

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
P41547	Calcitonin OS=Canis lupus familiaris GN=CALCA PE=1 SV=2 - [CALC_CANLF]	4618.25	98.26	1	25	25	1520	115	12.7	8.06
POA9K9	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1 - [SLYD_ECOLI]	453.58	71.43	1	12	12	217	196	20.8	5.05
POA6Y8	Chaperone protein DnaK OS=Escherichia coli (strain K12) GN=dnaK PE=1 SV=2 - [DNAK_ECOLI]	358.17	87.77	1	58	58	168	638	69.1	4.97
POA9A6	Cell division protein FtsZ OS=Escherichia coli (strain K12) GN=ftsZ PE=1 SV=1 - [FTSZ_ECOLI]	134.31	89.03	1	27	27	67	383	40.3	4.78
POAG67	30S ribosomal protein S1 OS=Escherichia coli (strain K12) GN=rpsA PE=1 SV=1 - [RS1_ECOLI]	81.98	56.73	1	25	25	33	557	61.1	4.98
POAFX4	Regulator of sigma D OS=Escherichia coli (strain K12) GN=rsd PE=1 SV=1 - [RSD_ECOLI]	80.42	56.33	1	8	8	32	158	18.2	6.02
POA6F5	60 kDa chaperonin OS=Escherichia coli (strain K12) GN=groL PE=1 SV=2 - [CH60_ECOLI]	79.79	69.16	1	27	27	41	548	57.3	4.94
POA6P1	Elongation factor Ts OS=Escherichia coli (strain K12) GN=tsf PE=1 SV=2 - [EFTS_ECOLI]	66.03	71.02	1	20	20	29	283	30.4	5.29
POA7G6	Protein RecA OS=Escherichia coli (strain K12) GN=recA PE=1 SV=2 - [RECA_ECOLI]	56.32	73.65	1	20	20	31	353	37.9	5.19
POA850	Trigger factor OS=Escherichia coli (strain K12) GN=tig PE=1 SV=1 - [TIG_ECOLI]	52.88	61.11	1	22	22	22	432	48.2	4.88
POAE08	Alkyl hydroperoxide reductase subunit C OS=Escherichia coli (strain K12) GN=ahpC PE=1 SV=2 - [AHP_C_ECOLI]	50.99	60.43	1	10	10	19	187	20.7	5.17
POCE47	Elongation factor Tu 1 OS=Escherichia coli (strain K12) GN=tufA PE=1 SV=1 - [EFTU1_ECOLI]	49.42	59.90	2	15	15	19	394	43.3	5.45
POAG86	Protein-export protein SecB OS=Escherichia coli (strain K12) GN=secB PE=1 SV=1 - [SECB_ECOLI]	46.66	58.06	1	7	7	16	155	17.3	4.37
POA6P9	Enolase OS=Escherichia coli (strain K12) GN=eno PE=1 SV=2 - [ENO_ECOLI]	46.00	57.87	1	14	14	23	432	45.6	5.48
POABK5	Cysteine synthase A OS=Escherichia coli (strain K12) GN=cysK PE=1 SV=2 - [CYSK_ECOLI]	42.51	69.66	1	13	14	18	323	34.5	6.06
POA7Z4	DNA-directed RNA polymerase subunit alpha OS=Escherichia coli (strain K12) GN=rpoA PE=1 SV=1 - [RPOA_ECOLI]	41.08	58.05	1	14	14	17	329	36.5	5.06
POAG55	50S ribosomal protein L6 OS=Escherichia coli (strain K12) GN=rplF PE=1 SV=2 - [RL6_ECOLI]	39.66	71.19	1	10	10	16	177	18.9	9.70
POA9P0	Dihydropyridyl dehydrogenase OS=Escherichia coli (strain K12) GN=lpdA PE=1 SV=2 - [DLDH_ECOLI]	37.17	33.12	1	10	10	14	474	50.7	6.15
POC0V0	Periplasmic serine endoprotease DegP OS=Escherichia coli (strain K12) GN=degP PE=1 SV=1 - [DEGP_ECOLI]	33.52	38.82	1	9	9	13	474	49.3	8.56
POABP8	Purine nucleoside phosphorylase DeoD-type OS=Escherichia coli (strain K12) GN=deoD PE=1 SV=2 - [DEOD_ECOLI]	32.99	58.58	1	9	9	14	239	25.9	5.66
POACF0	DNA-binding protein HU-alpha OS=Escherichia coli (strain K12) GN=hupA PE=1 SV=1 - [DBHA_ECOLI]	32.34	71.11	1	9	9	16	90	9.5	9.58
POA9Y6	Cold shock-like protein CspC OS=Escherichia coli (strain K12) GN=cspC PE=1 SV=2 - [CSPC_ECOLI]	31.93	60.87	1	4	4	13	69	7.4	7.24
PO2358	30S ribosomal protein S6 OS=Escherichia coli (strain K12) GN=rpsF PE=1 SV=1 - [RS6_ECOLI]	31.23	51.11	1	6	6	16	135	15.7	5.00
POA7R1	50S ribosomal protein L9 OS=Escherichia coli (strain K12) GN=rplI PE=1 SV=1 - [RL9_ECOLI]	30.89	71.81	1	9	9	13	149	15.8	6.58
POACF8	DNA-binding protein H-NS OS=Escherichia coli (strain K12) GN=hns PE=1 SV=2 - [HNS_ECOLI]	29.68	59.12	1	7	7	11	137	15.5	5.47
POA7K2	50S ribosomal protein L7/L12 OS=Escherichia coli (strain K12) GN=rplL PE=1 SV=2 - [RL7_ECOLI]	29.31	44.63	1	6	6	10	121	12.3	4.65
POA9B2	Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) GN=gapA PE=1 SV=2 - [G3P1_ECOLI]	29.30	63.14	2	11	11	14	331	35.5	7.11
P09372	Protein GrpE OS=Escherichia coli (strain K12) GN=grpE PE=1 SV=1 - [GRPE_ECOLI]	29.11	65.48	1	8	8	15	197	21.8	4.75
POAGD3	Superoxide dismutase [Fe] OS=Escherichia coli (strain K12) GN=sodB PE=1 SV=2 - [SODF_ECOLI]	27.11	88.08	1	10	10	12	193	21.3	5.95
P06959	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex OS=Escherichia coli (strain K12) GN=aceF PE=1 SV=3 - [ODP2_ECOLI]	26.80	34.60	1	14	14	15	630	66.1	5.17
POACC3	Iron-sulfur cluster insertion protein ErpA OS=Escherichia coli (strain K12) GN=erpA PE=1 SV=1 - [ERPA_ECOLI]	25.64	82.46	1	6	6	10	114	12.1	4.31
P35340	Alkyl hydroperoxide reductase subunit F OS=Escherichia coli (strain K12) GN=ahpF PE=1 SV=2 - [AHPF_ECOLI]	25.10	48.75	1	13	13	15	521	56.1	5.68
P64540	Uncharacterized protein YfcL OS=Escherichia coli (strain K12) GN=yfcL PE=4 SV=1 - [YFCL_ECOLI]	24.74	100.00	1	5	5	8	92	10.0	4.41
POA6A8	Acyl carrier protein OS=Escherichia coli (strain K12) GN=acpP PE=1 SV=2 - [ACP_ECOLI]	23.99	32.05	1	2	2	8	78	8.6	4.06
P61889	Malate dehydrogenase OS=Escherichia coli (strain K12) GN=mdh PE=1 SV=1 - [MDH_ECOLI]	23.75	67.95	1	11	11	11	312	32.3	5.77
POACF4	DNA-binding protein HU-beta OS=Escherichia coli (strain K12) GN=hupB PE=1 SV=1 - [DBHB_ECOLI]	23.73	74.44	1	7	7	11	90	9.2	9.70
P62707	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Escherichia coli (strain K12) GN=gpmA PE=1 SV=2 - [GPM_A_ECOLI]	23.69	66.80	1	13	13	13	250	28.5	6.18
POA7W1	30S ribosomal protein S5 OS=Escherichia coli (strain K12) GN=rpsE PE=1 SV=2 - [RS5_ECOLI]	22.41	56.89	1	6	6	9	167	17.6	10.11
POAED0	Universal stress protein A OS=Escherichia coli (strain K12) GN=uspA PE=1 SV=2 - [USPA_ECOLI]	20.52	70.14	1	6	6	9	144	16.1	5.29
POABT2	DNA protection during starvation protein OS=Escherichia coli (strain K12) GN=dps PE=1 SV=2 - [DPS_ECOLI]	19.60	54.49	1	9	9	10	167	18.7	6.11
P63284	Chaperone protein ClpB OS=Escherichia coli (strain K12) GN=clpB PE=1 SV=1 - [CLPB_ECOLI]	19.54	23.22	1	13	13	18	857	95.5	5.52
