Supporting Information

Chemoproteomic Profiling of Phosphoaspartate Modifications in Prokaryotes

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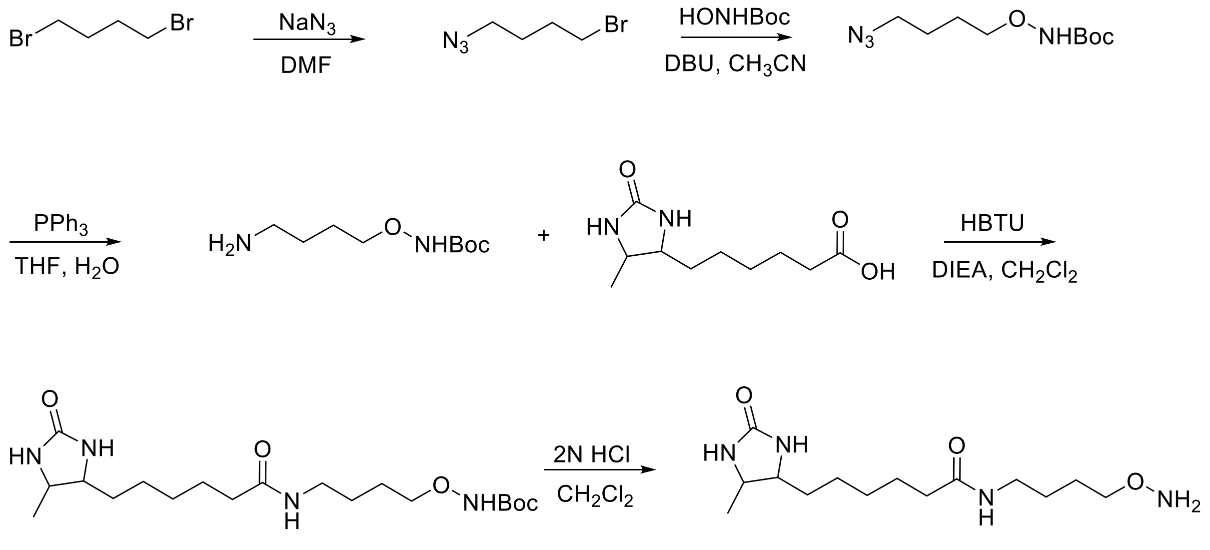
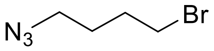
Synthesis of DBHA probe

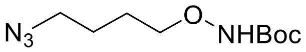


DBHA

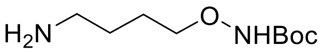
General Information: All commercially available chemicals were obtained from Aldrich, Acros, Fisher, Fluka and were used without further purification, except where noted. Dry solvents were obtained by passing through activated alumina columns. All reactions were carried out under inert nitrogen atmosphere using oven-baked glassware unless otherwise noted. Flash chromatography was performed using 230-400 mesh silica gel 60. NMR spectra were generated on a Bruker 400 MHz instrument. Chemical shifts were recorded in ppm relative to tetramethylsilane (TMS) with multiplicities given as s (singlet), bs (broad singlet), d (doublet), t (triplet), dt (doublet of triplets), q (quadruplet), qd (quadruplet of doublets), m (multiplet).



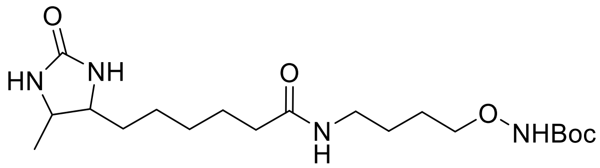
1-Azido-4-bromobutane.
Sodium azide (684 mg, 10.525 mmol) was added to a solution of 1,4-dibromobutane (2.5 g, 11.577 mmol) in dry DMF (20 mL) and allowed to stir for overnight at 50 °C under N_2 gas. To the reaction mixture was added cold H_2O and extracted with ethyl acetate 3 times. The organic layer was washed with brine two times and then dried over $MgSO_4$. The crude mixture after solvent evaporation was purified by silica gel flash chromatography (5% EtOAc/hexanes) to give 1-Azido-4-bromobutane as a clear oil (1.6 g, 80%).
^{1}H NMR (400 MHz, $CDCl_3$) δ 3.40 (t, *J* = 6.6 Hz, 2H), 3.31 (t, *J* = 6.6 Hz, 2H), 2.05-1.94 (m, 2H), 1.78-1.74 (m, 2H).



***tert*-butyl-4-azidobutoxycarbamate.**
N-Boc-hydroxylamine (1.3 g, 10.105 mmol) and DBU (2.2 g, 14.435 mmol) were added to a solution of 1-Azido-4-bromobutane (1.3 g, 7.217 mmol) in dry CH_3CN (25 mL) and allowed to stir for 24 hr at 50°C under N_2 gas. The reaction mixture was concentrated, added to H_2O and extracted with CH_2Cl_2 three times. The organic layer was washed with brine two times and then dried over $MgSO_4$. The crude mixture after solvent evaporation was purified by silica gel flash chromatography (10% EtOAc/hexanes) to give *tert*-butyl-4-azidobutoxycarbamate as a clear oil (1.2 g, 75%).
^{1}H NMR (400 MHz, $CDCl_3$) δ 3.82-3.84 (m, 2H), 3.31-3.25 (m, 2H), 1.72-1.68 (m, 4H), 1.42 (s, 9H); HRMS (ESI+) *m/z* calculated for $[M+H]^+$ $C_9H_{19}N_4O_3$: 231.2760, found 231.2758.



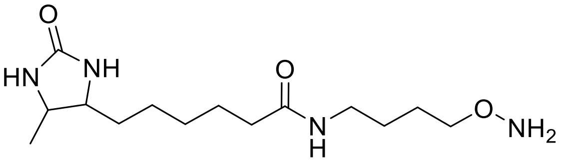
***tert*-butyl-4-aminobutoxycarbamate.**
Triphenylphosphine (666 mg, 2.540 mmol) was added to a solution of *tert*-butyl-4-azidobutoxycarbamate (450 mg, 1.954 mmol) in dry THF (8 mL) and H_2O (0.2 mL). The reaction mixture was stirred at room temperature for 12 hr. After removing THF under reduced pressure, the residue was purified by silica gel flash chromatography (85/15:CH_2Cl_2/MeOH) to give *tert*-butyl-4-aminobutoxycarbamate as a pale-yellow liquid (250 mg, 63%).
^{1}H NMR (400 MHz, $CDCl_3$) δ 3.82 (t, *J* = 6.6 Hz, 2H), 2.74 (t, *J* = 6.6 Hz, 2H), 1.62-1.60 (m, 2H), 1.52-1.46 (m, 2H), 1.43 (s, 9H); HRMS (ESI+) *m/z* calculated for $[M+H]^+$ $C_9H_{21}N_2O_3$: 205.2780, found 205.2782.



tert-butyl ((10-(5-methyl-2-oxoimidazolidin-4-yl)-5-oxodecyl)oxy)carbamate.

