

Protein name	Accession number	Protein molecular weight (Daltons)	Flight total cell protein ID probability*	Ground total cell protein ID probability*
sn-glycerol-3-phosphate dehydrogenase	gi 16766813	57 kDa	100% (100%)	99% (99%)
branched-chain-amino-acid transaminase	gi 96710	34 kDa	99% (99%)	100% (100%)
putative periplasmic protein	gi 16764930	39 kDa	100% (100%)	100% (100%)
6,7-dimethyl-8-ribityllumazine synthase	gi 16501685	16 kDa	100% (100%)	100% (100%)
thioredoxin reductase	gi 16502122	35 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L2	gi 16505152	30 kDa	100% (100%)	100% (100%)
30S ribosomal protein S10	gi 68057571	12 kDa	100% (100%)	100% (100%)
50S ribosomal protein L24	gi 15803836	11 kDa	100% (100%)	100% (100%)
serine hydroxymethyltransferase	gi 16503768	45 kDa	100% (100%)	100% (100%)
30s ribosomal protein S6	gi 16505516	15 kDa	100% (100%)	100% (100%)
30S ribosomal protein S22	gi 16502603	5 kDa	100% (100%)	100% (100%)
2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	gi 16763603	30 kDa	100% (100%)	100% (100%)
peptidyl-prolyl cis-trans isomerase B	gi 16501803	18 kDa	100% (100%)	100% (100%)
FKBP-type peptidyl-prolyl cis-trans isomerase	gi 16766744	21 kDa	100% (100%)	100% (100%)
ribosome recycling factor	gi 16501500	21 kDa	100% (100%)	100% (100%)
carbamoyl-phosphate synthase large subunit	gi 16763457	118 kDa	100% (100%)	100% (100%)
ATP synthase delta subunit	gi 16504763	19 kDa	100% (100%)	100% (100%)
FKBP-type peptidyl-prolyl cis-trans isomerase	gi 16766742	29 kDa	99% (99%)	100% (100%)
putative cytoplasmic protein	gi 56383221	12 kDa	99% (99%)	100% (100%)
D-3-phosphoglycerate dehydrogenase	gi 16766363	44 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L3	gi 16505149	22 kDa	100% (100%)	100% (100%)
ATP synthase alpha subunit	gi 16504764	55 kDa	100% (100%)	100% (100%)
serine endoprotease	gi 16766643	47 kDa	100% (100%)	100% (100%)
putative ABC-type transport system ATPase	gi 16763890	30 kDa	99% (99%)	100% (100%)
ATP synthase subunit B	gi 16504762	17 kDa	99% (99%)	100% (100%)
malate dehydrogenase	gi 16766654	32 kDa	99% (99%)	100% (100%)
RNase E	gi 16764541	119 kDa	100% (100%)	100% (100%)
osmotically inducible protein C	gi 16502605	15 kDa	99% (99%)	100% (100%)
polynucleotide phosphorylase	gi 16766580	77 kDa	100% (100%)	100% (100%)
glutamate dehydrogenase	gi 16764650	49 kDa	100% (100%)	100% (100%)
menaquinone biosynthesis protein	gi 16504650	17 kDa	99% (99%)	100% (100%)
50S ribosomal subunit protein L18	gi 16505166	13 kDa	99% (99%)	100% (100%)
phospho-2-dehydro-3-deoxyheptonate aldolase	gi 16503824	39 kDa	99% (99%)	100% (100%)
transketolase	gi 16766377	72 kDa	99% (99%)	100% (100%)
acetylglutamate kinase	gi 16767387	27 kDa	99% (99%)	100% (100%)
50S ribosomal protein L11	gi 15804573	15 kDa	99% (99%)	100% (100%)
cold shock protein CspC	gi 15802236	7 kDa	100% (100%)	100% (100%)
unnamed protein product	gi 47736	16 kDa	100% (100%)	100% (100%)
dihydropolipamide dehydrogenase	gi 16763544	51 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L29	gi 16505157	7 kDa	100% (100%)	100% (100%)
arginine-binding periplasmic protein 1 precursor	gi 16502093	27 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L10	gi 47916	18 kDa	100% (100%)	100% (100%)
