG_ECOLI	Elongation factor G (EF-G)	703	2	3	10
70	ODP1_ECOLI	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	886	3	7	15
71	LPP_ECOLI	Major outer membrane lipoprotein precursor (Murein-lipoprotein)	78	1	1	3
72	IF3_ECOLI	Translation initiation factor IF-3	180	0	0	3
73	GNTY_ECOLI	Protein gntY	191	0	0	1
74	DLDH_ECOLI	Dihydrolipoyl dehydrogenase (EC 1.8.1.4) (E3 component of pyruvate and 2-oxoglutarate dehydrogenases complexes) (Dihydrolipoamide dehydrogenase) (Glycine cleavage system L protein)	473	1	5	13
75	PPIC_ECOLI	Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase C) (Rotamase C) (Parvulin)	92	0	0	1
76	YOHL_ECOLI	Hypothetical protein yohL	90	1	1	3
77	YDHD_ECOLI	Probable monothiol glutaredoxin ydhD	115	1	2	3
78	NIKR_ECOLI	Nickel responsive regulator	133	1	1	1
79	YJBQ_ECOLI	Hypothetical UPF0047 protein yjbQ	138	0	0	2

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
80	USPG_ECOLI	Universal stress protein G	142	0	0	2
81	MOAC_ECOLI	Molybdenum cofactor biosynthesis protein C	160	0	0	4
82	YFHP_ECOLI	Hypothetical UPF0074 protein yfhP	162	0	0	4
83	GREA_ECOLI	Transcription elongation factor greA (Transcript cleavage factor greA)	158	0	0	2
84	PPIB_ECOLI	Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8) (PPIase B) (Rotamase B)	164	1	3	4
85	MOAB_ECOLI	Molybdenum cofactor biosynthesis protein B	169	0	3	7
86	DPS_ECOLI	DNA protection during starvation protein	166	0	1	3
87	NUOE_ECOLI	NADH-quinone oxidoreductase chain E (EC 1.6.99.5) (NADH dehydrogenase I, chain E) (NDH-1, chain E) (NUO5)	166	0	1	2
88	MUG_ECOLI	G/U mismatch-specific DNA glycosylase (EC 3.2.2.-) (Mismatch-specific uracil DNA-glycosylase) (UDG)	168	0	3	3
89	LUXS_ECOLI	S-ribosylhomocysteine lyase (EC 4.4.1.21) (Autoinducer-2 production protein luxS) (AI-2 synthesis protein)	170	0	0	1
90	AROK_ECOLI	Shikimate kinase I (EC 2.7.1.71) (SKI)	172	0	2	3
91	YFBU_ECOLI	UPF0304 protein yfbU	164	1	1	1
92	SEQA_ECOLI	SeqA protein	181	0	1	4
93	NUSG_ECOLI	Transcription antitermination protein nusG	180	1	2	2
94	RIMM_ECOLI	16S rRNA processing protein rimM (21K)	182	0	0	4
95	RIML_ECOLI	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-) (Acetylating enzyme for N-terminal of ribosomal protein L7/L12)	179	1	2	3

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
96	NUDH_ECOLI	(Di)nucleoside polyphosphate hydrolase (EC 3.6.1.-) (Ap5A pyrophosphatase)	176	1	1	3
97	PTH_ECOLI	Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH)	194	0	0	3
98	HEMG_ECOLI	Protoporphyrinogen oxidase (EC 1.3.3.4) (PPO)	181	0	1	2
99	TEHB_ECOLI	Tellurite resistance protein tehB	197	1	1	4
100	YIHX_ECOLI	Phosphatase yihX (EC 3.1.3.-)	199	0	1	7
101	THIE_ECOLI	Thiamine-phosphate pyrophosphorylase (EC 2.5.1.3) (TMP pyrophosphorylase) (TMP-PPase) (Thiamine-phosphate synthase)	211	2	4	4
102	YCIO_ECOLI	Protein yciO	206	0	3	5
103	ENGB_ECOLI	Probable GTP-binding protein engB	210	0	0	3
104	RCSB_ECOLI	Capsular synthesis regulator component B	216	1	3	7
105	YCBL_ECOLI	Hypothetical protein ycbL	215	1	2	4
106	UVRY_ECOLI	Response regulator uvrY	218	1	3	5
107	GLRX2_ECOLI	Glutaredoxin 2 (Grx2)	215	0	0	2
108	YODA_ECOLI	Metal-binding protein yodA precursor (Cadmium-induced protein yodA)	216	0	0	1
109	CAN_ECOLI	Carbonic anhydrase 2 (EC 4.2.1.1)	220	0	2	7
110	YGEA_ECOLI	Hypothetical protein ygeA	230	2	3	6
111	INAA_ECOLI	Protein inaA	216	1	1	3
112	TRMH_ECOLI	tRNA (Guanosine-2'-O-)-methyltransferase (EC 2.1.1.34) (tRNA [GM18] methyltransferase)	229	1	2	6
113	ARAD_ECOLI	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose isomerase)	231	0	3	6
114	PHOP_ECOLI	Transcriptional regulatory protein phoP	223	0	0	3