Desthiobiotin (46 mg, 0.214 mmol), HBTU (122 mg, 0.321 mmol) and DIEA (83 mg, 0.642 mmol) were added to a solution of *tert*-butyl-4-aminobutoxycarbamate (48 mg, 0.235 mmol) in dry CH_2Cl_2 (2 mL). The reaction mixture was stirred at room temperature overnight. The mixture was added to H_2O and extracted with CH_2Cl_2 three times. The organic layer was washed with brine two times and then dried over $MgSO_4$. The crude mixture after solvent evaporation was purified by silica gel flash chromatography (90/10:CH_2Cl_2/MeOH) to give *tert*-butyl ((10-(5-methyl-2-oxoimidazolidin-4-yl)-5-oxodecyl)oxy)carbamate as a pale-yellow liquid (70 mg, 82%).

^{1}H NMR (400 MHz, $CDCl_3$) δ 8.30 (bs, 1H), 6.80 (m, 1H), 6.18 (s, 1H), 5.42 (s, 1H), 3.87-3.84 (m, 3H), 3.70-3.68 (m, 1H), 3.27-3.25 (m, 2H), 2.84 (bs, 1H), 2.21-2.17 (t, J = 7.2 Hz, 2H), 1.64-1.63 (m, 5H), 1.39 (s, 9H), 1.37-1.26 (m, 6H), 1.12-1.10 (d, J = 6.6 Hz, 3H); HRMS (ESI+) *m/z* calculated for $[M+H]^+$ $C_{19}H_{37}N_4O_5$: 401.2764, found 401.2769.



4-(10-(aminooxy)-6-oxodecyl)-5-methylimidazolidin-2-one (DBHA).

2 N HCl (0.13 mL, 0.262 mmol) was slowly added to a solution of *tert*-butyl ((10-(5-methyl-2-oxoimidazolidin-4-yl)-5-oxodecyl)oxy)carbamate (70 mg, 0.175 mmol) in dry CH_2Cl_2 at 0 °C. The reaction mixture was stirred at 0 °C for 1 h and then warmed up to room temperature. The mixture was stirred at room temperatureovernight and reaction completion was monitored by thin layer chromatography. After removing solvent under reduced pressure, the crude mixture was dissolved in MeOH and added to Et_2O. The residue was collected by filtration and washed with Et_2O (5 mL) three times to give 4-(10-(aminooxy)-6-oxodecyl)-5-methylimidazolidin-2-one (DBHA) as a white solid (48 mg, 92%).

^{1}H NMR (400 MHz, *d6*-DMSO) δ 10.84 (bs, 2H), 7.82 (bs, 1H), 3.98-3.95 (t, J = 6.2 Hz, 2H), 3.61-3.58 (m, 1H), 3.49-3.47 (m, 1H), 3.11-3.08 (t, J = 6.6 Hz, 2H), 2.14-2.11 (t, J = 7.2 Hz, 2H), 1.59-1.47 (m, 7H), 1.39-1.22 (m, 6H), 1.00-0.98 (d, J = 6.6 Hz, 3H) ; HRMS (ESI+) *m/z* calculated for $[M+H]^+$ $C_{14}H_{29}N_4O_3$: 301.2240, found 301.2242.

Working solutions of DBHA probe.

Working solutions (~1 M) were prepared in H_2O from the DBHA chloride salts. The pH was titrated to 6.5–7 with concentrated sodium hydroxide using Colorphast pH indicator strips from pH 5–10 with 0.5 pH unit accuracy (EMD). Solutions were used immediately.

***E. coli* growth conditions and proteome harvesting.**

BL21 *E. coli* were transformed with empty pET28 vector to confer kanamycin-resistance, ensuring the purity of cultures studied. A 10 mL culture of lysogeny broth (LB, Fisher) containing kanamycin (kan, 50 μg/mL) was inoculated with a single colony from a fresh LB/kan agar plate. After 24 hr growth at 37 °C, 225 rpm, Cells were collected by centrifugation at mid-log phase (OD_{600} = 0.6) for 30 min at 4000 g, 4 °C and washed three times with ice-cold PBS. Cell pellets were resuspended in 2 mL ice-cold lysis buffer containing 6 M urea, protease and phosphatase inhibitors. Lysis was performed by sonication on ice, for 3 min at 30% amplitude, 1 s on, 5 s off. Following centrifugation for 15 min at 16000 g, 4 °C, protein concentration was measured by BCA assay (Pierce, #23225). Cell pellets were used immediately for gel-based or proteomic experiments.

Gel-based analysis of probe-labelled proteins.

Proteomes were diluted to 1 mg/mL in 6 M urea (30 μL total reaction volume) and incubated with DBHA probe at the indicated concentrations (1 μL of a 30x stock in H_2O) for 1 hr at 37 °C. Reactions were quenched with 4x SDS-PAGE loading buffer, followed by heating to 95 ˚C for 5 minutes, cooling to room temperature, and gel electrophoresis on NuPAGE Novex 4-12% Bis-Tris Protein Gels (Invitrogen, NP0322BOX). Half of each probe-labeled aliquot was set aside for Coomassie staining for protein loading comparison. PAGE gels were transferred onto nitrocellulose membranes, blocked in 2% BSA in TBS containing 0.1% tween-20 (TBST) and probed with IRDye®R-800CW Streptavidin (LI-COR, #926-32230, 1:1000). Blots were imaged on the OdysseyCLxImager (LI-COR).

Proteomic sample preparation with DBHA probe

Proteomes were diluted to 5 mg/mL in 6M urea (500 μL total reaction volume) and incubated with DBHA probe at the indicated concentrations for 1 hr at 37 °C. Sequential addition of and mixture with pre-chilled methanol (MeOH, 2 mL), chloroform ($CHCl_3$, 0.5 mL) and H_2O (1 mL) on ice quenched the reaction. The precipitated proteome was centrifuged (4,000 *g*, 5 min, 4 °C) to fractionate the protein interphase from the organic and aqueous solvent layers. The protein pellet was washed with cold 1:1 MeOH:$CHCl_3$ (3 × 1 mL), mildly sonicated in cold 4:1 MeOH:$CHCl_3$ (2.5 mL) and pelleted once more by centrifugation (4,000 *g*, 5 min, 4°C) to ensure excess DBHA probe was efficiently removed. The remaining protein precipitate was dissolved by mild sonication in a freshly prepared solution of proteomics-grade 6 M urea (500 μL). Disulfides were reduced with DTT (10 μL, 500 mM) for 30 min at 65 °C, and then alkylated by iodoacetamide (40 μL, 1 M) for 30 min at ambient temperature protected from light. After reduction and alkylation, one more time washed with MeOH/$CHCl_3$ to remove excess reagents. The protein pellet was resuspended in 500 μL digestion buffer containing 2 M urea and 1M Tris pH 8.0 (49:1, 2M Urea/1M Tris pH 8.0 ratio), $CaCl_2$ (1 mM) and digested with sequencing grade trypsin (10 μg; Thermo Pierce) at 37 ˚C while rotating for 4 hr. After 4 hr, the solution was incubated with streptavidin agarose resin (50 μL of 50% High Capacity Streptavidin resin, Pierce) for overnight at ambient temperature on a rotator. The streptavidin beads were collected by centrifugation (1,400 *g*, 2 min) and sequentially washed with PBS (5 × ~10 mL), and H_2O (5 × ~10 mL) to remove unbound protein, and small molecules. DBHA-modified peptides were eluted by adding 75 μL of Elution buffer (1:1 ACN/ H_2O, 0.1% TFA), incubated for 3 minutes, and transfer the eluate to a new a Protein LoBind tube (Eppendorf). Elution was repeated three times total. The samples were lyophilized and stored at –80 °C until analyzed or dissolved in LC-MS/MS Buffer A (H_2O with 0.1% formic acid, LC-MS grade, Sigma Aldrich) for LC-MS/MS analysis.

