

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
P0A799	Phosphoglycerate kinase OS=Escherichia coli (strain K12) GN=pgk PE=1 SV=2 - [PGK_ECOLI]	19.64	20.67	1	4	4	5	387	41.1	5.22
P0A853	Tryptophanase OS=Escherichia coli (strain K12) GN=tnaA PE=1 SV=1 - [TNA_A_ECOLI]	18.13	21.44	1	3	3	6	471	52.7	6.23
P0A9B2	Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) GN=gapA PE=1 SV=2 - [G3P1_ECOLI]	14.90	16.92	1	2	2	4	331	35.5	7.11
P0A9Q7	Aldehyde-alcohol dehydrogenase OS=Escherichia coli (strain K12) GN=adhE PE=1 SV=2 - [ADHE_ECOLI]	13.00	4.38	1	1	1	3	891	96.1	6.79
P0AE08	Alkyl hydroperoxide reductase subunit C OS=Escherichia coli (strain K12) GN=ahpC PE=1 SV=2 - [AHPC_ECOLI]	9.25	12.30	1	1	1	2	187	20.7	5.17
P27302	Transketolase 1 OS=Escherichia coli (strain K12) GN=tktA PE=1 SV=5 - [TKT1_ECOLI]	8.90	5.43	1	1	1	2	663	72.2	5.67
P37689	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Escherichia coli (strain K12) GN=gpmI PE=1 SV=1 - [GPMI_ECOLI]	8.44	5.64	1	1	1	2	514	56.2	5.29
P0A8N5	Lysine--tRNA ligase, heat inducible OS=Escherichia coli (strain K12) GN=lysJ PE=1 SV=2 - [SYK2_ECOLI]	8.41	6.34	1	1	1	2	505	57.8	5.24
P0A8M6	UPF0265 protein YeeX OS=Escherichia coli (strain K12) GN=yeeX PE=1 SV=1 - [YEE_X_ECOLI]	7.93	25.69	1	1	1	2	109	12.8	9.31
P75682	Probable 2-keto-3-deoxy-galactonate aldolase YagE OS=Escherichia coli (strain K12) GN=yagE PE=1 SV=2 - [YAGE_ECOLI]	7.07	10.60	1	1	1	2	302	32.5	6.44
P0ACF0	DNA-binding protein HU-alpha OS=Escherichia coli (strain K12) GN=hupA PE=1 SV=1 - [DBHA_ECOLI]	6.48	32.22	1	1	1	2	90	9.5	9.58
P69902	Formyl-CoA:oxalate CoA-transferase OS=Escherichia coli (strain K12) GN=frc PE=1 SV=1 - [FCTA_ECOLI]	4.88	1.92	1	1	1	2	416	45.8	5.58
P0AG86	Protein-export protein SecB OS=Escherichia coli (strain K12) GN=secB PE=1 SV=1 - [SECB_ECOLI]	4.75	22.58	1	1	1	2	155	17.3	4.37
P0ABV2	DNA-directed RNA polymerase subunit beta OS=Escherichia coli (strain K12) GN=rpoB PE=1 SV=1 - [RPOB_ECOLI]	4.52	3.28	1	1	1	1	1342	150.5	5.26
P77286	Uncharacterized protein YdeU OS=Escherichia coli (strain K12) GN=ydeU PE=5 SV=1 - [YDEU_ECOLI]	4.12	9.44	1	1	1	1	466	50.5	5.97
P09373	Formate acetyltransferase 1 OS=Escherichia coli (strain K12) GN=pfkB PE=1 SV=2 - [PFLB_ECOLI]	4.10	3.68	1	1	1	1	760	85.3	6.01
P0A9G6	Isocitrate lyase OS=Escherichia coli (strain K12) GN=aceA PE=1 SV=1 - [ACEA_ECOLI]	4.03	9.45	1	1	1	1	434	47.5	5.31
P41547	Calcitonin OS=Canis lupus familiaris GN=CALCA PE=1 SV=2 - [CALC_CANLNF]	4.00	17.39	1	1	1	1	115	12.7	8.06
P77211	Cation efflux system protein CusC OS=Escherichia coli (strain K12) GN=cusC PE=1 SV=1 - [CUSC_ECOLI]	3.95	4.60	1	1	1	2	457	50.2	6.40
P0ACF4	DNA-binding protein HU-beta OS=Escherichia coli (strain K12) GN=hupB PE=1 SV=1 - [DBHB_ECOLI]	3.92	33.33	1	1	1	1	90	9.2	9.70
P0A8T7	DNA-directed RNA polymerase subunit beta' OS=Escherichia coli (strain K12) GN=rpoC PE=1 SV=1 - [RPOC_ECOLI]	3.87	2.42	1	1	1	1	1407	155.1	7.08
P39308	Uncharacterized protein Yjz OS=Escherichia coli (strain K12) GN=yjz PE=4 SV=1 - [YJZ_ECOLI]	3.86	14.02	1	1	1	1	264	29.7	6.73
P12758	Uridine phosphorylase OS=Escherichia coli (strain K12) GN=udp PE=1 SV=3 - [UDP_ECOLI]	3.66	11.86	1	1	1	1	253	27.1	6.21
P77596	Uncharacterized protein YagF OS=Escherichia coli (strain K12) GN=yagF PE=3 SV=1 - [YAGF_ECOLI]	3.53	7.18	1	1	1	1	655	69.4	6.42
P0A6M8	Elongation factor G OS=Escherichia coli (strain K12) GN=fusA PE=1 SV=2 - [EFG_ECOLI]	3.46	5.11	1	1	1	1	704	77.5	5.38
P0CE47	Elongation factor Tu 1 OS=Escherichia coli (strain K12) GN=tufA PE=1 SV=1 - [EFTU1_ECOLI]	3.36	4.31	2	1	1	1	394	43.3	5.45
P0A9Q9	Aspartate-semialdehyde dehydrogenase OS=Escherichia coli (strain K12) GN=asd PE=1 SV=1 - [DHAS_ECOLI]	2.82	10.63	1	1	1	1	367	40.0	5.58
P0A6P9	Enolase OS=Escherichia coli (strain K12) GN=eno PE=1 SV=2 - [ENO_ECOLI]	2.44	7.18	1	1	1	1	432	45.6	5.48