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
115	FABG_ECOLI	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) (3-ketoacyl- acyl carrier protein reductase)	244	2	2	6
116	PROQ_ECOLI	ProP effector	232	0	0	0
117	CPXR_ECOLI	Transcriptional regulatory protein cpxR	232	0	1	5
118	PYRF_ECOLI	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase) (OMPDCase) (OMPdecase)	245	1	1	4
119	OMPR_ECOLI	Transcriptional regulatory protein ompR	239	0	0	4
120	LPXA_ECOLI	Acyl-[acyl-carrier-protein]–UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase)	262	2	6	8
121	YBFF_ECOLI	Esterase ybfF (EC 3.1.-.-)	254	1	2	5
122	PSTB_ECOLI	Phosphate import ATP-binding protein pstB (EC 3.6.3.27) (Phosphate- transporting ATPase) (ABC phosphate transporter)	256	2	4	7
123	YJJV_ECOLI	Putative deoxyribonuclease yjjV (EC 3.1.21.-)	259	0	1	3
124	CYSE_ECOLI	Serine acetyltransferase (EC 2.3.1.30) (SAT)	273	0	3	7
125	KDSA_ECOLI	2-dehydro-3-deoxyphosphooctonate aldolase (EC 2.5.1.55) (Phospho-2- dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase) (KDOPS)	284	0	2	4
126	YFFS_ECOLI	Hypothetical protein yffS	279	0	2	3

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	5	4
127	YPT2_ECOLI	Hypothetical 31.7 kDa protein in traX-finO intergenic region (ORFC)	286	2	2	6
128	YBBN_ECOLI	Protein ybbN	284	1	2	11
129	YIJO_ECOLI	Putative HTH-type transcriptional regulator yijO	283	1	4	7
130	YNIA_ECOLI	Hypothetical protein yniA	286	4	6	9
131	HSLO_ECOLI	33 kDa chaperonin (Heat shock protein 33) (HSP33)	292	1	4	8
132	RLUB_ECOLI	Ribosomal large subunit pseudouridine synthase B (EC 5.4.99.-) (rRNA- uridine isomerase B) (rRNA pseudouridylate synthase B)	291	0	2	4
133	ROB_ECOLI	Right origin-binding protein	289	1	3	8
134	YCJZ_ECOLI	Putative HTH-type transcriptional regulator ycjZ	299	0	3	4
135	YADB_ECOLI	Hypothetical protein yadB	298	1	2	6
136	YDHF_ECOLI	Hypothetical oxidoreductase ydhF (EC 1.-.-.-)	298	2	2	4
137	KPRS_ECOLI	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) (RPPK) (Phosphoribosyl pyrophosphate synthetase) (P-Rib-PP synthetase) (PRPP synthetase)	314	1	2	6
138	OXYR_ECOLI	Hydrogen peroxide-inducible genes activator (Morphology and auto- aggregation control protein)	305	2	4	9
139	YEAT_ECOLI	Putative HTH-type transcriptional regulator yeaT	307	2	3	10
140	YBIB_ECOLI	Hypothetical protein ybiB	320	0	2	6