TMT labeling with high and low osmolarity proteomes sample.

For osmolarity studies, Nutrient broth (NB, Sigma #70122) was made, autoclaved, treated with kan to 50 μg/mL, and supplemented with 20% w/v sucrose, or left unmodified. After 16 hr of growth at 37 °C, 225 rpm, flasks of 300 mL LB or NB media were inoculated 1:1000 with overnight culture. After 24 hr growth at 37 °C, 225 rpm, Cells were collected by centrifugation at mid-log phase (OD_{600} =

0.6) for 30 min at 4000 g, 4 °C and washed three times with ice-cold PBS, and lysed as for all proteome preparations. “High osmolarity” and “Low osmolarity” proteomes were diluted to 5 mg/mL in 6M urea (500 µL total reaction volume) and incubated with DBHA probe at the indicated concentrations for 1 hr at 37 °C. Washed proteomes with MeOH/$CHCl_3$ to remove excess DBHA probe. The protein precipitate was resuspended by mild sonication in a freshly prepared solution of proteomics-grade 6 M urea (500 µL). Disulfides were reduced with DTT (10 µL, 500 mM) for 30 min at 65 °C. Reduced thiols were then alkylated by iodoacetamide (40 µL, 1 M) for 30 min at ambient temperature protected from light. The solution was diluted with PBS (~5 mL) and incubated with pre-equilibrated streptavidin agarose resin (50 µL column volume, Pierce) for ~1.5–2 hr at ambient temperature on a rotator. The streptavidin beads were collected by centrifugation (1,400 *g*, 1–2 min) and sequentially washed with PBS (3 × ~10 mL), and H_2O (3 × ~10 mL) to remove unbound protein and small molecules. The resin was transferred to a Protein LoBind tube (Eppendorf or BioPioneer) and bound proteins were digested on-bead overnight at 37 °C in ~200 µL total volume containing sequencing grade porcine trypsin (4 µg, Promega) in the presence of urea (2 M Urea in PBS) and $CaCl_2$ (1 mM). The proteolyzed supernatant was transferred to a fresh Protein LoBind tube and acidified with formic acid (5%) to inactivate trypsin. Peptides were then desalted with ZipTip C18 tips (100 µL, Millipore), dried under vacuum, resuspended with LC-MS grade water (Sigma Aldrich) and then lyophilized. Lyophilized peptides were labeled with 10-plex isobaric tandem mass tags (90406, Thermo Scientific) according to manufacturer’s protocol with slight modification. TMT reagents were reconstituted to 8 mg/mL in anhydrous acetonitrile (Sigma) and added to lyophilized peptides dissolved in 100 uL of 200 mM HEPES buffer, pH 8.0 (~8:1 reagent/peptide ratio). Labeling reaction was carried out in room temperature for 1 hr with gentle shaking, and quenched with 5 uL of 5% hydroxylamine (Thermo Scientific). Labeled peptides were combined into a single pool per experiment, acidified with formic acid (pH 2-3), desalted using ZipTip C18 tips (100 µL, Millipore). The samples were lyophilized and stored at –80 °C until analyzed or dissolved in LC-MS/MS Buffer A (H_2O with 0.1% formic acid, LC-MS grade, Sigma Aldrich) for LC-MS/MS analysis.

For bulk protein level quantification by LC-MS/MS, “High osmolarity” and “Low osmolarity” proteomes were diluted to 5 mg/mL in 6M urea (500 µL total reaction volume). Reduction and alkylation of cysteine residues were performed by addition of DTT (10 µL, 500 mM) for 30 min at 65 °C, followed iodoacetamide (40 µL, 1 M) for 30 min at ambient temperature protected from light. The proteome solution was diluted 4-fold with ammonium bicarbonate solution (50 mM, pH 8.0), $CaCl_2$ added (1 mM) and digested with sequencing grade trypsin (~1:100 enzyme/protein ratio; Thermo Pierce) at 37 ˚C while rotating overnight. Peptide digestion reactions were quenched by acidification to pH 2-3 with 1% formic acid, and peptides were then desalted with Sep-Pak C18 cartridges (50mg, Waters), dried under vacuum, resuspended with LC-MS grade water (Sigma Aldrich) and then lyophilized. TMT labeling samples were prepared as described above.