P61714	6,7-dimethyl-8-ribityllumazine synthase OS=Escherichia coli (strain K12) GN=ribE PE=1 SV=1 - [RISB_ECOLI]	18.70	78.21	1	6	6	10	156	16.1	5.25
P28635	D-methionine-binding lipoprotein MetQ OS=Escherichia coli (strain K12) GN=metQ PE=1 SV=2 - [METQ_ECOLI]	18.22	36.90	1	5	5	10	271	29.4	5.29
POA862	Thiol peroxidase OS=Escherichia coli (strain K12) GN=tpx PE=1 SV=2 - [TPX_ECOLI]	18.09	47.62	1	5	5	6	168	17.8	4.92
POA805	Ribosome-recycling factor OS=Escherichia coli (strain K12) GN=frr PE=1 SV=1 - [RRF_ECOLI]	17.84	56.22	1	6	6	7	185	20.6	6.89
POAFG0	Transcription termination/antitermination protein NusG OS=Escherichia coli (strain K12) GN=nusG PE=1 SV=2 - [NUSG_ECOLI]	17.29	53.59	1	5	5	9	181	20.5	6.81
P69441	Adenylate kinase OS=Escherichia coli (strain K12) GN=adk PE=1 SV=1 - [KAD_ECOLI]	16.74	57.94	1	8	8	10	214	23.6	5.76
P63020	Fe/S biogenesis protein NfuA OS=Escherichia coli (strain K12) GN=nfuA PE=1 SV=1 - [NFUA_ECOLI]	16.72	37.70	1	4	4	7	191	21.0	4.64
POAA04	Phosphocarrier protein HPr OS=Escherichia coli (strain K12) GN=ptsH PE=1 SV=1 - [PTHP_ECOLI]	16.57	78.82	1	4	4	9	85	9.1	5.83
P68919	50S ribosomal protein L25 OS=Escherichia coli (strain K12) GN=rplY PE=1 SV=1 - [RL25_ECOLI]	16.46	42.55	1	4	4	6	94	10.7	9.60
POA7V0	30S ribosomal protein S2 OS=Escherichia coli (strain K12) GN=rpsB PE=1 SV=2 - [RS2_ECOLI]	16.38	43.57	1	6	6	7	241	26.7	7.14
P69828	Galactitol-specific phosphotransferase enzyme IIA component OS=Escherichia coli (strain K12) GN=gatA PE=3 SV=1 - [PTKA_ECOLI]	15.99	59.33	1	6	6	12	150	16.9	5.29
POAA43	Ribosomal small subunit pseudouridine synthase A OS=Escherichia coli (strain K12) GN=rsuA PE=1 SV=1 - [RSUA_ECOLI]	15.88	54.98	1	7	7	7	231	25.8	6.18
POA7J7	50S ribosomal protein L11 OS=Escherichia coli (strain K12) GN=rplK PE=1 SV=2 - [RL11_ECOLI]	15.67	38.03	1	5	5	6	142	14.9	9.63
POAE06	Multidrug efflux pump subunit AcrA OS=Escherichia coli (strain K12) GN=acrA PE=1 SV=1 - [ACRA_ECOLI]	15.41	23.93	1	6	6	8	397	42.2	7.99

POA8E7	UPF0234 protein YajQ OS=Escherichia coli (strain K12) GN=yajQ PE=1 SV=2 - [YAJQ_ECOLI]	15.31	33.13	1	5	5	9	163	18.3	6.24
P69783	Glucose-specific phosphotransferase enzyme IIA component OS=Escherichia coli (strain K12) GN=crr PE=1 SV=2 - [PTGA_ECOLI]	15.21	59.76	1	8	8	8	169	18.2	4.84
POAGE0	Single-stranded DNA-binding protein OS=Escherichia coli (strain K12) GN=ssb PE=1 SV=2 - [SSB_ECOLI]	15.17	47.19	1	6	6	6	178	19.0	5.58
POAE52	Putative peroxiredoxin bcp OS=Escherichia coli (strain K12) GN=bcp PE=1 SV=1 - [BCP_ECOLI]	15.04	42.31	1	5	5	9	156	17.6	5.24
P13029	Catalase-peroxidase OS=Escherichia coli (strain K12) GN=katG PE=1 SV=2 - [KATG_ECOLI]	14.68	16.12	1	6	6	6	726	80.0	5.31
P76344	Metal-binding protein ZinT OS=Escherichia coli (strain K12) GN=zinT PE=1 SV=1 - [ZINT_ECOLI]	14.41	29.17	1	5	5	7	216	24.7	6.37
POA855	Protein TolB OS=Escherichia coli (strain K12) GN=tolB PE=1 SV=1 - [TOLB_ECOLI]	13.79	23.49	1	5	5	6	430	45.9	7.59
P45523	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA OS=Escherichia coli (strain K12) GN=fkpA PE=1 SV=1 - [FKBA_ECOLI]	13.72	18.52	1	4	4	5	270	28.9	8.47
POAA25	Thioredoxin-1 OS=Escherichia coli (strain K12) GN=trxA PE=1 SV=2 - [THIO_ECOLI]	13.43	58.72	1	5	5	6	109	11.8	4.88
P16456	Selenide, water dikinase OS=Escherichia coli (strain K12) GN=selD PE=1 SV=1 - [SELD_ECOLI]	13.23	20.17	1	3	3	5	347	36.7	5.43
POA7L0	50S ribosomal protein L1 OS=Escherichia coli (strain K12) GN=rplA PE=1 SV=2 - [RL1_ECOLI]	12.85	36.32	1	7	7	7	234	24.7	9.64
POA858	Triosephosphate isomerase OS=Escherichia coli (strain K12) GN=tpiA PE=1 SV=1 - [TPIS_ECOLI]	12.77	34.90	1	3	3	6	255	27.0	5.96
POA6H5	ATP-dependent protease ATPase subunit HslU OS=Escherichia coli (strain K12) GN=hslU PE=1 SV=1 - [HSLU_ECOLI]	12.71	30.02	1	8	8	8	443	49.6	5.35
POA6Z6	Nickel-responsive regulator OS=Escherichia coli (strain K12) GN=nikR PE=1 SV=1 - [NIKR_ECOLI]	12.50	54.89	1	4	4	5	133	15.1	6.24
POA6M8	Elongation factor G OS=Escherichia coli (strain K12) GN=fusA PE=1 SV=2 - [EFG_ECOLI]	12.39	15.77	1	6	6	6	704	77.5	5.38
POA9A9	Ferric uptake regulation protein OS=Escherichia coli (strain K12) GN=fur PE=1 SV=1 - [FUR_ECOLI]	12.35	52.70	1	7	7	9	148	16.8	6.11
P60438	50S ribosomal protein L3 OS=Escherichia coli (strain K12) GN=rplC PE=1 SV=1 - [RL3_ECOLI]	12.33	32.54	1	5	5	6	209	22.2	9.91
POA8N5	Lysine--tRNA ligase, heat inducible OS=Escherichia coli (strain K12) GN=lysU PE=1 SV=2 - [SYK2_ECOLI]	12.24	15.84	1	5	5	6	505	57.8	5.24
P69811	Multiphosphoryl transfer protein OS=Escherichia coli (strain K12) GN=fruB PE=2 SV=1 - [PTFAH_ECOLI]	12.17	29.79	1	5	5	6	376	39.6	4.94
POA7M9	50S ribosomal protein L31 OS=Escherichia coli (strain K12) GN=rpmE PE=1 SV=1 - [RL31_ECOLI]	12.14	41.43	1	2	2	4	70	7.9	9.32
POA7A9	Inorganic pyrophosphatase OS=Escherichia coli (strain K12) GN=ppa PE=1 SV=2 - [IPYR_ECOLI]	11.91	22.16	1	3	3	5	176	19.7	5.17
POA836	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12) GN=sucC PE=1 SV=1 - [SUCC_ECOLI]	11.85	13.92	1	4	4	4	388	41.4	5.52
POAFL3	Peptidyl-prolyl cis-trans isomerase A OS=Escherichia coli (strain K12) GN=ppiA PE=1 SV=1 - [PPIA_ECOLI]	11.73	48.95	1	4	4	6	190	20.4	8.85
P64588	Transcriptional regulator YqjI OS=Escherichia coli (strain K12) GN=yqjI PE=1 SV=1 - [YQJI_ECOLI]	11.50	25.60	1	5	5	6	207	23.4	6.74
POA8M3	Threonine--tRNA ligase OS=Escherichia coli (strain K12) GN=thrS PE=1 SV=1 - [SYT_ECOLI]	11.27	8.57	1	3	3	5	642	74.0	6.19
P30859	Putative ABC transporter arginine-binding protein 2 OS=Escherichia coli (strain K12) GN=arti PE=1 SV=3 - [ARTI_ECOLI]	10.95	32.51	1	5	5	5	243	26.9	6.10