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
141	ACCA_ECOLI	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	318	0	4	4
142	CYSB_ECOLI	HTH-type transcriptional regulator cysB (Cys regulon transcriptional activator)	324	0	2	3
143	DUSA_ECOLI	tRNA-dihydrouridine synthase A (EC 1.-.-.-)	330	0	3	8
144	MREB_ECOLI	Rod shape-determining protein mreB	347	2	8	13
145	MOAA_ECOLI	Molybdenum cofactor biosynthesis protein A	329	0	0	6
146	GATD_ECOLI	Galactitol-1-phosphate 5-dehydrogenase (EC 1.1.1.251)	346	1	5	8
147	RSMC_ECOLI	Ribosomal RNA small subunit methyltransferase C (EC 2.1.1.52) (rRNA (guanine-N(2)-)-methyltransferase) (16S rRNA m2G1207 methyltransferase)	342	2	8	8
148	INH5_ECOLI	Transposase insH for insertion sequence element IS5Y	326	1	1	2
149	YIHE_ECOLI	Hypothetical protein yihE	328	0	1	6
150	TAS_ECOLI	Tas protein	346	1	2	4
151	PYRC_ECOLI	Dihydroorotase (EC 3.5.2.3) (DHOase)	347	2	4	5
152	YGHZ_ECOLI	Hypothetical protein yghZ	346	1	2	4
153	ALF_ECOLI	Fructose-bisphosphate aldolase class II (EC 4.1.2.13) (FBP aldolase)	358	3	3	6
154	DCUP_ECOLI	Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD)	354	2	3	5
155	INSH_ECOLI	Transposase insH for insertion sequence element IS5	338	2	2	3

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	5	4
156	OMPF_ECOLI	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	362	1	3	6
157	SERC_ECOLI	Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT)	361	1	2	9
158	YBBB_ECOLI	Hypothetical protein ybbB	364	1	2	8
159	ENTC_ECOLI	Isochorismate synthase entC (EC 5.4.4.2) (Isochorismate mutase)	391	2	3	13
160	ARGM_ECOLI	Succinylornithine transaminase (EC 2.6.1.-) (Succinylornithine aminotransferase) (Carbon starvation protein C)	406	1	2	10
161	ODO2_ECOLI	Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex (EC 2.3.1.61) (E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex)	404	0	2	7
162	ISCS_ECOLI	Cysteine desulfurase (EC 2.8.1.7) (ThiI transpersulfidase) (NifS protein homolog)	404	1	2	5
163	GLPB_ECOLI	Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.99.5) (Anaerobic G-3-P dehydrogenase subunit B) (Anaerobic G3Pdhase B)	419	4	6	9
164	GSA_ECOLI	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT)	426	2	3	10
165	YADE_ECOLI	Hypothetical protein yadE precursor	409	2	4	10

TABLE 4: (continued)

				GroES repeats		
No.	Swiss-Prot ID	Protein	Seq. length	6	5	4
166	AVTA_ECOLI	Valine–pyruvate aminotransferase (EC 2.6.1.66) (Transaminase C) (Alanine–valine transaminase)	417	0	5	13
167	RHLB_ECOLI	ATP-dependent RNA helicase rhlB (EC 3.6.1.-)	420	2	4	9
168	RHO_ECOLI	Transcription termination factor rho	419	1	5	9
169	DHNA_ECOLI	NADH dehydrogenase (EC 1.6.99.3)	433	6	8	10
170	CISY_ECOLI	Citrate synthase (EC 2.3.3.1)	427	0	1	8
171	YGAF_ECOLI	Hypothetical protein ygaF	444	1	7	12
172	PAAK_ECOLI	Phenylacetate-coenzyme A ligase (EC 6.2.1.30) (Phenylacetyl-CoA ligase) (PA-CoA ligase)	437	0	3	5
173	NUOF_ECOLI	NADH-quinone oxidoreductase chain F (EC 1.6.99.5) (NADH dehydrogenase I, chain F) (NDH-1, chain F) (NUO6)	445	2	3	7
174	ACCC_ECOLI	Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA carboxylase) (EC 6.4.1.2) (ACC)	449	2	4	12
175	YEGD_ECOLI	Hypothetical chaperone protein yegD	450	1	4	9
176	YCAJ_ECOLI	Hypothetical protein ycaJ	447	1	5	15
177	STHA_ECOLI	Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1) (STH) (NAD(P)(+) transhydrogenase [B-specific])	465	1	3	6
178	DCEA_ECOLI	Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha)	466	1	3	14
179	TNAA_ECOLI	Tryptophanase (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase)	471	1	4	12
180	YDCR_ECOLI	Hypothetical protein ydcR	468	3	5	12
181	PCNB_ECOLI	Poly(A) polymerase (EC 2.7.7.19) (PAP) (Plasmid copy number protein)	472	0	0	4