hyperosmotically-inducible periplasmic protein	gi 16505665	21 kDa	100% (100%)	100% (100%)
bacterioferritin comigratory protein	gi 16503708	18 kDa	100% (100%)	100% (100%)
glutamate/aspartate transporter	gi 16764042	34 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L17	gi 16505176	14 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L6	gi 16505165	19 kDa	100% (100%)	100% (100%)
fructose 1,6-bisphosphate aldolase	gi 16504152	39 kDa	100% (100%)	100% (100%)
30S ribosomal protein S3	gi 16131193	26 kDa	100% (100%)	100% (100%)
5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase	gi 16767235	85 kDa	100% (100%)	100% (100%)
phosphate acetyltransferase	gi 16765665	77 kDa	99% (99%)	100% (100%)
inorganic pyrophosphatase	gi 16505542	20 kDa	100% (100%)	100% (100%)
phase 1 flagellin	gi 50830926	52 kDa	99% (99%)	100% (100%)
histone like DNA-binding protein HU-alpha (NS2) (HU-2)	gi 16504591	10 kDa	100% (100%)	100% (100%)
Iron transport protein, periplasmic-binding protein	gi 16503939	34 kDa	100% (100%)	100% (100%)
conserved hypothetical protein	gi 16503804	14 kDa	100% (100%)	100% (100%)
ribosomal protein S7	gi 47922	18 kDa	100% (100%)	100% (100%)
ATP synthase beta subunit	gi 16504766	50 kDa	100% (100%)	100% (100%)
30S ribosomal protein S2	gi 16501497	27 kDa	100% (100%)	100% (100%)
glucose-specific PTS system enzyme IIA component	gi 47658	18 kDa	100% (100%)	100% (100%)
probable peroxidase	gi 16501671	22 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L5	gi 16505162	20 kDa	100% (100%)	100% (100%)
argininosuccinate lyase	gi 16767388	50 kDa	100% (100%)	100% (100%)
RNA polymerase, alpha subunit	gi 24053769	37 kDa	100% (100%)	100% (100%)
glycine/betaine/proline transport protein	gi 16766122	36 kDa	100% (100%)	100% (100%)
elongation factor Ts	gi 16501498	30 kDa	100% (100%)	100% (100%)
inositol-5-monophosphate dehydrogenase	gi 16765831	52 kDa	100% (100%)	100% (100%)
putative outer membrane lipoprotein	gi 16763634	29 kDa	100% (100%)	100% (100%)
DNA-directed RNA polymerase, beta-subunit	gi 16504603	155 kDa	100% (100%)	100% (100%)
GroEL protein	gi 16505460	57 kDa	100% (100%)	100% (100%)
enolase	gi 16504025	46 kDa	100% (100%)	100% (100%)
glyceraldehyde 3-phosphate dehydrogenase A	gi 16502901	36 kDa	100% (100%)	100% (100%)
translation elongation factor EF-Tu.A	gi 96718	43 kDa	100% (100%)	100% (100%)
iron-dependent alcohol dehydrogenase	gi 16765093	96 kDa	100% (100%)	100% (100%)
phosphoglycerate kinase	gi 16504153	41 kDa	100% (100%)	100% (100%)
putative hydrogenase membrane component precursor	gi 16764429	38 kDa	100% (100%)	100% (100%)
formate acetyltransferase 1	gi 16502136	85 kDa	100% (100%)	100% (100%)
30S ribosomal protein S1	gi 16502144	61 kDa	100% (100%)	100% (100%)
elongation factor G	gi 47923	78 kDa	100% (100%)	100% (100%)
30S ribosomal subunit protein S5	gi 24053777	18 kDa	100% (100%)	100% (100%)
O-Acetylserine Sulfhydrylase	gi 11514514	34 kDa	100% (100%)	100% (100%)
trigger factor	gi 16501718	48 kDa	100% (100%)	100% (100%)
Glutamine Synthetase	gi 9256972	52 kDa	100% (100%)	100% (100%)
molecular chaperone DnaK	gi 16763402	69 kDa	100% (100%)	100% (100%)
arginine-binding periplasmic protein 2 precursor	gi 16502090	27 kDa	100% (100%)	100% (100%)