POABD3	Bacterioferritin OS=Escherichia coli (strain K12) GN=bfr PE=1 SV=1 - [BFR_ECOLI]	10.90	46.84	1	6	6	6	158	18.5	4.81
POA6F9	10 kDa chaperonin OS=Escherichia coli (strain K12) GN=groS PE=1 SV=1 - [CH10_ECOLI]	10.90	72.16	1	5	5	6	97	10.4	5.24
POAC69	Glutaredoxin-4 OS=Escherichia coli (strain K12) GN=grxD PE=1 SV=1 - [GLRX4_ECOLI]	10.71	39.13	1	4	4	4	115	12.9	4.75
P60624	50S ribosomal protein L24 OS=Escherichia coli (strain K12) GN=rplX PE=1 SV=2 - [RL24_ECOLI]	10.57	44.23	1	4	4	4	104	11.3	10.21
POA7J3	50S ribosomal protein L10 OS=Escherichia coli (strain K12) GN=rplJ PE=1 SV=2 - [RL10_ECOLI]	10.49	43.64	1	4	4	4	165	17.7	8.98
POA9X4	Rod shape-determining protein MreB OS=Escherichia coli (strain K12) GN=mreB PE=1 SV=1 - [MREB_ECOLI]	10.43	37.46	1	9	9	11	347	36.9	5.26
POA8B5	Nucleoid-associated protein YbaB OS=Escherichia coli (strain K12) GN=ybaB PE=1 SV=1 - [YBAB_ECOLI]	10.32	39.45	1	3	3	4	109	12.0	5.07
POABS1	RNA polymerase-binding transcription factor DksA OS=Escherichia coli (strain K12) GN=dksA PE=1 SV=1 - [DKSA_ECOLI]	10.28	29.14	1	3	3	4	151	17.5	5.12
POA705	Translation initiation factor IF-2 OS=Escherichia coli (strain K12) GN=infB PE=1 SV=1 - [IF2_ECOLI]	10.05	23.60	1	9	9	10	890	97.3	6.07
P45578	S-ribosylhomocysteine lyase OS=Escherichia coli (strain K12) GN=luxS PE=1 SV=3 - [LUXS_ECOLI]	9.67	35.67	1	3	3	6	171	19.4	5.36
P08200	Isoctrate dehydrogenase [NADP] OS=Escherichia coli (strain K12) GN=icd PE=1 SV=1 - [IDH_ECOLI]	9.35	15.14	1	4	4	4	416	45.7	5.26
POA9L3	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase OS=Escherichia coli (strain K12) GN=fkib PE=1 SV=2 - [FKBB_ECOLI]	9.12	35.44	1	6	6	6	206	22.2	4.89
POAFG6	Dihydrolypoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Escherichia coli (strain K12) GN=sucB PE=1 SV=2 - [ODO2_ECOLI]	9.02	20.74	1	6	6	6	405	44.0	5.81
POA6X3	RNA-binding protein Hfq OS=Escherichia coli (strain K12) GN=hfq PE=1 SV=2 - [HFQ_ECOLI]	9.00	83.33	1	4	4	5	102	11.2	7.65
P02413	50S ribosomal protein L15 OS=Escherichia coli (strain K12) GN=rplO PE=1 SV=1 - [RL15_ECOLI]	8.85	27.08	1	3	3	3	144	15.0	11.18
POAAN9	Anti-adapter protein IraP OS=Escherichia coli (strain K12) GN=iraP PE=1 SV=1 - [IRAP_ECOLI]	8.77	44.19	1	2	2	3	86	9.9	4.92
P06999	ATP-dependent 6-phosphofructokinase isozyme 2 OS=Escherichia coli (strain K12) GN=pfkB PE=1 SV=2 - [PFKB_ECOLI]	8.67	25.89	1	3	3	4	309	32.4	5.36
P18843	NH(3)-dependent NAD(+) synthetase OS=Escherichia coli (strain K12) GN=nadE PE=1 SV=2 - [NADE_ECOLI]	8.51	28.73	1	4	4	4	275	30.6	5.59
POA7J0	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Escherichia coli (strain K12) GN=ribB PE=1 SV=1 - [RIBB_ECOLI]	8.17	49.31	1	4	4	4	217	23.3	5.01
POA8M6	UPF0265 protein YeeX OS=Escherichia coli (strain K12) GN=yeeX PE=1 SV=1 - [YEEX_ECOLI]	8.13	14.68	1	1	1	3	109	12.8	9.31
P23869	Peptidyl-prolyl cis-trans isomerase B OS=Escherichia coli (strain K12) GN=ppiB PE=1 SV=2 - [PPIB_ECOLI]	7.99	28.05	1	4	4	4	164	18.1	5.80
POA825	Serine hydroxymethyltransferase OS=Escherichia coli (strain K12) GN=glyA PE=1 SV=1 - [GLYA_ECOLI]	7.92	10.55	1	3	3	3	417	45.3	6.48
POC054	Small heat shock protein IbpA OS=Escherichia coli (strain K12) GN=ibpA PE=1 SV=1 - [IBPA_ECOLI]	7.88	26.28	1	3	3	3	137	15.8	5.83
POA7M6	50S ribosomal protein L29 OS=Escherichia coli (strain K12) GN=rpmC PE=1 SV=1 - [RL29_ECOLI]	7.74	49.21	1	3	3	4	63	7.3	9.99
POAD10	Uncharacterized protein YecJ OS=Escherichia coli (strain K12) GN=yecJ PE=4 SV=1 - [YECJ_ECOLI]	7.71	38.55	1	2	2	3	83	9.1	5.05
POA912	Peptidoglycan-associated lipoprotein OS=Escherichia coli (strain K12) GN=pal PE=1 SV=1 - [PAL_ECOLI]	7.69	21.39	1	2	2	4	173	18.8	6.80
POADE8	tRNA-modifying protein YgfZ OS=Escherichia coli (strain K12) GN=ygfZ PE=1 SV=2 - [YGFZ_ECOLI]	7.60	18.40	1	4	4	6	326	36.1	5.27
P39099	Periplasmic pH-dependent serine endoprotease DegQ OS=Escherichia coli (strain K12) GN=degQ PE=1 SV=1 - [DEGQ_ECOLI]	7.53	24.92	1	6	6	9	455	47.2	5.95
P69503	Adenine phosphoribosyltransferase OS=Escherichia coli (strain K12) GN=apt PE=1 SV=1 - [APT_ECOLI]	7.48	46.99	1	4	4	4	183	19.8	5.41
POA6Y5	33 kDa chaperonin OS=Escherichia coli (strain K12) GN=hslo PE=1 SV=1 - [HSLO_ECOLI]	7.42	19.86	1	4	4	4	292	32.5	4.49

P0A7Z0	Ribose-5-phosphate isomerase A OS=Escherichia coli (strain K12) GN=rpiA PE=1 SV=1 - [RPIA_ECOLI]	7.32	26.48	1	3	3	6	219	22.8	5.40
P17846	Sulfite reductase [NADPH] hemoprotein beta-component OS=Escherichia coli (strain K12) GN=cysI PE=1 SV=4 - [CYST_ECOLI]	7.30	24.04	1	7	7	7	570	64.0	7.64
P39310	Uncharacterized protein YtfB OS=Escherichia coli (strain K12) GN=ytfB PE=4 SV=2 - [YTFB_ECOLI]	7.25	21.23	1	2	2	4	212	23.5	5.22
P76177	Protein YdgH OS=Escherichia coli (strain K12) GN=ydgH PE=1 SV=1 - [YDGH_ECOLI]	7.17	20.06	1	4	4	5	314	33.9	9.28
P0AF93	2-iminobutanoate/2-iminopropanoate deaminase OS=Escherichia coli (strain K12) GN=ridA PE=1 SV=2 - [RIDA_ECOLI]	7.08	62.50	1	4	4	5	128	13.6	5.50
P0ACR9	Transcriptional repressor MprA OS=Escherichia coli (strain K12) GN=mprA PE=2 SV=1 - [MPRA_ECOLI]	6.99	25.57	1	2	2	3	176	20.6	6.21
P39177	Universal stress protein G OS=Escherichia coli (strain K12) GN=uspG PE=1 SV=2 - [USPG_ECOLI]	6.88	66.90	1	5	5	5	142	15.9	6.52
P0A8A2	Probable transcriptional regulatory protein YeeN OS=Escherichia coli (strain K12) GN=yeeN PE=1 SV=1 - [YEEN_ECOLI]	6.88	9.24	1	1	1	5	238	25.9	4.82
P08839	Phosphoenolpyruvate-protein phosphotransferase OS=Escherichia coli (strain K12) GN=ptsI PE=1 SV=1 - [PTI_ECOLI]	6.86	8.70	1	3	3	3	575	63.5	4.87
P0AEQ3	Glutamine-binding periplasmic protein OS=Escherichia coli (strain K12) GN=glnH PE=1 SV=1 - [GLNH_ECOLI]	6.76	21.37	1	3	3	3	248	27.2	8.51