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	5	4
182	MGLA_ECOLI	Galactoside transport ATP-binding protein mglA	506	2	6	13
183	TYPA_ECOLI	GTP-binding protein typA/BipA (Tyrosine phosphorylated protein A)	607	3	7	13
184	NUOCD_ECOLI	NADH-quinone oxidoreductase chain C/D (EC 1.6.99.5) (NADH dehydrogenase I, chain C/D) (NDH-1, chain C/D) (NUO3/NUO4)	600	1	4	10
185	DNAK_ECOLI	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	637	0	2	8
186	GIDA_ECOLI	Glucose inhibited division protein A	629	3	4	13
187	YDCP_ECOLI	Putative protease ydcP precursor (EC 3.4.-.-)	653	1	2	7
188	SYT_ECOLI	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine–tRNA ligase) (ThrRS)	642	1	5	11
189	SPOT_ECOLI	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.2) ((ppGpp)ase) (Penta-phosphate guanosine-3'-pyrophosphohydrolase)	702	1	2	7
190	LON_ECOLI	ATP-dependent protease La (EC 3.4.21.53)	784	1	2	8
191	RNR_ECOLI	Ribonuclease R (EC 3.1.-.-) (RNase R) (VacB protein)	813	2	3	7
192	ADHE_ECOLI	Aldehyde-alcohol dehydrogenase [Includes: Alcohol dehydrogenase (EC 1.1.1.1) (ADH); Acetaldehyde dehydrogenase [acetylating] (EC 1.2.1.10) (ACDH); Pyruvate-formate-lyase deactivase (PFL deactivase)]	890	5	13	22
193	GYRA_ECOLI	DNA gyrase subunit A (EC 5.99.1.3)	875	1	7	17

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	5	4
194	IF2_ECOLI	Translation initiation factor IF-2	890	5	8	11
195	GLND_ECOLI	[Protein-PII] uridylyltransferase (EC 2.7.7.59) (PII uridylyl- transferase) (Uridylyl removing enzyme) (UTase)	890	1	3	19
196	ODO1_ECOLI	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) (Alpha- ketoglutarate dehydrogenase)	933	0	7	16
197	PUR4_ECOLI	Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) (FGAM synthase) (FGAMS) (Formylglycinamide ribotide amidotransferase) (FGARAT) (Formylglycinamide ribotide synthetase)	1295	4	13	28
198	HRPA_ECOLI	ATP-dependent helicase hrpA	1300	3	5	15
199	RPOB_ECOLI	DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (RNAP beta subunit) (Transcriptase beta chain) (RNA polymerase beta subunit)	1342	1	7	17
200	RPOC_ECOLI	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (RNAP beta' subunit) (Transcriptase beta' chain) (RNA polymerase beta' subunit)	1407	5	15	27
201	YBAK_ECOLI	Protein ybaK	159	1	3	3
202	HLPA_ECOLI	Histone-like protein HLP-1 precursor (DNA-binding 17 kDa protein)	161	0	2	2
203	SSRP_ECOLI	SsrA-binding protein (Small protein B)	159	1	3	6
204	RSD_ECOLI	Regulator of sigma D	158	0	0	1
205	UBIC_ECOLI	Chorismate–pyruvate lyase (EC 4.-.-.-)	164	0	1	4
206	YQAB_ECOLI	Phosphatase yqaB (EC 3.1.3.-)	188	1	2	4

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
207	YCFP_ECOLI	Hypothetical UPF0227 protein ycfP	180	0	0	1
208	RFBC_ECOLI	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) (dTDP-4-keto-6- deoxyglucose 3,5-epimerase) (dTDP-L-rhamnose synthetase)	185	1	2	4
209	RIMJ_ECOLI	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) (Acetylating enzyme for N-terminal of ribosomal protein S5)	194	1	1	4
210	YAJB_ECOLI	Hypothetical protein yajB	193	0	0	5
211	YQJI_ECOLI	Hypothetical protein yqjI	207	0	1	1
212	CRP_ECOLI	Catabolite gene activator (cAMP receptor protein) (cAMP-regulatory protein)	210	0	1	5
213	FTSE_ECOLI	Cell division ATP-binding protein ftsE	222	1	4	7
214	GCH1_ECOLI	GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I)	221	1	1	4
215	TRMB_ECOLI	tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase)	239	0	0	2
216	FUCR_ECOLI	L-fucose operon activator	243	1	1	5
217	PFLA_ECOLI	Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4) (PFL- activating enzyme) (Formate-C-acetyltransferase-activating enzyme 1)	245	0	1	5
218	TRMD_ECOLI	tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (M1G- methyltransferase) (tRNA [GM37] methyltransferase)	255	1	3	4
219	GLCC_ECOLI	Glc operon transcriptional activator	254	1	2	4
220	SUHB_ECOLI	Inositol-1-monophosphatase (EC 3.1.3.25) (IMPase) (Inositol-1- phosphatase) (I-1-Pase)	267	1	3	8
221	YCFH_ECOLI	Putative deoxyribonuclease ycfH (EC 3.1.21.-)	265	0	0	4