alkyl hydroperoxide reductase c22 protein	gi 16501859	21 kDa	100% (100%)	100% (100%)

50S ribosomal protein L9	gi 16767640	16 kDa	100% (100%)	100% (100%)
outer membrane protein OmpH precursor	gi 16501506	18 kDa	100% (100%)	100% (100%)
glutamine-binding periplasmic protein precursor	gi 16502041	27 kDa	100% (100%)	100% (100%)
GroES protein	gi 16505459	10 kDa	100% (100%)	100% (100%)
50S ribosomal subunit protein L1	gi 16504607	25 kDa	100% (100%)	100% (100%)
outer membrane protein C	gi 16503494	41 kDa	100% (100%)	100% (100%)
dipeptide transport protein	gi 16766917	60 kDa	100% (100%)	
PTS system protein HPr	gi 24052838	9 kDa	100% (100%)	
50S ribosomal subunit protein L7/L12	gi 47917	12 kDa	100% (100%)	
50S ribosomal subunit protein L32	gi 24051382	6 kDa	100% (100%)	
oligopeptide transport protein	gi 39546324	61 kDa	100% (100%)	
high-affinity branched-chain amino acid transporter	gi 16766853	39 kDa	100% (100%)	
30S ribosomal protein S20	gi 16501327	10 kDa	100% (100%)	
phosphoribosylaminoimidazole carboxylase catalytic subunit	gi 16763914	18 kDa	100% (100%)	
putative translation initiation inhibitor	gi 16505567	14 kDa	100% (100%)	
putative multicopper oxidase	gi 16763558	59 kDa	100% (100%)	
DNA protection during starvation protein	gi 16502042	19 kDa	100% (100%)	
thioredoxin	gi 67005950	12 kDa	100% (100%)	
sulfate transport protein	gi 16767329	37 kDa	100% (100%)	
ribulose-phosphate 3-epimerase	gi 16766771	24 kDa	99% (99%)	
cytoplasmic ferritin	gi 16765276	19 kDa	99% (99%)	
osmotically inducible lipoprotein E precursor	gi 16502880	12 kDa	100% (100%)	
fructose-bisphosphate aldolase class I	gi 16503381	38 kDa	100% (100%)	
30S ribosomal protein S13	gi 16766707**	13 kDa	100% (100%)	
thiosulfate transport protein	gi 16765764	38 kDa	100% (100%)	
histidine-binding periplasmic protein	gi 47731	28 kDa	100% (100%)	
RecA protein	gi 16503906	38 kDa	100% (100%)	
aspartate semialdehyde dehydrogenase	gi 2353187	43 kDa	100% (100%)	
transcription elongation factor NusA	gi 16766585**	55 kDa	100% (100%)	
pyruvate kinase	gi 16764728	51 kDa	99% (99%)	
30S ribosomal protein S11	gi 16766706**	14 kDa	99% (99%)	
DNA-directed RNA polymerase omega subunit	gi 15804190	10 kDa	99% (99%)	
single-strand DNA-binding protein	gi 16505243	19 kDa	99% (99%)	
DNA-binding protein HU-beta	gi 581767	9 kDa	99% (99%)	
putative cytoplasmic protein	gi 6851082	19 kDa	99% (99%)	
succinyl-CoA synthetase beta chain	gi 16501970	41 kDa	99% (99%)	
50S ribosomal subunit protein A	gi 56383471	7 kDa	99% (99%)	
ATPase subunit	gi 7594817	46 kDa	99% (99%)	
ketol-acid reductoisomerase	gi 16767185	54 kDa	98% (98%)	
DNA ligase	gi 16765747	73 kDa	99% (99%)	
30S ribosomal subunit protein S19	gi 16505153	10 kDa	100% (100%)	
NifU-like protein involved in Fe-S cluster formation	gi 16503756	14 kDa	99% (99%)	
putative sigma(54) modulation protein	gi 16503819	13 kDa	99% (99%)	
3-isopropylmalate dehydrogenase	gi 16763502**	40 kDa	99% (99%)	
bacterioferrin	gi 16766732**	18 kDa	99% (99%)	
glycerate kinase II	gi 16763905**	39 kDa	99% (99%)	
DNA polymerase I	gi 16767264	103 kDa	99% (99%)	
putative periplasmic protein	gi 16764812	54 kDa	99% (99%)	
threonine dehydratase	gi 16767181	56 kDa	98% (98%)	