P0AEK2	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Escherichia coli (strain K12) GN=fabG PE=1 SV=1 - [FABG_ECOLI]	6.74	14.75	1	2	2	2	244	25.5	7.42
P0AEM0	FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase OS=Escherichia coli (strain K12) GN=fkpB PE=1 SV=2 - [FKBX_ECOLI]	6.73	30.87	1	2	2	2	149	16.1	4.44
P0A8W8	UPF0304 protein YfbU OS=Escherichia coli (strain K12) GN=yfbU PE=1 SV=1 - [YFBU_ECOLI]	6.69	38.41	1	4	4	4	164	19.5	6.52
P0AC59	Glutaredoxin-2 OS=Escherichia coli (strain K12) GN=grxB PE=1 SV=1 - [GLRX2_ECOLI]	6.60	26.05	1	4	4	4	215	24.3	7.96
P0A9M8	Phosphate acetyltransferase OS=Escherichia coli (strain K12) GN=pta PE=1 SV=2 - [PTA_ECOLI]	6.37	8.96	1	4	4	4	714	77.1	5.41
P0AEU7	Chaperone protein Skp OS=Escherichia coli (strain K12) GN=skp PE=1 SV=1 - [SKP_ECOLI]	6.34	39.13	1	4	4	4	161	17.7	9.70
P0AD33	UPF0381 protein YfcZ OS=Escherichia coli (strain K12) GN=yfcZ PE=3 SV=1 - [YFCZ_ECOLI]	6.31	27.66	1	2	2	2	94	10.3	4.36
P0A7T3	30S ribosomal protein S16 OS=Escherichia coli (strain K12) GN=rpsP PE=1 SV=1 - [RS16_ECOLI]	6.30	32.93	1	2	2	2	82	9.2	10.55
P0A7N4	50S ribosomal protein L32 OS=Escherichia coli (strain K12) GN=rpmF PE=1 SV=2 - [RL32_ECOLI]	6.20	52.63	1	3	3	3	57	6.4	11.03
P0ADP9	Protein YihD OS=Escherichia coli (strain K12) GN=yihD PE=1 SV=1 - [YIHD_ECOLI]	6.11	57.30	1	3	3	5	89	10.3	5.26
P02925	Ribose import binding protein RbsB OS=Escherichia coli (strain K12) GN=rbsB PE=1 SV=1 - [RBSB_ECOLI]	5.98	17.57	1	2	2	2	296	30.9	7.47
P0A6K6	Phosphopentomutase OS=Escherichia coli (strain K12) GN=deoB PE=1 SV=1 - [DEOB_ECOLI]	5.86	11.79	1	4	4	4	407	44.3	5.29
P0AG63	30S ribosomal protein S17 OS=Escherichia coli (strain K12) GN=rpsQ PE=1 SV=2 - [RS17_ECOLI]	5.83	22.62	1	1	1	2	84	9.7	9.60
P0AAC8	Iron-binding protein IscA OS=Escherichia coli (strain K12) GN=iscA PE=1 SV=1 - [ISCA_ECOLI]	5.78	45.79	1	3	3	3	107	11.5	4.88
P67603	UPF0267 protein YqfB OS=Escherichia coli (strain K12) GN=yqfB PE=1 SV=1 - [YQFB_ECOLI]	5.77	56.31	1	3	3	3	103	11.9	4.82
P0AFM6	Phage shock protein A OS=Escherichia coli (strain K12) GN=pspA PE=1 SV=2 - [PSPA_ECOLI]	5.67	16.67	1	2	2	2	222	25.5	5.49
P0A7K6	50S ribosomal protein L19 OS=Escherichia coli (strain K12) GN=rplS PE=1 SV=2 - [RL19_ECOLI]	5.61	24.35	1	3	3	3	115	13.1	10.62
P0A800	DNA-directed RNA polymerase subunit omega OS=Escherichia coli (strain K12) GN=rpoZ PE=1 SV=1 - [RPOZ_ECOLI]	5.58	30.77	1	2	2	2	91	10.2	4.92
P0ADS2	Cell division protein ZapA OS=Escherichia coli (strain K12) GN=zapA PE=1 SV=1 - [ZAPA_ECOLI]	5.51	25.69	1	2	2	2	109	12.6	5.25
P0A8J4	UPF0250 protein YbeD OS=Escherichia coli (strain K12) GN=ybeD PE=1 SV=1 - [YBED_ECOLI]	5.45	37.93	1	2	2	2	87	9.8	5.76
P00448	Superoxide dismutase [Mn] OS=Escherichia coli (strain K12) GN=sodA PE=1 SV=2 - [SODM_ECOLI]	5.42	9.71	1	2	2	3	206	23.1	6.96
P0ACE7	HIT-like protein HinT OS=Escherichia coli (strain K12) GN=hinT PE=1 SV=1 - [HINT_ECOLI]	5.36	42.86	1	2	2	3	119	13.2	6.18
P15288	Cytosol non-specific dipeptidase OS=Escherichia coli (strain K12) GN=pepD PE=1 SV=3 - [PEPD_ECOLI]	5.28	8.66	1	2	2	2	485	52.9	5.39
P0A746	Peptide methionine sulfoxide reductase MsrB OS=Escherichia coli (strain K12) GN=msrB PE=1 SV=1 - [MSRB_ECOLI]	5.27	28.47	1	2	2	3	137	15.4	5.94
P64596	Uncharacterized protein YraP OS=Escherichia coli (strain K12) GN=yraP PE=3 SV=1 - [YRAP_ECOLI]	5.19	20.42	1	3	3	3	191	20.0	8.98
P0A9W9	Protein YrdA OS=Escherichia coli (strain K12) GN=yrdA PE=1 SV=1 - [YRDA_ECOLI]	5.12	15.22	1	2	2	2	184	20.2	5.55
P0ABD8	Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli (strain K12) GN=accB PE=1 SV=1 - [BCCP_ECOLI]	5.09	15.38	1	2	2	2	156	16.7	4.65
P0ADN2	UPF0438 protein YifE OS=Escherichia coli (strain K12) GN=yifE PE=1 SV=2 - [YIFE_ECOLI]	5.09	43.75	1	3	3	3	112	13.1	6.55
P37188	Galactitol-specific phosphotransferase enzyme IIB component OS=Escherichia coli (strain K12) GN=gatB PE=1 SV=2 - [PTKB_ECOLI]	5.00	46.81	1	2	2	2	94	10.2	6.27
P0A6T9	Glycine cleavage system H protein OS=Escherichia coli (strain K12) GN=gcvH PE=1 SV=2 - [GCSH_ECOLI]	4.98	19.38	1	2	2	2	129	13.8	4.09
P0ADY1	Peptidyl-prolyl cis-trans isomerase D OS=Escherichia coli (strain K12) GN=ppiD PE=1 SV=1 - [PPID_ECOLI]	4.97	17.34	1	5	5	7	623	68.1	5.07
P0A6Y1	Integration host factor subunit beta OS=Escherichia coli (strain K12) GN=ihfB PE=1 SV=1 - [IHFB_ECOLI]	4.90	34.04	1	3	3	3	94	10.6	9.35
P33014	UPF0033 protein YeeD OS=Escherichia coli (strain K12) GN=yeeD PE=1 SV=1 - [YEED_ECOLI]	4.88	22.67	1	2	2	2	75	8.1	4.28
P0A870	Transaldolase B OS=Escherichia coli (strain K12) GN=talB PE=1 SV=2 - [TALB_ECOLI]	4.80	11.67	2	2	2	2	317	35.2	5.21
P06616	GTPase Era OS=Escherichia coli (strain K12) GN=era PE=1 SV=2 - [ERA_ECOLI]	4.77	9.63	1	2	2	2	301	33.8	7.25
P0A8K5	UPF0253 protein YaeP OS=Escherichia coli (strain K12) GN=yaeP PE=1 SV=1 - [YAEF_ECOLI]	4.76	56.06	1	2	2	2	66	7.2	4.56
P05055	Polyribonucleotide nucleotidyltransferase OS=Escherichia coli (strain K12) GN=pnp PE=1 SV=3 - [PNP_ECOLI]	4.73	6.33	1	3	3	3	711	77.1	5.21
P0A6Z1	Chaperone protein HscA OS=Escherichia coli (strain K12) GN=hscA PE=1 SV=1 - [HSCA_ECOLI]	4.73	12.50	1	3	3	3	616	65.6	5.16
P0A9Q1	Aerobic respiration control protein ArcA OS=Escherichia coli (strain K12) GN=arcA PE=1 SV=1 - [ARCA_ECOLI]	4.70	20.59	1	3	3	3	238	27.3	5.33
P0A707	Translation initiation factor IF-3 OS=Escherichia coli (strain K12) GN=infC PE=1 SV=1 - [IF3_ECOLI]	4.67	18.89	1	2	2	2	180	20.6	9.52
P0A7V8	30S ribosomal protein S4 OS=Escherichia coli (strain K12) GN=rpsD PE=1 SV=2 - [RS4_ECOLI]	4.61	27.67	1	4	4	4	206	23.5	10.05
P0AB52	Protein YchN OS=Escherichia coli (strain K12) GN=ychn PE=1 SV=1 - [YCHN_ECOLI]	4.49	28.21	1	2	2	2	117	12.7	5.11