TABLE 4: (continued)

				GroES repeats		
No.	Swiss-Prot ID	Protein	Seq. length	6	5	4
222	YAFD_ECOLI	Hypothetical UPF0294 protein yafD	266	1	4	8
223	GATY_ECOLI	Tagatose-1,6-bisphosphate aldolase gatY (EC 4.1.2.-) (TBPA)	284	2	3	7
224	DAPA_ECOLI	Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPS)	292	1	2	4
225	AMIA_ECOLI	Probable N-acetylmuramoyl-L-alanine amidase amiA precursor (EC 3.5.1.28)	289	2	3	9
226	END4_ECOLI	Endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV)	285	0	1	4
227	YPT1_ECOLI	Hypothetical 31.7 kDa protein in traX-finO intergenic region	286	2	2	6
228	YNEB_ECOLI	Putative aldolase yneB (EC 4.2.1.-)	291	1	4	8
229	NANA_ECOLI	N-acetylneuraminate lyase (EC 4.1.3.3) (N-acetylneuraminic acid aldolase) (N-acetylneuraminate pyruvate-lyase) (Sialic acid lyase) (Sialate lyase) (Sialic acid aldolase) (NALase)	296	1	2	7
230	YHBJ_ECOLI	Hypothetical UPF0042 protein yhbJ	284	1	3	6
231	METF_ECOLI	5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	296	1	2	6
232	ARAC_ECOLI	Arabinose operon regulatory protein	292	3	5	7
233	ICIA_ECOLI	Chromosome initiation inhibitor (OriC replication inhibitor)	297	3	5	10
234	DUSC_ECOLI	tRNA-dihydrouridine synthase C (EC 1.-.-.-)	315	2	4	5

TABLE 4: (continued)

				GroES repeats		
No.	Swiss-Prot ID	Protein	Seq. length	6	5	4
235	HEM2_ECOLI	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) (Porphobilinogen synthase) (ALAD) (ALADH)	323	1	2	6
236	DUSB_ECOLI	tRNA-dihydrouridine synthase B (EC 1.-.-.-)	321	1	2	3
237	RLUC_ECOLI	Ribosomal large subunit pseudouridine synthase C (EC 5.4.99.-) (rRNA- uridine isomerase C) (rRNA pseudouridylate synthase C)	319	0	0	6
238	LIPA_ECOLI	Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase) (Lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipA) (Lip-syn)	321	1	1	3
239	ADD_ECOLI	Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	333	2	3	3
240	YAJO_ECOLI	Hypothetical oxidoreductase yajO (EC 1.-.-.-)	324	0	0	4
241	LTAE_ECOLI	Low-specificity L-threonine aldolase (EC 4.1.2.5) (Low-specificity L- TA)	333	3	5	12
242	NAGZ_ECOLI	Beta-hexosaminidase (EC 3.2.1.52) (N-acetyl-beta-glucosaminidase) (Beta-N-acetylhexosaminidase)	341	3	4	9
243	YFIF_ECOLI	Hypothetical tRNA/rRNA methyltransferase yfiF (EC 2.1.1.-)	345	0	1	6
244	ALF1_ECOLI	Fructose-bisphosphate aldolase class I (EC 4.1.2.13) (FBP aldolase)	349	1	3	7
245	YBJS_ECOLI	Hypothetical protein ybjS	337	0	2	6
246	ALR2_ECOLI	Alanine racemase, catabolic (EC 5.1.1.1)	356	1	3	6
247	YJJU_ECOLI	Hypothetical protein yjjU	357	2	6	8

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	5	4
248	DHAS_ECOLI	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH)	367	1	1	6
249	HIS7_ECOLI	Histidine biosynthesis bifunctional protein hisB [Includes: Histidinol-phosphatase (EC 3.1.3.15); Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) (IGPD)]	355	0	0	5
250	PHOL_ECOLI	PhoH-like protein	359	1	2	5
251	THIK_ECOLI	Thiamine kinase (EC 2.7.1.89)	274	0	4	8
252	DNAJ_ECOLI	Chaperone protein dnaJ (Heat shock protein J) (HSP40)	375	1	2	6
253	BIOF_ECOLI	8-amino-7-oxononanoate synthase (EC 2.3.1.47) (AONS) (8-amino-7- ketopelargonate synthase) (7-keto-8-amino-pelargonic acid synthetase) (7-KAP synthetase) (L-alanine–pimelyl CoA ligase)	384	1	4	12
254	METK_ECOLI	S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine adenosyltransferase) (AdoMet synthetase) (MAT)	383	3	5	12
255	TRMA_ECOLI	tRNA (Uracil-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54)- methyltransferase) (RUMT)	366	0	3	7
256	RSMD_ECOLI	Putative ribosomal RNA small subunit methyltransferase D (EC 2.1.1.52) (rRNA (guanine-N(2)-)-methyltransferase) (16S rRNA m2G966 methyltransferase)	378	4	5	10