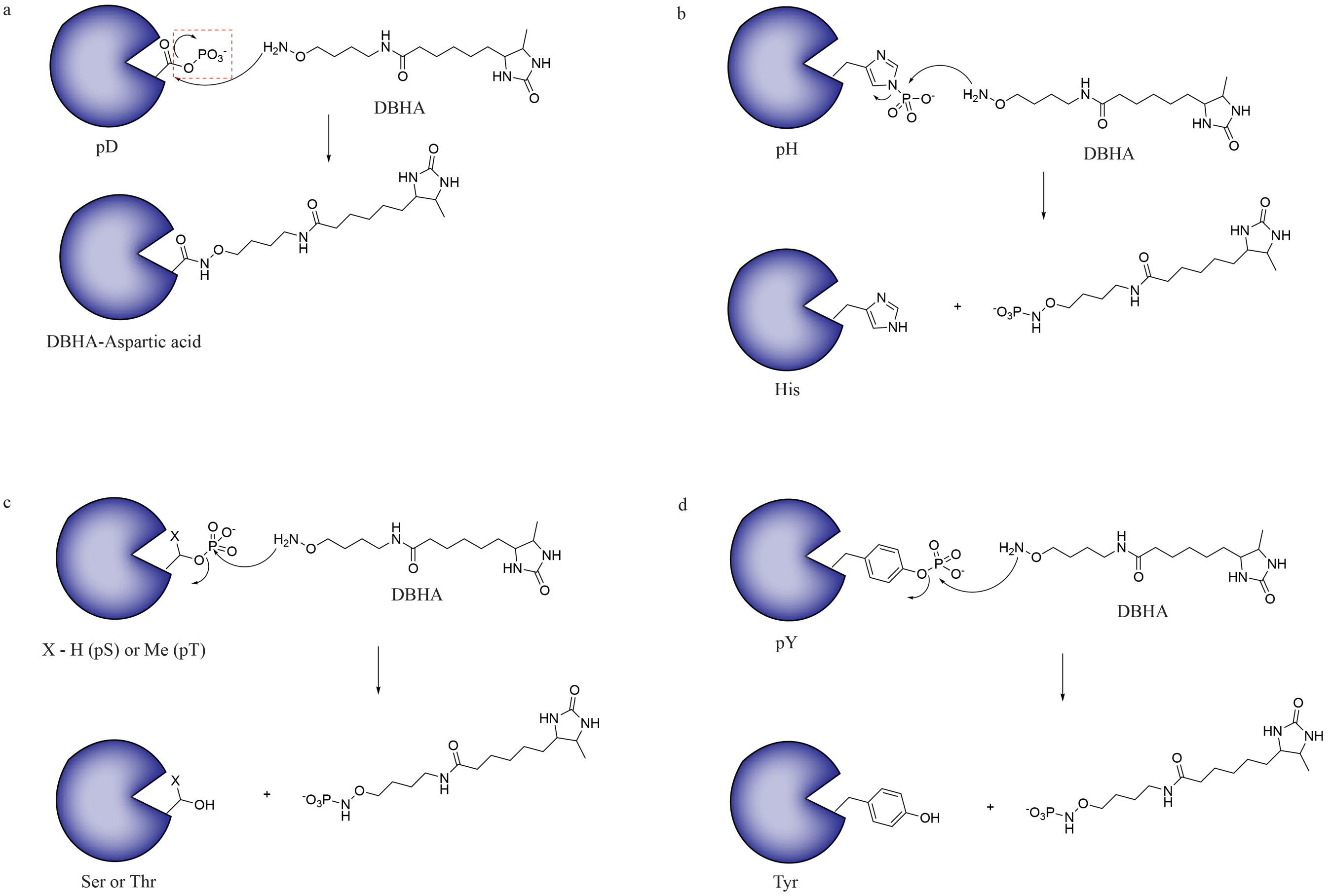
Proteomic LC-MS/MS and Data Analysis.
LC-MS/MS experiments were performed with an Easy-nLC 1000 ultra-high pressure LC system (ThermoFisher) using a PepMap RSLC C18 column (column: 75 µm x 15 cm; 3 µm, 100 Å) coupled to a Q Exactive HF orbitrap and Easy-Spray nanosource (ThermoFisher). Enriched peptides with DBHA probe (500 ng) were injected onto the column in buffer A (0.1% Formic acid water) and separated using the following linear gradient of buffer B (0.1% Formic acid acetonitrile) at 300 nL/min: 0-2% buffer B over 10 minutes, 2-40% buffer B over 120 minutes, 40-70% buffer B over 10 minutes, 70-100% buffer B over 5 minutes, keep 100% buffer B over 5 minutes, re-stabilized to 0% buffer B over 10 minutes, keep 0% buffer B over 5 minutes, 0-100% buffer B over 5 minutes, keep 100% buffer B over 5 minutes, re-stabilized to 0% buffer B over 5 minutes, and then keep 0% buffer B over 5 minutes. MS/MS spectra were collected from 0 to 150 minutes using a data-dependent, top-20 ion setting. Data acquisition for differential modification searches were performed with the following settings: Full MS scans were acquired at a resolution of 120,000, scan range of 400-1600 m/z, maximum IT of 50 ms, AGC target of 1e6, and data type in profile mode. Sequencing was performed by HCD fragmentation with a resolution of 15,000, AGC target of 1e5, maximum IT of 30 ms, NCE of 26, and data type in centroid mode. Isolation window for precursor ions was set to 1.5 m/*z* with an underfill ratio of 0.5%. Peptides with charge state >5, 1 and undefined were excluded and dynamic exclusion was set to 5.0 seconds. Furthermore, S-lens RF level was set to 60 with a spray voltage value of 2.60kV.

TMT-labeled digested peptides were injected onto the column and separated using the following gradient of buffer B (0.1% Formic acid acetonitrile) at 300 nL/min: 0-5% buffer B in 5 minutes, 5-32% buffer B in 115 minutes, 32-90% buffer B over 6 minutes, and hold at 90% for 20mins. MS/MS spectra were collected from 0 to 150 minutes using a data-dependent, top-10 ion setting with the following settings: full MS scans were acquired at a resolution of 120,000, scan range of 375-1500 m/z, maximum IT of 60 ms, AGC target of 1e6, and data collection in profile mode. MS2 scans was performed by HCD fragmentation with a resolution of 60,000, AGC target of 1e5, maximum IT of 60 ms, NCE of 30, and data type in centroid mode. Isolation window for precursor ions was set to 1.0 m/z with an underfill ratio of 0.5%. Peptides with charge state 1 and undefined were excluded and dynamic exclusion was set to 20 seconds. Furthermore, S-lens RF level was set to 60 with a spray voltage value of 2.60kV and ionization chamber temperature of 300˚C.

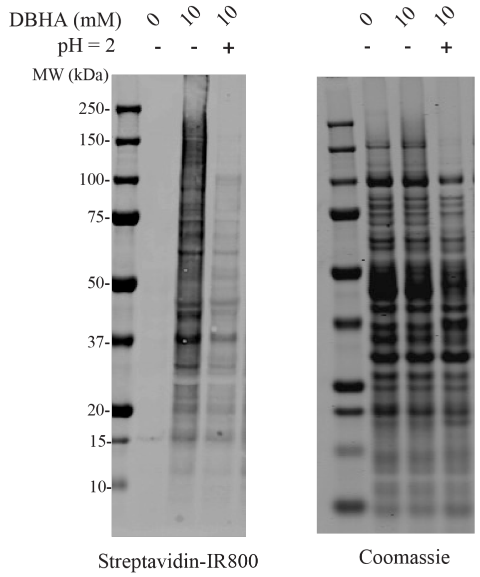
For Enriched peptides with DBHA, MS2 files were generated and searched using the ProLuCID algorithm in the Integrated Proteomics Pipeline (IP2) software platform. *E.coli* proteome data were searched using a concatenated target/decoy UniProt database (UniProt_E_coli_02-14-2011_reversed.fasta). Basic searches were performed with the following search parameters: HCD fragmentation method; monoisotopic precursor ions; high resolution mode (3 isotopic peaks); precursor mass range 600-6000 and initial fragment tolerance at 600 p.p.m. C-terminal enzyme cleavage specificity at lysine and arginine residues with 3 missed cleavage sites permitted; static modification of +57.02146 on cysteines (carboxyamidomethylation); two total differential modification sites per peptide including oxidized methionine (+15.9949), pD-modified aspartic acid (+282.2056); primary scoring type by XCorr and secondary by Zscore; minimum peptide length of six residues with a candidate peptide threshold of 500. A minimum of one peptide per protein and half-tryptic peptide specificity were required. Starting statistics were performed with a Δmass cutoff = 10 p.p.m. with modstat, and trypstat settings. False-discovery rates of peptide (sfp) were set to 0%, peptide modification requirement (-m) was set to 0, and spectra display mode (-t) was set to 1. Through subsequent FP-rate adjustment, filtering according to Xcorr (>2.0) and ΔCn (>0.2) statistics, and manual removal of peptides containing singleton pD-modified peptides containing more than one missed tryptic site, false-positive rates of less than 0.8% were achieved in individual technical replicates. The target list was further refined by requiring that each DBHA-modification site was detected in a minimum of six of eight technical replicates in the 10 mM DBHA dataset (4 biological samples x 2 technical runs), or four of six technical replicates (3 biological samples x 2 technical runs) in the 100 mM DBHA dataset. These combined filters place the realized false positive rate below 0.1%