P0AD49	Ribosome-associated inhibitor A OS=Escherichia coli (strain K12) GN=raiA PE=1 SV=2 - [RAIA_ECOLI]	4.44	30.97	1	2	2	2	113	12.8	6.68
P27434	Cytoskeleton protein RodZ OS=Escherichia coli (strain K12) GN=rodZ PE=1 SV=2 - [RODZ_ECOLI]	4.44	15.13	1	3	3	3	337	36.2	5.80
P0A9D8	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Escherichia coli (strain K12) GN=dapD PE=1 SV=1 - [DAPD_ECOLI]	4.19	15.69	1	3	3	3	274	29.9	5.74
P0ADU5	Protein YgiW OS=Escherichia coli (strain K12) GN=ygiW PE=1 SV=1 - [YGIW_ECOLI]	4.16	8.46	1	1	1	2	130	14.0	5.26

P0C0L9	Protein IscX OS=Escherichia coli (strain K12) GN=iscX PE=1 SV=1 - [ISCX_ECOLI]	3.99	36.36	1	1	1	1	66	7.7	4.12
P0AB61	Protein YciN OS=Escherichia coli (strain K12) GN=yciN PE=1 SV=1 - [YGIN_ECOLI]	3.85	31.33	1	2	2	2	83	9.4	5.73
POA955	KHG/KDPG aldolase OS=Escherichia coli (strain K12) GN=eda PE=1 SV=1 - [ALKH_ECOLI]	3.82	15.02	1	2	2	2	213	22.3	5.67
P68688	Glutaredoxin-1 OS=Escherichia coli (strain K12) GN=grxA PE=1 SV=1 - [GLRX1_ECOLI]	3.80	18.82	1	1	1	1	85	9.7	4.97
P65556	Uncharacterized Nudix hydrolase YfcD OS=Escherichia coli (strain K12) GN=yfcD PE=1 SV=1 - [YFCD_ECOLI]	3.69	12.78	1	1	1	1	180	20.4	4.72
P0A799	Phosphoglycerate kinase OS=Escherichia coli (strain K12) GN=pgk PE=1 SV=2 - [PGK_ECOLI]	3.66	10.08	1	2	2	2	387	41.1	5.22
POA6Z3	Chaperone protein HtpG OS=Escherichia coli (strain K12) GN=htpG PE=1 SV=1 - [HTPG_ECOLI]	3.50	7.21	1	3	3	4	624	71.4	5.21
P69776	Major outer membrane lipoprotein Lpp OS=Escherichia coli (strain K12) GN=lpp PE=1 SV=1 - [LPP_ECOLI]	3.49	15.38	1	1	1	1	78	8.3	9.25
POAEG4	Thiol:disulfide interchange protein DsbA OS=Escherichia coli (strain K12) GN=dsbA PE=1 SV=1 - [DSBA_ECOLI]	3.42	13.94	1	1	1	1	208	23.1	6.34
P27838	Protein CyaY OS=Escherichia coli (strain K12) GN=cyaY PE=1 SV=1 - [CYAY_ECOLI]	3.40	11.32	1	1	1	1	106	12.2	4.41
POAF28	Nitrate/nitrite response regulator protein NarL OS=Escherichia coli (strain K12) GN=narL PE=1 SV=1 - [NARL_ECOLI]	3.25	11.57	1	1	1	1	216	23.9	6.07
P09394	Glycerophosphoryl diester phosphodiesterase OS=Escherichia coli (strain K12) GN=glpQ PE=1 SV=2 - [GLPQ_ECOLI]	3.21	3.35	1	1	1	1	358	40.8	5.60
POA7B8	ATP-dependent protease subunit HslV OS=Escherichia coli (strain K12) GN=hslV PE=1 SV=2 - [HSLV_ECOLI]	3.20	6.25	1	1	1	1	176	19.1	6.39
P45955	Uncharacterized protein YbgF OS=Escherichia coli (strain K12) GN=ybgF PE=1 SV=2 - [YBGF_ECOLI]	3.14	16.35	1	1	1	2	263	28.2	8.65
P22259	Phosphoenolpyruvate carboxykinase [ATP] OS=Escherichia coli (strain K12) GN=pckA PE=1 SV=2 - [PCKA_ECOLI]	3.07	4.63	1	1	1	1	540	59.6	5.71
POA1I3	ATP-dependent zinc metalloprotease FtsH OS=Escherichia coli (strain K12) GN=ftsH PE=1 SV=1 - [FTSH_ECOLI]	3.07	2.64	1	1	1	1	644	70.7	6.24
P76270	Free methionine-R-sulfoxide reductase OS=Escherichia coli (strain K12) GN=msrC PE=1 SV=2 - [MSRC_ECOLI]	3.03	9.70	1	1	1	1	165	18.1	4.83
P37349	PTS-dependent dihydroxyacetone kinase, phosphotransferase subunit DhaM OS=Escherichia coli (strain K12) GN=dhaM PE=1 SV=3 - [DHAM_ECOLI]	3.02	7.42	1	2	2	2	472	51.4	4.73
POAFW8	Protein of OS=Escherichia coli (strain K12) GN=rof PE=1 SV=1 - [ROF_ECOLI]	2.95	17.86	1	1	1	1	84	9.5	4.74
POA7T7	30S ribosomal protein S18 OS=Escherichia coli (strain K12) GN=rpsR PE=1 SV=2 - [RS18_ECOLI]	2.91	16.00	1	1	1	1	75	9.0	10.59
P46859	Thermoresistant gluconokinase OS=Escherichia coli (strain K12) GN=gntK PE=1 SV=4 - [GNTK_ECOLI]	2.91	13.71	1	1	1	2	175	19.5	6.73
P68191	Stationary-phase-induced ribosome-associated protein OS=Escherichia coli (strain K12) GN=sra PE=1 SV=1 - [SRA_ECOLI]	2.90	40.00	1	1	1	1	45	5.1	11.05
POADY3	50S ribosomal protein L14 OS=Escherichia coli (strain K12) GN=rplN PE=1 SV=1 - [RL14_ECOLI]	2.84	14.63	1	2	2	2	123	13.5	10.42
P42596	Ribosomal RNA large subunit methyltransferase G OS=Escherichia coli (strain K12) GN=rImG PE=1 SV=2 - [RLMG_ECOLI]	2.81	9.52	1	1	1	1	378	42.3	6.80
POAC62	Glutaredoxin-3 OS=Escherichia coli (strain K12) GN=grxC PE=1 SV=2 - [GLRX3_ECOLI]	2.78	18.07	1	1	1	1	83	9.1	7.24
POA6X7	Integration host factor subunit alpha OS=Escherichia coli (strain K12) GN=ihfA PE=1 SV=1 - [IHFA_ECOLI]	2.75	11.11	1	1	1	1	99	11.3	9.35
POA8G6	NAD(P)H dehydrogenase (quinone) OS=Escherichia coli (strain K12) GN=wrbA PE=1 SV=2 - [NQOR_ECOLI]	2.74	9.09	1	1	1	1	198	20.8	5.86
POA7S9	30S ribosomal protein S13 OS=Escherichia coli (strain K12) GN=rpsM PE=1 SV=2 - [RS13_ECOLI]	2.74	27.97	1	2	2	2	118	13.1	10.78
POABU5	Enhancing lycopene biosynthesis protein 2 OS=Escherichia coli (strain K12) GN=elbB PE=1 SV=1 - [ELBB_ECOLI]	2.72	12.44	1	1	1	1	217	23.0	4.77
P69222	Translation initiation factor IF-1 OS=Escherichia coli (strain K12) GN=infA PE=1 SV=2 - [IF1_ECOLI]	2.68	25.00	1	1	1	1	72	8.2	9.25
P67095	Phosphodiesterase YfcE OS=Escherichia coli (strain K12) GN=yfcE PE=1 SV=1 - [YFCE_ECOLI]	2.68	14.67	1	1	1	2	184	20.1	6.05
POAFG8	Pyruvate dehydrogenase E1 component OS=Escherichia coli (strain K12) GN=aceE PE=1 SV=2 - [ODP1_ECOLI]	2.64	3.38	1	2	2	2	887	99.6	5.68
P19926	Glucose-1-phosphatase OS=Escherichia coli (strain K12) GN=agp PE=1 SV=1 - [AGP_ECOLI]	2.63	10.65	1	2	2	3	413	45.7	5.73
POA6A3	Acetate kinase OS=Escherichia coli (strain K12) GN=ackA PE=1 SV=1 - [ACKA_ECOLI]	2.62	10.00	1	2	2	4	400	43.3	6.28
P68206	UPF0337 protein YjbJ OS=Escherichia coli (strain K12) GN=yjbJ PE=1 SV=1 - [YJB1_ECOLI]	2.62	26.09	1	1	1	1	69	8.3	5.55
P50466	Aerotaxis receptor OS=Escherichia coli (strain K12) GN=aer PE=1 SV=1 - [AER_ECOLI]	2.62	5.34	1	1	1	1	506	55.0	7.99
P24232	Flavohepomeprotein OS=Escherichia coli (strain K12) GN=hmp PE=1 SV=1 - [HMP_ECOLI]	2.59	5.56	1	1	1	1	396	43.8	5.77