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats 6	5	4
257	ARGE_ECOLI	Acetylornithine deacetylase (EC 3.5.1.16) (Acetylornithinase) (AO) (N- acetylornithinase) (NAO)	383	0	4	8
258	LLDD_ECOLI	L-lactate dehydrogenase (Cytochrome) (EC 1.1.2.3)	396	2	2	11
259	FABF_ECOLI	3-oxoacyl-[acyl-carrier-protein] synthase II (EC 2.3.1.41) (Beta- ketoacyl-ACP synthase II) (KAS II)	412	1	2	7
260	PHEA_ECOLI	P-protein [Includes: Chorismate mutase (EC 5.4.99.5) (CM); Prephenate dehydratase (EC 4.2.1.51) (PDT)]	386	3	5	9
261	THIH_ECOLI	Thiazole biosynthesis protein thiH	376	1	2	8
262	INTS_ECOLI	Putative prophage CPS-53 integrase	385	0	2	4
263	SUFS_ECOLI	Cysteine desulfurase (EC 2.8.1.7) (Selenocysteine lyase) (EC 4.4.1.16) (Selenocysteine reductase) (Selenocysteine beta-lyase) (SCL)	406	2	5	10
264	YFBQ_ECOLI	Probable aminotransferase yfbQ (EC 2.6.1.-)	405	1	3	7
265	RSPA_ECOLI	Starvation sensing protein rspA	404	0	1	3
266	GATZ_ECOLI	Putative tagatose 6-phosphate kinase gatZ (EC 2.7.1.144)	420	0	0	8
267	TYPH_ECOLI	Thymidine phosphorylase (EC 2.4.2.4) (TdRPase)	440	1	5	14
268	DADA_ECOLI	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)	432	2	3	4
269	PMBA_ECOLI	PmbA protein (TldE protein)	450	0	3	7

TABLE 4: (continued)

No.	Swiss-Prot ID	Protein	Seq. length	GroES repeats		
				6	5	4
270	EUTB_ECOLI	Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7) (Ethanolamine ammonia-lyase large subunit)	453	1	4	12
271	XYLA_ECOLI	Xylose isomerase (EC 5.3.1.5) (D-xylulose keto-isomerase)	440	0	4	10
272	RHLE_ECOLI	Putative ATP-dependent RNA helicase rhlE	454	1	5	8
273	PEPQ_ECOLI	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase)	443	1	4	11
274	TLDD_ECOLI	TldD protein	481	2	6	13
275	UXAC_ECOLI	Uronate isomerase (EC 5.3.1.12) (Glucuronate isomerase) (Uronic isomerase)	470	0	1	5
276	AMPA_ECOLI	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Aminopeptidase A/I)	503	4	9	13
277	ARAA_ECOLI	L-arabinose isomerase (EC 5.3.1.4)	500	4	4	10
278	ALDB_ECOLI	Aldehyde dehydrogenase B (EC 1.2.1.-)	512	2	6	15
279	DHSA_ECOLI	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	588	3	5	12
280	FRDA_ECOLI	Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	601	1	4	15
281	DEAD_ECOLI	Cold-shock DEAD-box protein A (ATP-dependent RNA helicase deaD)	628	1	5	10
282	YCBY_ECOLI	Hypothetical UPF0020/UPF0064 protein ycbY	702	4	7	13
283	PARC_ECOLI	Topoisomerase IV subunit A (EC 5.99.1.-)	752	3	8	20
284	PHSM_ECOLI	Maltodextrin phosphorylase (EC 2.4.1.1)	796	6	8	19

GroES patterns are G_IVL_G_A ($N_C = 6$ contacts), G_IVL_G ($N_C = 5$ contacts), and G_IVL ($N_C = 4$ contacts). Any separation along the sequence between identified patterns is considered. The requirement of a sequence spacer of 10 residues between binding motifs results in slightly fewer motifs per protein.

I. REFERENCES

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