For TMT-labeled digested peptides, basic searches were performed with the following search parameters: HCD fragmentation method; monoisotopic precursor ions; high resolution mode (3 isotopic peaks); precursor mass range 600- 6,000 and initial fragment tolerance at 600 p.p.m.; enzyme cleavage specificity at C-terminal lysine and arginine residues with 3 missed cleavage sites permitted; static modification of +57.02146 on cysteine (carboxyamidomethylation), +229.1629 on N-terminal and lysine for TMT-10-plex tag; 2

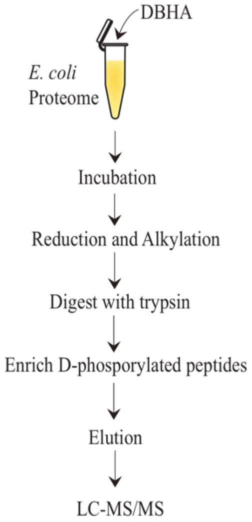
differential modification sites per peptide, including oxidized methionine (+15.9949), and pD-modified aspartic acid (+282.2056); primary scoring type by XCorr and secondary by Zscore; minimum peptide length of six residues with a candidate peptide threshold of 500. A minimum of one peptide per protein and half-tryptic peptide specificity were required. Starting statistics were performed with a Δmass cutoff = 10 p.p.m. with modstat, and trypstat settings. False-discovery rates of peptide (sfp) were set to 0%, peptide modification requirement (-m) was set to 1, and spectra display mode (-t) was set to 1. TMT quantification was performed using the isobaric labeling 10-plex labeling algorithm, with a mass tolerance of 5.0 p.p.m. or less in cases where co-eluting peptide interfere. Reporter ions 129.13779, 130.134825 were used for relative quantification. In general, all quantified peptides have mass error of < 5 p.p.m..



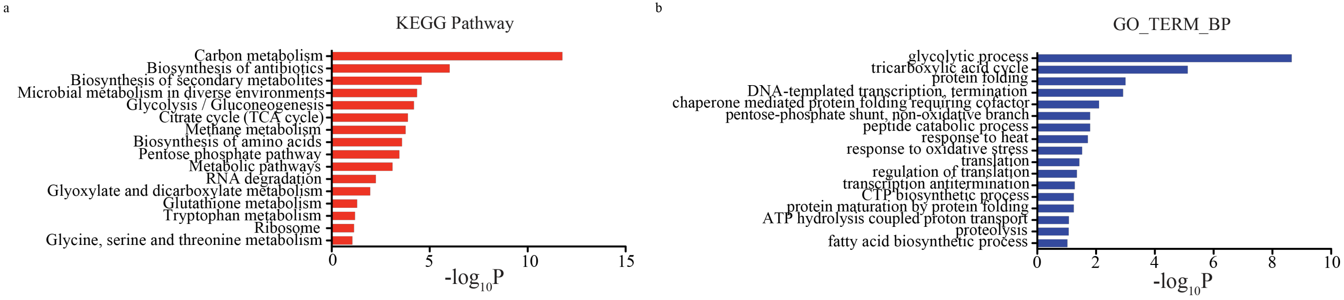
Supplemental Figure 1. Schematic depicting the peptide-level identification of DBHA-modification sites. DBHA-treated proteomes are reduced and alkylated in urea, trypsinized, enriched on streptavidin-agarose, modified peptides are eluted in 1:1 CH_3CN/H_2O with 0.1% TFA, and peptides are desalted for LC-MS/MS detection. Differential modification searching for DBHA-modified aspartic acids results in modification site identification.



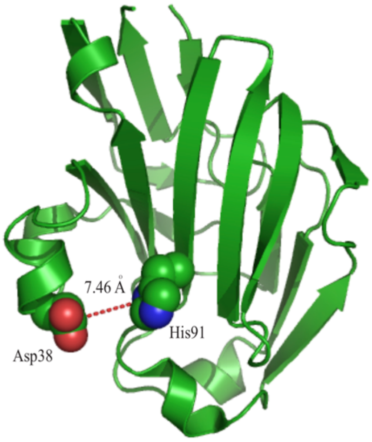
Supplemental Figure 2. Schematic depicting the peptide-level identification of DBHA-modification sites. DBHA-treated proteomes are reduced and alkylated in urea, trypsinized, enriched on streptavidin-agarose, modified peptides are eluted in 1:1 CH_3CN/H_2O with 0.1% TFA, and peptides are desalted for LC-MS/MS detection. Differential modification searching for DBHA-modified aspartic acids results in modification site identification.



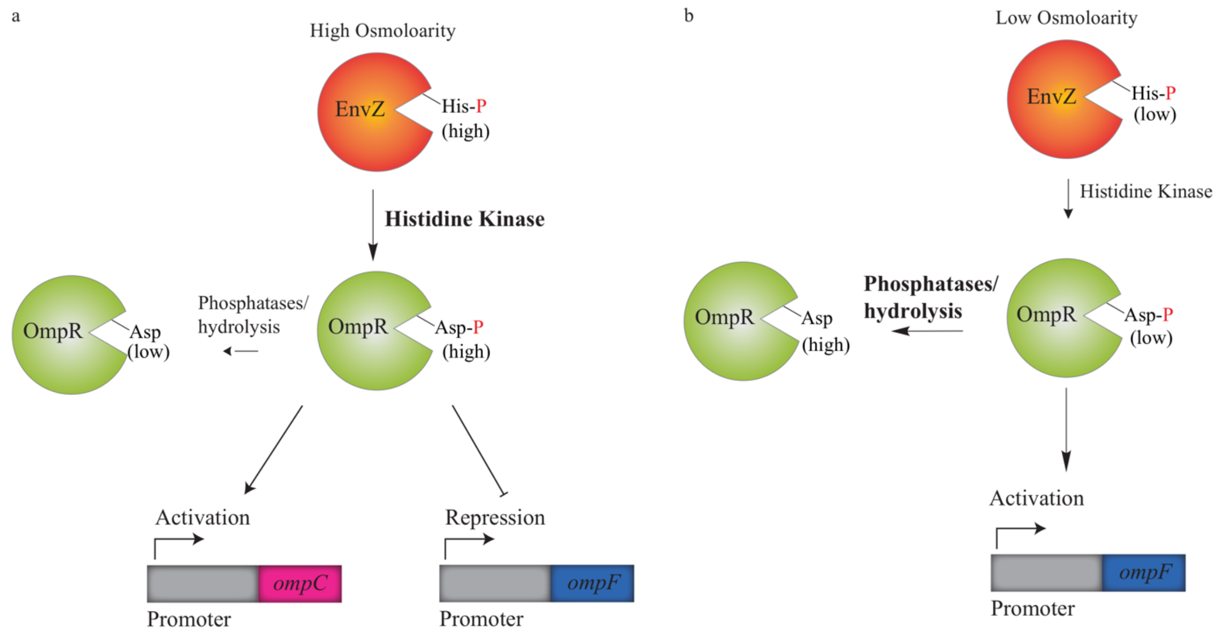
Supplemental Figure 3. Schematic depicting the peptide-level identification of DBHA-modification sites. DBHA-treated proteomes are reduced and alkylated in urea, trypsinized, enriched on streptavidin-agarose, modified peptides are eluted in 1:1 CH_3CN/H_2O with 0.1% TFA, and peptides are desalted for LC-MS/MS detection. Differential modification searching for DBHA-modified aspartic acids results in modification site identification.