POA7W7	30S ribosomal protein S8 OS=Escherichia coli (strain K12) GN=rpsH PE=1 SV=2 - [RS8_ECOLI]	2.59	23.85	1	1	1	1	130	14.1	9.42
POA7E5	CTP synthase OS=Escherichia coli (strain K12) GN=pyrG PE=1 SV=2 - [PYRG_ECOLI]	2.57	10.28	1	3	3	3	545	60.3	5.94
P11557	Cell division protein DamX OS=Escherichia coli (strain K12) GN=damX PE=1 SV=2 - [DAMX_ECOLI]	2.55	2.10	1	1	1	1	428	46.1	5.81
POADZ0	50S ribosomal protein L23 OS=Escherichia coli (strain K12) GN=rplW PE=1 SV=1 - [RL23_ECOLI]	2.55	12.00	1	1	1	1	100	11.2	9.94
P60422	50S ribosomal protein L2 OS=Escherichia coli (strain K12) GN=rplB PE=1 SV=2 - [RL2_ECOLI]	2.55	8.06	1	1	1	1	273	29.8	10.93
POAEN8	L-fucose mutarotase OS=Escherichia coli (strain K12) GN=fucJ PE=1 SV=1 - [FUCM_ECOLI]	2.54	17.14	1	2	2	2	140	15.5	5.86
POA9Z1	Nitrogen regulatory protein P-II 1 OS=Escherichia coli (strain K12) GN=glnB PE=1 SV=1 - [GLNB_ECOLI]	2.53	9.82	1	1	1	1	112	12.4	5.34
POAEG6	Thiol:disulfide interchange protein DsbC OS=Escherichia coli (strain K12) GN=dsbC PE=1 SV=1 - [DSBC_ECOLI]	2.53	6.78	1	1	1	1	236	25.6	6.79
POA7R5	30S ribosomal protein S10 OS=Escherichia coli (strain K12) GN=rpsJ PE=1 SV=1 - [RS10_ECOLI]	2.46	37.86	1	3	3	4	103	11.7	9.69
P75779	PKHD-type hydroxylase YbiX OS=Escherichia coli (strain K12) GN=ybiX PE=3 SV=2 - [YBIX_ECOLI]	2.44	10.67	1	1	1	1	225	25.5	6.42
POAA16	Transcriptional regulatory protein OmpR OS=Escherichia coli (strain K12) GN=ompR PE=1 SV=1 - [OMPR_ECOLI]	2.39	13.39	1	2	2	2	239	27.3	6.39
POA903	Outer membrane protein assembly factor BamC OS=Escherichia coli (strain K12) GN=bamC PE=1 SV=1 - [BAMC_ECOLI]	2.39	11.92	1	2	2	2	344	36.8	5.57
P32662	Phosphoglycolate phosphatase OS=Escherichia coli (strain K12) GN=gph PE=1 SV=1 - [GPH_ECOLI]	2.39	10.32	1	1	1	2	252	27.4	4.72
P10100	Rare lipoprotein A OS=Escherichia coli (strain K12) GN=rIpA PE=1 SV=1 - [RLPA_ECOLI]	2.39	3.87	1	1	1	1	362	37.5	5.73
POA7U7	30S ribosomal protein S20 OS=Escherichia coli (strain K12) GN=rpsT PE=1 SV=2 - [RS20_ECOLI]	2.38	12.64	1	1	1	1	87	9.7	11.18
P0C0L2	Peroxioredoxin OsmC OS=Escherichia coli (strain K12) GN=osmC PE=1 SV=2 - [OSMC_ECOLI]	2.36	15.38	1	1	1	1	143	15.1	5.86
POC8I8	D-tagatose-1,6-bisphosphate aldolase subunit GatZ OS=Escherichia coli (strain K12) GN=gatZ PE=1 SV=1 - [GATZ_ECOLI]	2.35	11.43	1	2	2	2	420	47.1	5.77
POAG44	50S ribosomal protein L17 OS=Escherichia coli (strain K12) GN=rplQ PE=1 SV=1 - [RL17_ECOLI]	2.35	11.81	1	1	1	1	127	14.4	11.05
P61175	50S ribosomal protein L22 OS=Escherichia coli (strain K12) GN=rplV PE=1 SV=1 - [RL22_ECOLI]	2.34	10.00	1	1	1	1	110	12.2	10.23

P75874	Uncharacterized protein YccU OS=Escherichia coli (strain K12) GN=yccU PE=1 SV=2 - [YCCU_ECOLI]	2.33	13.14	1	1	1	1	137	14.7	7.34
P16700	Thiosulfate-binding protein OS=Escherichia coli (strain K12) GN=cysP PE=1 SV=1 - [CYSP_ECOLI]	2.31	9.76	1	2	2	3	338	37.6	8.15
POA6J1	Adenyllyl-sulfate kinase OS=Escherichia coli (strain K12) GN=cysC PE=1 SV=2 - [CYSC_ECOLI]	2.23	7.96	1	1	1	1	201	22.3	6.37
POAEU0	Histidine-binding periplasmic protein OS=Escherichia coli (strain K12) GN=hisJ PE=1 SV=1 - [HISJ_ECOLI]	2.22	4.23	1	1	1	1	260	28.5	5.60
P76002	Inhibitor of g-type lysozyme OS=Escherichia coli (strain K12) GN=pliG PE=1 SV=1 - [PLIG_ECOLI]	2.21	20.30	1	1	1	1	133	14.9	9.50
POAG78	Sulfate-binding protein OS=Escherichia coli (strain K12) GN=sbp PE=1 SV=1 - [SUBI_ECOLI]	2.21	3.95	1	1	1	1	329	36.6	7.15
POA6H1	ATP-dependent Clp protease ATP-binding subunit ClpX OS=Escherichia coli (strain K12) GN=clpX PE=1 SV=2 - [CLPX_ECOLI]	2.19	13.21	1	3	3	3	424	46.3	5.35
P76027	Oligopeptide transport ATP-binding protein OppD OS=Escherichia coli (strain K12) GN=oppD PE=3 SV=2 - [OPPD_ECOLI]	2.18	5.93	1	1	1	1	337	37.2	6.10
P62768	UPF0325 protein YaeH OS=Escherichia coli (strain K12) GN=yaeH PE=3 SV=1 - [YAEH_ECOLI]	2.17	9.38	1	1	1	1	128	15.1	7.18
P31802	Nitrate/nitrite response regulator protein NarP OS=Escherichia coli (strain K12) GN=narP PE=3 SV=1 - [NARP_ECOLI]	2.16	5.58	1	1	1	1	215	23.6	4.97
P22524	Chromosome partition protein MukE OS=Escherichia coli (strain K12) GN=mukE PE=1 SV=5 - [MUKE_ECOLI]	2.14	5.13	1	1	1	1	234	27.0	5.00
ASA614	UPF0509 protein YciZ OS=Escherichia coli (strain K12) GN=yicZ PE=3 SV=1 - [YCIZ_ECOLI]	2.13	70.18	1	2	2	2	57	6.4	4.65
P10408	Protein translocase subunit SecA OS=Escherichia coli (strain K12) GN=secA PE=1 SV=2 - [SECA_ECOLI]	2.12	3.00	1	1	1	3	901	102.0	5.60
POA6N8	Elongation factor P-like protein OS=Escherichia coli (strain K12) GN=yefP PE=1 SV=1 - [EFPL_ECOLI]	2.11	5.26	1	1	1	1	190	21.5	5.02
POABA4	ATP synthase subunit delta OS=Escherichia coli (strain K12) GN=atpH PE=1 SV=1 - [ATPD_ECOLI]	2.10	19.77	1	2	2	3	177	19.3	5.02
POAB71	Fructose-bisphosphate aldolase class 2 OS=Escherichia coli (strain K12) GN=fbaA PE=1 SV=2 - [ALF_ECOLI]	2.10	16.43	1	2	2	3	359	39.1	5.86
POABZ6	Chaperone SurA OS=Escherichia coli (strain K12) GN=surA PE=1 SV=1 - [SJURA_ECOLI]	2.10	5.14	1	2	2	2	428	47.3	6.98
P18390	Uncharacterized protein YjjA OS=Escherichia coli (strain K12) GN=yjjA PE=3 SV=3 - [YJJA_ECOLI]	2.07	14.02	1	1	1	1	164	17.3	5.94
P39173	Putative glucose-6-phosphate 1-epimerase OS=Escherichia coli (strain K12) GN=yead PE=1 SV=2 - [YEAD_ECOLI]	2.07	15.99	1	2	2	2	294	32.6	6.34
P24251	Sigma factor-binding protein Crl OS=Escherichia coli (strain K12) GN=crl PE=1 SV=5 - [CRL_ECOLI]	2.07	9.02	1	1	1	1	133	15.6	6.79
P31979	NADH-quinone oxidoreductase subunit F OS=Escherichia coli (strain K12) GN=nuoF PE=1 SV=3 - [NUOF_ECOLI]	2.06	3.60	1	1	1	1	445	49.3	6.86
POAD05	Uncharacterized protein YecA OS=Escherichia coli (strain K12) GN=yecA PE=4 SV=1 - [YECA_ECOLI]	2.06	7.69	1	1	1	2	221	25.0	4.59