putative universal stress protein UspA	gi 16501866	16 kDa	99% (99%)	
ferric uptake regulator Fur	gi 16501929	17 kDa	99% (99%)	
Cell division protease ftsH	gi 16504361	71 kDa	99% (99%)	
flavodoxin	gi 16764064	20 kDa	99% (99%)	
nitrate reductase 2 beta subunit	gi 16764922	59 kDa	99% (99%)	
keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	gi 16765226	22 kDa	99% (99%)	
carbon storage regulator CsrA	gi 24053109	7 kDa	99% (99%)	
rmlC dTDP-4,deoxyrhamnose 3,5 epimerase	gi 581655	21 kDa	99% (99%)	
TonB-dependent siderophore receptor protein	gi 16766089	79 kDa		100% (100%)
N-succinyl-diaminopimelate-aminotransferase/acylornithine transaminase	gi 16766756	44 kDa		100% (100%)
DNA-directed RNA polymerase beta subunit	gi 16767407	151 kDa		100% (100%)
argininosuccinate synthase	gi 39546365	50 kDa		100% (100%)
outer membrane lipoprotein SlyB precursor	gi 16502764	16 kDa		100% (100%)
thiol peroxidase	gi 16765025	18 kDa		100% (100%)
50S ribosomal subunit protein L14	gi 49613467	14 kDa		100% (100%)
triosephosphate isomerase	gi 16767347	27 kDa		100% (100%)
lipoprotein	gi 16765808**	37 kDa		100% (100%)
oligopeptidase A	gi 16766880	77 kDa		100% (100%)
phosphoribosylamine--glycine ligase	gi 16767429	46 kDa		100% (100%)
phosphoglyceromutase	gi 16764136	28 kDa		100% (100%)
cystathionine gamma-synthase	gi 16767366	42 kDa		100% (100%)
glucose-6-phosphate isomerase	gi 16767471	61 kDa		100% (100%)
50S ribosomal subunit protein L33	gi 24054147	6 kDa		100% (100%)
ribosomal protein S4	gi 2780215	23 kDa		100% (100%)
PEP-protein phosphotransferase	gi 16765752**	63 kDa		100% (100%)
Lpp1 major outer membrane lipoprotein	gi 37785814	8 kDa		100% (100%)
aldose 1-epimerase	gi 16764640**	33 kDa		100% (100%)
putative outer membrane porin precursor	gi 16764916**	40 kDa		99% (99%)
50S ribosomal protein L4	gi 15803846	22 kDa		100% (100%)
outer membrane ferric enterobactin receptor precursor	gi 16763962	83 kDa		100% (100%)
hypothetical protein STM2795 putative LysM domain	gi 16766106**	16 kDa		100% (100%)
phosphoribosylaminoimidazole-succinocarboxamide synthase	gi 16503704	27 kDa		100% (100%)
ornithine carbamoyltransferase	gi 312706	24 kDa		100% (100%)
ribonucleoside-diphosphate reductase	gi 1184247	81 kDa		100% (100%)
biotin carboxylase	gi 16504442	49 kDa		100% (100%)
3-ketoacyl-(acyl-carrier-protein) reductase	gi 16764550	26 kDa		100% (100%)
6-phosphofructokinase II	gi 16764677	33 kDa		100% (100%)
uroporphyrinogen III methylase	gi 16767207	42 kDa		100% (100%)

*Peptide samples obtained from MudPIT were analyzed using Sequest and X!Tandem software, and the data was organized using the Scaffold program. To be considered a positive identification in Scaffold, the following parameters were used: a minimum of 2 peptides from a given protein identified with peptide and protein thresholds of 80% to give an overall protein identification (ID) probability of at least 80%. Note that a protein ID probability of greater than 80% in at least one of the samples warranted inclusion in the table so as to allow identification of possible differential expression of a given protein.

** Peptides encoded by genes or operons also found to be differentially regulated in spaceflight or ground based modeled microgravity in LB medium