Supplemental Figure 4. All significantly enriched KEGG pathways and Gene-ontology biological process categories among DBHA-modified proteins.



Supplemental Figure 5. Crystal structure of the *E. coli* histidine kinase protein Crr is shown with relevant residues (PDB: 1F3G). Histidine 91 is a known pHis site, and is located in high proximity to D38, which was detected with a DBHA-modification in our dataset, suggesting that transient phosphotransfer may occur and result in DBHA labeling.



Supplementary Figure 6. Schematic diagram of EnvZ/OmpR signaling in response to altered osmolarity. Briefly, high osmolarity results in increased OmpR phosphorylation, followed by transcriptional repression of OmpF, and activation of OmpC.

Supplementary Table 1. Comprehensive list of DBHA-modified proteins and peptides. All modification sites were detected in at last four LC-MS/MS replicate runs and exhibited suitable spectral statistics, as described in Methods.

Supplementary Table 2. Quantitative proteomic profiling of changes to protein level and DBHA-enrichment in response to high osmolarity. All ratios depict the aggregate of TMT channel quantification of individual tryptic peptides from replicate runs.

Author Contributions

J.W.C. and R.E.M. conceived the study. J.W.C. designed, performed and analyzed chemical syntheses, biochemical experiments, cell-based experiments, mass spectrometry experiments, and analyzed data. G.L. designed, performed and analyzed chemical syntheses and mass spectrometry experiments. J.E.M. performed and analyzed cell-based and mass spectrometry experiments. R.E.M. supervised the study, designed and analyzed experiments, and wrote the manuscript. All authors contributed to writing the manuscript.

Supplementary Table 1

Protein Descriptions	sequence	Charge State	XCorr	DeltCN	Conf%	Calc M+H+	ppm	Prob	TotalIntensity	SpR	IonProportion	Redundancy	globalFLR	localFLR
[P0A4D0 30S ribosomal protein S6 OS=Escherichia coli O6 GN=rpsF]	R.HYEIVFMVHPD(282.2056)QSEQVPGMIER.Y	4	3.67925	0.46065	100	2923.459	-2.27	7.736944	971238.3	1	30.8	2	2.99E-11	1.95E-11
[P0A6F6 60 kDa chaperonin OS=Escherichia coli O6 GN=groL]	R.QIVLNCGEEPSVVANTVKGGD(282.2056)GNYGYNAATEEYGNMIDMGILDPTKVTR.S	4	6.1333	0.527	100	5542.693	2.4	6.990459	2.79E+07	1	22.9	2	2.32E-06	7.89E-05
	K.ANDAAGD(282.2056)GTTTATVLAQAIITEGLK.A	3	3.6972	0.33672	100	2684.447	-4.2	6.555434	4321054	1	41.1	1	1.91E-05	0.002746
	K.ATLED(282.2056)LGQAK.R	2	2.3862	0.3082	100	1327.758	2.05	5.275362	990745.6	1	66.7	1	8.31E-10	3.65E-10
	K.GGD(282.2056)GNYGYNAATEEYGNMIDMGILDPTK.V	3	3.474067	0.496967	100	3248.488	-4.46667	7.869935	2290685	1	33.3	1	0.005934	0.005883
[P0A6M9 Elongation factor G OS=Escherichia coli O6 GN=fusA]	K.IGEVHD(282.2056)GAATMDWMEQEQER.G	3	3.21565	0.34395	100	2614.202	2.2	7.654236	828667	1	39.7	1	1.08E-09	4.80E-10
	R.VYSGVVNSGD(282.2056)TVLNSVK.A	2	3.08035	0.323867	100	2020.107	-3.75167	9.856055	470954.7	1	48.3	1	4.88E-05	1.90E-03
[P0A6N2 Elongation factor Tu OS=Escherichia coli O6 GN=tufA]	K.ALEGD(282.2056)AEWEAK.I	2	2.950333	0.3413	100	1500.769	1.2	7.734511	8804118	1	84.2	3	7.98E-06	2.43E-04
	K.CD(282.2056)MVDDEELLELVEMEVR.E	3	4.621333	0.550533	100	2506.187	4	6.172545	682017.7	1	32.2	1	0.007787	0.041945
	R.GITINTSHVEYD(282.2056)TPTR.H	3	4.174867	0.5751	100	2086.093	-0.4	7.424041	1905338	1	28.3	1	2.81E-10	1.20E-10
	R.HYAHVD(282.2056)CPGHADYVK.N	3	3.614663	0.370588	99.9	2050.992	4.241667	7.242086	3.54E+07	1	48.6	6	8.86E-06	3.88E-04
	R.TTDVTGTIELPEGVEMVMPGD(282.2056)NIK.M	3	4.47854	0.4519	100	2828.442	-3.98	5.422923	5292609	1	36.6	1	1.02E-04	1.97E-03
	K.ILELAGFLD(282.2056)SYIPEPER.A	2	3.4161	0.369467	100	2244.228	0.833333	6.629926	3185363	1	65.5	2	7.03E-10	3.13E-10
	R.AIDKPFLLPIED(282.2056)VFSISGR.G	3	3.41445	0.37765	100	2399.37	2.775	5.85866	1.66E+07	1	50	1	8.40E-10	3.74E-10
[P0A6P2 Elongation factor Ts OS=Escherichia coli O6 GN=tsf]	R.VAALEGD(282.2056)VLGSYQHGAR.I	3	2.73305	0.31745	99.4	2025.088	2.05	5.498847	2701511	1	44.9	1	5.50E-10	2.48E-10
[P0A6Q0 Enolase OS=Escherichia coli O6 GN=eno]	K.AAGYELGKDITLAMD(282.2056)CAASEFYK.D	3	5.5646	0.376375	99.7	2806.379	-1.7	8.321842	1.57E+07	1	60.7	2	4.64E-10	1.79E-10
	K.D(282.2056)QAGIDKIMIDLDGTENK.S	3	3.1615	0.431867	100	2258.17	-4.76667	8.13407	3419412	2	43.9	1	0.002519	0.004123
[P0A6R1 3-oxoacyl-[acyl-carrier-protein] synthase 3 OS=Escherichia coli O6 GN=fabH]	R.HGNTSAASVPCALD(282.2056)EAVRDGR.I	3	3.560975	0.56875	100	2465.231	4.725	8.879271	5888089	1	41.7	1	0.006535	0.004363
[P0A6Y9 Chaperone protein dnaK OS=Escherichia coli O6 GN=dnaK]	K.AKIELSSAQQTD(282.2056)VNLPYITADATGPK.H	3	3.30865	0.3723	100	3013.62	-4.6	6.549933	1086749	1	29.5	2	1.53E-05	7.42E-04
	K.HSQVFSTAED(282.2056)NQSAVTIHVLQGER.K	4	4.0662	0.458625	100	2935.502	-4.3875	7.801736	2971210	1	37.6	2	2.11E-09	7.27E-10
	K.TAEDYLGEPVTEAVITVPAYFND(282.2056)AQR.Q	3	3.93696	0.4947	100	3151.595	-3.06	7.7471	5419710	1	41.9	1	8.10E-05	1.75E-03
[P0A718 Ribose-phosphate pyrophosphokinase OS=Escherichia coli O6 GN=prs]	R.ANVSQVMHIIGDVAGRDCVLVDDMID(282.2056)TGGTLCK.A	4	6.3795	0.513643	100	3841.907	3.742857	7.172724	4.25E+07	1	34.7	3	1.32E-10	4.07E-11
[P0A7A0 Phosphoglycerate kinase OS=Escherichia coli O6 GN=pgk]	K.FAD(282.2056)VACAGPLLAAELDALGK.A	3	4.028738	0.460413	100	2284.237	4.3375	6.907443	2889038	1	38.5	1	2.20E-08	1.14E-06
	K.IAD(282.2056)QLIVGGGIANTFIAAQGHDVGK.S	3	4.38462	0.47388	100	2747.52	-2.89	10.3797	3904082	1	50.6	1	6.61E-03	1.41E-03
[P0A7E6 CTP synthase OS=Escherichia coli O6 GN=pyrG]	R.SGDD(282.2056)QLVEIIEVPNHPWFVACQFHPEFTSTPR.D	4	4.66885	0.51245	100	4034.986	-1.15	6.024978	2.03E+07	1	30.4	1	1.07E-04	3.39E-03
[P0A7J4 50S ribosomal protein L10 OS=Escherichia coli O6 GN=rplJ]	R.AVEGTPFECLKD(282.2056)AFVGPTLIAYSMEHPGAAAR.L	3	6.15025	0.51823	100	3687.866	1.025	6.631363	1411936	1	17.8	1	1.40E-10	6.11E-11
[P0A7V1 30S ribosomal protein S2 OS=Escherichia coli O6 GN=rpsB]	K.DAALSCD(282.2056)QFFVNHR.W	3	2.939533	0.406933	99.6	1961.965	-2.1	6.698929	7438513	1	56.8	3	1.84E-03	2.94E-02