P10121	Signal recognition particle receptor FtsY OS=Escherichia coli (strain K12) GN=ftsY PE=1 SV=1 - [FTSY_ECOLI]	2.04	3.82	1	1	1	1	497	54.5	4.50
POABH0	Cell division protein FtsA OS=Escherichia coli (strain K12) GN=ftsA PE=1 SV=1 - [FTSA_ECOLI]	2.00	4.29	1	1	1	1	420	45.3	6.24
POAA10	50S ribosomal protein L13 OS=Escherichia coli (strain K12) GN=rplM PE=1 SV=1 - [RL13_ECOLI]	1.98	7.75	1	1	1	1	142	16.0	9.91
POA6C8	Acetylglutamate kinase OS=Escherichia coli (strain K12) GN=argB PE=1 SV=1 - [ARGB_ECOLI]	1.95	14.34	1	2	2	2	258	27.1	5.62
POA6W5	Transcription elongation factor GreA OS=Escherichia coli (strain K12) GN=greA PE=1 SV=1 - [GREA_ECOLI]	1.93	13.29	1	1	1	1	158	17.6	4.79
P76576	UPF0070 protein YfgM OS=Escherichia coli (strain K12) GN=yfgM PE=3 SV=1 - [YFGM_ECOLI]	1.89	8.74	1	1	1	1	206	22.2	5.16
POA910	Outer membrane protein A OS=Escherichia coli (strain K12) GN=ompA PE=1 SV=1 - [OMPA_ECOLI]	1.83	3.76	1	1	1	1	346	37.2	6.42
P39325	ABC transporter periplasmic-binding protein YtfQ OS=Escherichia coli (strain K12) GN=ytfQ PE=1 SV=1 - [YTFQ_ECOLI]	1.81	5.03	1	1	1	1	318	34.3	7.14
POA734	Cell division topological specificity factor OS=Escherichia coli (strain K12) GN=minE PE=1 SV=1 - [MINE_ECOLI]	1.81	22.73	1	1	1	1	88	10.2	5.24
POACX3	Putative monooxygenase YdhR OS=Escherichia coli (strain K12) GN=ydhR PE=1 SV=1 - [YDHR_ECOLI]	1.80	14.85	1	1	1	1	101	11.3	5.15
POA7Q1	50S ribosomal protein L35 OS=Escherichia coli (strain K12) GN=rplM PE=1 SV=2 - [RL35_ECOLI]	1.79	20.00	1	1	1	1	65	7.3	11.78
POAC19	Dihydroneopterin triphosphate 2'-epimerase OS=Escherichia coli (strain K12) GN=folX PE=1 SV=2 - [FOLX_ECOLI]	1.77	10.00	1	1	1	1	120	14.1	7.06
POAFH8	Osmotically-inducible protein Y OS=Escherichia coli (strain K12) GN=osmY PE=1 SV=1 - [OSMY_ECOLI]	1.77	11.44	1	2	2	2	201	21.1	6.81
POAF36	Cell division protein ZapB OS=Escherichia coli (strain K12) GN=zapB PE=1 SV=1 - [ZAPB_ECOLI]	1.73	34.57	1	2	2	3	81	9.6	4.67
P27842	Uncharacterized protein YigF OS=Escherichia coli (strain K12) GN=yigF PE=4 SV=1 - [YIGF_ECOLI]	1.72	10.32	1	1	1	1	126	14.5	9.60
POA6K3	Peptide deformylase OS=Escherichia coli (strain K12) GN=def PE=1 SV=2 - [DEF_ECOLI]	1.71	6.51	1	1	1	1	169	19.3	5.35
POAD56	Uncharacterized protein YggE OS=Escherichia coli (strain K12) GN=yggE PE=4 SV=1 - [YGGE_ECOLI]	1.70	6.10	1	1	1	1	246	26.6	6.57
P76014	PTS-dependent dihydroxyacetone kinase, ADP-binding subunit DhaL OS=Escherichia coli (strain K12) GN=dhaL PE=1 SV=3 - [DHAL_ECOLI]	1.70	6.19	1	1	1	1	210	22.6	5.41
P00961	Glycine-tRNA ligase beta subunit OS=Escherichia coli (strain K12) GN=glyS PE=1 SV=4 - [SYGB_ECOLI]	1.69	10.16	1	3	3	3	689	76.8	5.44
POAG51	50S ribosomal protein L30 OS=Escherichia coli (strain K12) GN=rplM PE=1 SV=2 - [RL30_ECOLI]	1.69	15.25	1	1	1	1	59	6.5	10.96
P60723	50S ribosomal protein L4 OS=Escherichia coli (strain K12) GN=rplD PE=1 SV=1 - [RL4_ECOLI]	1.69	7.46	1	1	1	1	201	22.1	9.73
POA8P3	Probable Fe(2+)-trafficking protein OS=Escherichia coli (strain K12) GN=yggX PE=1 SV=2 - [FETP_ECOLI]	1.68	15.38	1	1	1	1	91	10.9	6.30
POAGG4	Thioredoxin-2 OS=Escherichia coli (strain K12) GN=trxC PE=1 SV=1 - [THIO2_ECOLI]	1.65	17.27	1	2	2	2	139	15.5	5.17
POA9Q5	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Escherichia coli (strain K12) GN=accD PE=1 SV=1 - [ACCD_ECOLI]	1.63	4.28	1	1	1	1	304	33.3	7.68
POACX5	Uncharacterized protein YdhZ OS=Escherichia coli (strain K12) GN=ydhZ PE=4 SV=1 - [YDHZ_ECOLI]	1.62	17.39	1	1	1	1	69	7.9	9.31
POADU2	Probable quinol monooxygenase YgiN OS=Escherichia coli (strain K12) GN=ygiN PE=1 SV=1 - [YGIN_ECOLI]	1.62	8.65	1	1	1	1	104	11.5	6.24
POAD24	UPF0352 protein YejL OS=Escherichia coli (strain K12) GN=yejL PE=1 SV=1 - [YEJL_ECOLI]	0.00	38.67	1	1	1	1	75	8.3	5.78
POA8R4	Protein SlyX OS=Escherichia coli (strain K12) GN=slyX PE=3 SV=1 - [SLYX_ECOLI]	0.00	29.17	1	1	1	1	72	8.2	4.92
POA6D0	Arginine repressor OS=Escherichia coli (strain K12) GN=argR PE=1 SV=1 - [ARGR_ECOLI]	0.00	14.74	1	1	1	1	156	17.0	5.03
POA9X9	Cold shock protein CspA OS=Escherichia coli (strain K12) GN=cspA PE=1 SV=2 - [CSPA_ECOLI]	0.00	21.43	1	1	1	1	70	7.4	5.95
P28631	DNA polymerase III subunit delta' OS=Escherichia coli (strain K12) GN=holB PE=1 SV=2 - [HOLB_ECOLI]	0.00	10.48	1	1	1	1	334	36.9	7.05
P23827	Ecotin OS=Escherichia coli (strain K12) GN=eco PE=1 SV=1 - [ECOT_ECOLI]	0.00	8.64	1	1	1	1	162	18.2	7.12
POA6R3	DNA-binding protein Fis OS=Escherichia coli (strain K12) GN=fis PE=1 SV=1 - [FIS_ECOLI]	0.00	27.55	1	1	1	1	98	11.2	9.35
P61949	Flavodoxin-1 OS=Escherichia coli (strain K12) GN=fldA PE=1 SV=2 - [FLAV_ECOLI]	0.00	10.80	1	1	1	1	176	19.7	4.39

P0A9M5	Xanthine phosphoribosyltransferase OS=Escherichia coli (strain K12) GN=gpt PE=1 SV=1 - [XGPT_ECOLI]	0.00	25.66	1	2	2	2	152	17.0	5.85
P0A780	N utilization substance protein B OS=Escherichia coli (strain K12) GN=nusB PE=1 SV=1 - [NUSB_ECOLI]	0.00	5.76	1	1	1	1	139	15.7	7.18
P0AFZ3	Stringent starvation protein B OS=Escherichia coli (strain K12) GN=sspB PE=1 SV=1 - [SSPB_ECOLI]	0.00	16.97	1	2	2	2	165	18.3	4.55
P19934	Protein TolA OS=Escherichia coli (strain K12) GN=tolA PE=1 SV=1 - [TOLA_ECOLI]	0.00	2.38	1	1	1	1	421	43.1	9.07
P0A8X0	UPF0307 protein YjgA OS=Escherichia coli (strain K12) GN=yjgA PE=1 SV=1 - [YJGA_ECOLI]	0.00	11.48	1	1	1	1	183	21.3	5.45
P0AAX8	Probable L,D-transpeptidase YbiS OS=Escherichia coli (strain K12) GN=ybiS PE=1 SV=1 - [YBIS_ECOLI]	0.00	8.82	1	1	1	1	306	33.3	6.40
P0AB33	Biofilm regulator BssS OS=Escherichia coli (strain K12) GN=bssS PE=2 SV=1 - [BSSS_ECOLI]	0.00	14.29	1	1	1	1	84	9.7	4.92
P16095	L-serine dehydratase 1 OS=Escherichia coli (strain K12) GN=sdaA PE=1 SV=3 - [SDHL_ECOLI]	0.00	7.93	1	1	1	1	454	48.9	5.34
P23857	Thiosulfate sulfurtransferase PspE OS=Escherichia coli (strain K12) GN=pspE PE=1 SV=1 - [PSPE_ECOLI]	0.00	21.15	1	1	1	1	104	11.5	8.15
P0A763	Nucleoside diphosphate kinase OS=Escherichia coli (strain K12) GN=ndk PE=1 SV=2 - [NDK_ECOLI]	0.00	22.38	1	2	2	2	143	15.5	5.81
P0A815	tRNA (guanine-N(7)-)-methyltransferase OS=Escherichia coli (strain K12) GN=trmB PE=1 SV=1 - [TRMB_ECOLI]	0.00	5.02	1	1	1	1	239	27.3	6.92
P62399	50S ribosomal protein L5 OS=Escherichia coli (strain K12) GN=rplE PE=1 SV=2 - [RL5_ECOLI]	0.00	18.44	1	2	2	2	179	20.3	9.48
P0A5E6	DNA gyrase subunit B OS=Escherichia coli (strain K12) GN=gyrB PE=1 SV=2 - [GYRB_ECOLI]	0.00	5.10	1	2	2	2	804	89.9	6.06
P0A988	DNA polymerase III subunit beta OS=Escherichia coli (strain K12) GN=dnaN PE=1 SV=1 - [DPO3B_ECOLI]	0.00	7.10	1	1	1	2	366	40.6	5.39
P0A9Q9	Aspartate-semialdehyde dehydrogenase OS=Escherichia coli (strain K12) GN=asd PE=1 SV=1 - [DHAS_ECOLI]	0.00	10.63	1	1	1	2	367	40.0	5.58
P0A7N9	50S ribosomal protein L33 OS=Escherichia coli (strain K12) GN=rpmG PE=1 SV=2 - [RL33_ECOLI]	0.00	30.91	1	1	1	1	55	6.4	10.24
P0AF50	Uncharacterized protein Yjbr OS=Escherichia coli (strain K12) GN=yjbr PE=1 SV=1 - [YJBR_ECOLI]	0.00	8.47	1	1	1	1	118	13.5	6.52
P0A6N4	Elongation factor P OS=Escherichia coli (strain K12) GN=efp PE=1 SV=2 - [EFP_ECOLI]	0.00	6.38	1	1	1	1	188	20.6	5.02
P0AF90	Regulator of ribonuclease activity B OS=Escherichia coli (strain K12) GN=rraB PE=1 SV=1 - [RRAB_ECOLI]	0.00	23.91	1	1	1	1	138	15.6	3.80
P75770	Inner membrane protein YbhN OS=Escherichia coli (strain K12) GN=ybhN PE=1 SV=1 - [YBHN_ECOLI]	0.00	5.97	1	1	1	1	318	35.8	9.77
P0AAV6	Uncharacterized protein YbgS OS=Escherichia coli (strain K12) GN=ybgS PE=3 SV=1 - [YBGS_ECOLI]	0.00	15.87	1	1	1	1	126	12.9	4.88
P0AB14	Uncharacterized protein YccJ OS=Escherichia coli (strain K12) GN=yccJ PE=1 SV=1 - [YCCJ_ECOLI]	0.00	25.33	1	1	1	1	75	8.5	4.74
P45807	Uncharacterized protein YbaM OS=Escherichia coli (strain K12) GN=ybaM PE=4 SV=1 - [YBAM_ECOLI]	0.00	39.62	1	1	1	1	53	6.0	4.61
P0AEY5	Modulator of drug activity B OS=Escherichia coli (strain K12) GN=mdaB PE=1 SV=1 - [MDAB_ECOLI]	0.00	9.84	1	1	1	1	193	21.9	6.29
P69922	L-fucose isomerase OS=Escherichia coli (strain K12) GN=fucI PE=1 SV=1 - [FUCI_ECOLI]	0.00	2.03	1	1	1	1	591	64.9	5.90
P00562	Bifunctional aspartokinase/homoserine dehydrogenase 2 OS=Escherichia coli (strain K12) GN=metL PE=1 SV=3 - [AK2H_ECOLI]	0.00	4.69	1	1	1	1	810	88.8	5.59
P38489	Oxygen-insensitive NAD(P)H nitroreductase OS=Escherichia coli (strain K12) GN=nfsB PE=1 SV=1 - [NFSB_ECOLI]	0.00	11.06	1	1	1	1	217	23.9	6.23
P06968	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Escherichia coli (strain K12) GN=dut PE=1 SV=1 - [DUT_ECOLI]	0.00	13.91	1	1	1	1	151	16.1	5.26
P0ACU7	HTH-type transcriptional regulator YjdC OS=Escherichia coli (strain K12) GN=yjdC PE=3 SV=1 - [YJDC_ECOLI]	0.00	12.57	1	1	1	1	191	21.9	5.08
P0AAG5	Multidrug resistance-like ATP-binding protein MdlB OS=Escherichia coli (strain K12) GN=mdlB PE=1 SV=1 - [MDLB_ECOLI]	0.00	4.89	1	1	1	1	593	65.2	6.02
P0AD65	Penicillin-binding protein 2 OS=Escherichia coli (strain K12) GN=mrdA PE=1 SV=1 - [PBP2_ECOLI]	0.00	3.00	1	1	1	1	633	70.8	8.82
P77173	Cell division protein ZipA OS=Escherichia coli (strain K12) GN=zipA PE=1 SV=3 - [ZIPA_ECOLI]	0.00	5.79	1	1	1	1	328	36.5	5.99
P07639	3-dehydroquinate synthase OS=Escherichia coli (strain K12) GN=aroB PE=1 SV=1 - [AROB_ECOLI]	0.00	6.08	1	1	1	1	362	38.9	6.05
Q46920	NADPH-dependent 7-cyano-7-deazaguanine reductase OS=Escherichia coli (strain K12) GN=queF PE=1 SV=1 - [QUEF_ECOLI]	0.00	8.16	1	1	1	1	282	32.6	6.13
P00393	NADH dehydrogenase OS=Escherichia coli (strain K12) GN=ndh PE=1 SV=2 - [DHNA_ECOLI]	0.00	4.15	1	1	1	1	434	47.3	8.85
P05825	Ferrierterobactin receptor OS=Escherichia coli (strain K12) GN=fepA PE=1 SV=2 - [FEPB_ECOLI]	0.00	3.89	1	1	1	1	746	82.1	5.59
P0A8W5	UPF0301 protein YqgE OS=Escherichia coli (strain K12) GN=yqgE PE=1 SV=1 - [YQGE_ECOLI]	0.00	8.56	1	1	1	1	187	20.7	5.57
P30860	ABC transporter arginine-binding protein 1 OS=Escherichia coli (strain K12) GN=artJ PE=1 SV=2 - [ARTJ_ECOLI]	0.00	8.23	1	1	1	1	243	26.8	7.36
P36928	Uncharacterized chaperone protein YegD OS=Escherichia coli (strain K12) GN=yegD PE=3 SV=2 - [YEGD_ECOLI]	0.00	1.56	1	1	1	1	450	49.3	5.25
P0AEB7	RutC family protein YoaB OS=Escherichia coli (strain K12) GN=yoaB PE=3 SV=1 - [YOAB_ECOLI]	0.00	12.28	1	1	1	1	114	12.5	5.16
P69434	Poly-beta-1,6-N-acetyl-D-glucosamine export protein OS=Escherichia coli (strain K12) GN=pgaA PE=1 SV=1 - [PGAA_ECOLI]	0.00	3.22	1	1	1	1	807	92.2	6.58
P75966	Ribosomal large subunit pseudouridine synthase E OS=Escherichia coli (strain K12) GN=rluE PE=1 SV=2 - [RLUE_ECOLI]	0.00	7.37	1	1	1	1	217	24.9	10.02
P76536	Probable deferriochelatase/peroxidase YfeX OS=Escherichia coli (strain K12) GN=yfeX PE=1 SV=2 - [YFEX_ECOLI]	0.00	12.04	1	2	2	3	299	33.0	5.54
P0AD17	Isochorismatase family protein YecD OS=Escherichia coli (strain K12) GN=yecD PE=1 SV=2 - [YECD_ECOLI]	0.00	15.43	1	1	1	1	188	20.4	5.57
P76172	Uncharacterized protein YnfD OS=Escherichia coli (strain K12) GN=ynfD PE=1 SV=2 - [YNFD_ECOLI]	0.00	21.78	1	1	1	1	101	10.5	4.94
P38038	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Escherichia coli (strain K12) GN=cysJ PE=1 SV=4 - [CYSJ_ECOLI]	0.00	3.17	1	1	1	1	599	66.2	5.02
P0AB20	Heat shock protein HspQ OS=Escherichia coli (strain K12) GN=hspQ PE=1 SV=2 - [HSPQ_ECOLI]	0.00	32.38	1	1	1	1	105	11.8	4.67
P0A9K3	PhoH-like protein OS=Escherichia coli (strain K12) GN=ybeZ PE=1 SV=2 - [PHOL_ECOLI]	0.00	4.05	1	1	1	1	346	39.0	5.97