Protein Descriptions	sequence	Charge State	XCorr	DeltCN	Conf%	Calc M+H+	ppm	Prob	TotalIntensity	SpR	IonProportion	Redundancy	globalFLR	localFLR
[P0A7V9 30S ribosomal protein S4 OS=Escherichia coli O6 GN=rpsD]	R.VVNIASYQVSPND(282.2056)VVSIR.E	3	3.3272	0.4166	100	2242.255	-2.24167	6.922903	2450059	1	50.9	1	1.04E-06	5.80E-05
[P0A826 Serine hydroxymethyltransferase OS=Escherichia coli O6 GN=glyA]	K.ELAGWMCD(282.2056)VLDSINDEAVIER.I	3	5.29888	0.50782	100	2717.327	-0.255	7.433316	1.72E+07	1	50	1	0.001256	0.001109
[P0A837 Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O6 GN=sucC]	R.LVTYQTD(282.2056)ANGQPVNQILVEAATDIAK.E	3	4.038	0.4673	99.8	3054.647	-1.63333	7.218959	5725411	1	34.2	2	2.27E-08	1.29E-06
[P0A8G7 Flavoprotein wrbA OS=Escherichia coli O6 GN=wrbA]	R.GGTPYGATTIAGGD(282.2056)GSRQPSQEELSIAR.Y	3	3.29535	0.4015	100	3058.555	-3.35	5.988062	975994.8	1	22.2	1	1.09E-09	4.81E-10
[P0A8V3 DNA-directed RNA polymerase subunit beta OS=Escherichia coli O6 GN=rpoB]	R.LSLGDLDTLMPQD(282.2056)MINAKPISAAVK.E	3	5	0.492433	100	2923.6	-1.99167	7.246008	9968577	1	27.8	1	4.37E-03	3.90E-03
[P0A956 KHG/KDPG aldolase OS=Escherichia coli O6 GN=eda]	K.AATEGTIPLIPGISTVSELMLGMD(282.2056)YGLKEFKFFPAEANGGVK.A	4	5.7366	0.52555	100	4681.466	-4.46667	6.526991	5031395	1	32.8	1	8.85E-11	8.85E-11
[P0A999 Ferritin-1 OS=Escherichia coli O6 GN=ftnA]	R.INTVESPFAEYSSLD(282.2056)ELFQETYKHEQLITQK.I	4	5.007	0.459033	100	3970.012	-1.68333	7.154652	1.49E+07	1	33	3	5.65E-11	2.39E-11
	R.LFD(282.2056)YLTDTGNLPR.I	3	2.47002	0.4318	100	1806.975	0.54	6.848366	1708776	1	39.5	1	1.11E-10	7.13E-11
[P0A9B3 Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli O6 GN=gapA]	K.VIND(282.2056)NFGIIEGLMTTVHATTATQK.T	3	5.7368	0.386113	100	2856.529	-4.125	7.260034	9381950	1	50.7	2	2.49E-09	7.68E-10
[P0A9G7 Isocitrate lyase OS=Escherichia coli O6 GN=aceA]	R.TDADAADLITSD(282.2056)CDPYDSEFITGER.T	3	4.289625	0.513813	100	3059.379	2.3375	10.05186	2.71E+07	2	45.8	1	1.31E-10	3.96E-11
[P0A9L0 FKBP-type peptidyl-prolyl cis-trans isomerase slyD OS=Escherichia coli O6 GN=slyD]	R.FLAETD(282.2056)QGPVPVEITAVEDDHVVVDGNHMLAGQNLK.F	4	3.2496	0.3567	99.8	4140.107	-2.65833	5.93886	1178425	1	12.6	1	1.18E-10	8.10E-11
[P0A9S6 Glycerol dehydrogenase OS=Escherichia coli O6 GN=gldA]	K.ALAHFMGVPVAIAPTIASTD(282.2056)APCSALSVIYTDEGEFDR.Y	3	3.575557	0.357571	100	4275.147	-1.44286	6.566715	1646127	1	29.8	1	9.92E-10	4.33E-10
[P0AA17 Transcriptional regulatory protein ompR OS=Escherichia coli O6 GN=ompR]	R.ESFHLMVLD(282.2056)LMLPGEDGLSICR.R	3	4.632738	0.31695	100	2814.435	2.075	8.332836	2493783	1	47.7	1	1.11E-09	4.83E-10
[P0AA26 Thioredoxin-1 OS=Escherichia coli O6 GN=trxA]	K.LNID(282.2056)QNPGTAPK.Y	2	2.504225	0.38055	100	1549.87	5.908752	766150.1	1	50	1	9.11E-10	4.05E-10	9.11E-10
[P0AAI6 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Escherichia coli O6 GN=fabF]	K.SMTGHLLGAAGAVESIYSILALRDQAVPPTINLDNPDEGCD(282.2056)LDFVPHEAR.Q	5	5.68332	0.52692	100	5627.826	2.48	8.794396	1.64E+07	1	36.9	2	1.33E-10	4.06E-11
[P0AAJ0 Malonyl CoA-acyl carrier protein transacylase OS=Escherichia coli O6 GN=fabD]	K.ITFNAPTVPVVNNVD(282.2056)VKCETNGDAIRDALVR.Q	4	4.2335	0.405833	99.6	3679.959	3.233333	6.955297	2.87E+07	2	33.9	1	0.000762	0.001653
[P0ABB1 ATP synthase subunit alpha OS=Escherichia coli O6 GN=atpA]	R.IHGLAD(282.2056)CMQGEMISLPGNR.Y	3	4.06826	0.44816	99.8	2381.189	-0.505	6.457961	1443956	1	42	1	4.04E-10	2.02E-10
[P0ABB5 ATP synthase subunit beta OS=Escherichia coli O6 GN=atpD]	R.AAPSYEELSNSQELLETGIKVID(282.2056)LMCPFAK.G	4	6.707	0.549675	99.7	3635.87	3.6	7.216695	5.72E+07	1	32.7	5	4.64E-06	1.91E-04
[P0ABH8 Citrate synthase OS=Escherichia coli O6 GN=gltA]	R.D(282.2056)SHPMAVMCGITGALAAFYHDSLDVNNPR.H	4	7.981388	0.6695	100	3441.65	-1.8625	11.94151	3.40E+07	1	37.7	4	5.12E-10	2.48E-10
	R.ETCHEVLKELGTKDD(282.2056)LLEVAMELENIALNDPYFIEK.K	5	4.668967	0.518867	99.8	4501.288	2.933333	6.973507	1.87E+07	2	31	1	1.33E-10	4.11E-11
	R.GFPIDQLATD(282.2056)SNYLEVCYILLNGEKPTQEQYDEFKTTVTR.H	4	7.406	0.54855	100	4978.482	3.125	9.410625	2.21E+07	2	31.7	9	1.90E-03	1.94E-03
	K.ITFIDGD(282.2056)EGILLHR.G	3	3.117067	0.327767	100	1881.059	2.866667	7.416337	2250791	1	45.5	1	6.29E-04	0.004688
[P0AC42 Succinate dehydrogenase flavoprotein subunit OS=Escherichia coli O6 GN=sdhA]	R.AGVPVQD(282.2056)MEMWQFHPTGIAGAGVLVTEGCR.G	3	4.309533	0.502667	99.8	3495.733	-1.01667	7.6584	1.44E+07	1	33.1	2	1.38E-04	3.86E-03
	K.GSDYIGD(282.2056)QDAIEYMCK.T	2	2.5696	0.4905	100	2146.978	-4.7	9.019269	833211.8	1	50	1	0.001312	0.007776
[P0ACD5 NifU-like protein OS=Escherichia coli O6 GN=nifU]	K.SLDEAQAIKNTDIAEELELPPVKIHCSILAED(282.2056)AIK.A	3	5.581967	0.41205	99.9	4156.221	-3.18333	6.412707	1.45E+07	1	40.6	1	6.13E-04	1.23E-03
[P0ACF1 DNA-binding protein HU-alpha OS=Escherichia coli O6 GN=hupA]	K.AALESTLAAITESLKEGD(282.2056)AVQLVGFGTFK.V	3	5.6069	0.463	100	3248.778	-4.95	5.470314	5703632	2	30.7	1	1.88E-09	7.64E-10
[P0ACF9 DNA-binding protein H-NS OS=Escherichia coli O6 GN=hns]	R.EMLIADGID(282.2056)PNELLNSLAAVK.S	2	3.24635	0.465875	100	2508.374	-3.67083	7.928573	4607238	1	40.6	1	1.12E-10	7.21E-11
[P0ADY4 50S ribosomal protein L14 OS=Escherichia coli O6 GN=rplN]	R.YAGVGD(282.2056)IIKITIKEAIPR.G	3	4.007533	0.4364	100	2239.354	-3.525	9.016177	1621799	1	40.6	2	4.38E-10	2.06E-10
[P0AE09 Alkyl hydroperoxide reductase subunit C OS=Escherichia coli O6 GN=ahpC]	R.ATFVVD(282.2056)PQGIIQAIEVTAEGIGR.D	2	3.407975	0.518075	100	2666.488	-3.7925	9.759778	956110.7	1	31.3	2	3.94E-11	2.57E-11

Protein Descriptions	sequence	Charge State	XCorr	DeltCN	Conf%	Calc M+H+	ppm	Prob	TotalIntensity	SpR	IonProportion	Redundancy	globalFLR	localFLR
	R.NFDNMRED(282.2056)EGLADR.A	3	2.319125	0.3452	99.8	1963.929	0.175	6.586012	3687123	1	35.4	1	1.06E-10	6.93E-11
	R.WSVFFFYPAD(282.2056)FTFVCPTELGDVADHYEELQK.L	4	4.87235	0.433725	99.7	4039.925	2.55	7.689168	6581791	1	29.2	2	5.30E-05	1.66E-03
[P0AEP4 UTP--glucose-1-phosphate uridylyltransferase OS=Escherichia coli O6 GN=galU]	K.GLGHAVLCAHPVVGD(282.2056)EPVAVILPDVILDEYESDLSQDNLAEMIR.R	4	6.015757	0.513986	100	5051.585	1.457143	6.652686	673079.3	1	9.7	1	3.86E-03	2.96E-03
[P0AEU1 Histidine-binding periplasmic protein OS=Escherichia coli O6 GN=hisJ]	K.GIEIVSYQGQD(282.2056)NIYSDLTAGR.I	3	2.9582	0.4322	100	2581.326	-4.625	6.797157	4106664	1	39.3	1	5.30E-05	0.002047
[P0AEU8 Chaperone protein skp OS=Escherichia coli O6 GN=skp]	K.D(282.2056)ITADVLK.Q	2	2.2374	0.324867	100	1156.694	0.9	6.444761	3211289	1	85.7	1	9.29E-11	6.07E-11
[P0AFF7 Transcription elongation protein nusA OS=Escherichia coli O6 GN=nusA]	R.GVCTLED(282.2056)LAEQGIDDLADIEGLTDEKAGALIMAAR.N	5	7.3384	0.5854	99.7	3955.999	3.622222	8.079259	2222568	1	21.8	1	6.37E-05	2.00E-03
[P0AFG4 2-oxoglutarate dehydrogenase E1 component OS=Escherichia coli O6 GN=sucA]	R.STFQQLPGTGVKPD(282.2056)QFHSQTR.E	4	2.9251	0.3077	99.9	2641.385	-1.2	6.095705	4818985	1	36.2	1	6.64E-10	2.63E-10
[P0AFH9 Osmotically-inducible protein Y OS=Escherichia coli O6 GN=osmY]	K.GYAGD(282.2056)TATTSEIK.A	2	2.24955	0.36305	100	1595.828	1.85	7.314196	642619.8	1	66.7	1	9.84E-10	4.44E-10
	K.VETTDGVVQLSGTVD(282.2056)SQAQSDRAESIAK.A	3	2.914933	0.4465	100	3173.628	-4.5	7.402868	226161.9	2	20.6	1	1.01E-07	1.87E-05
[P0AFL4 Peptidyl-prolyl cis-trans isomerase A OS=Escherichia coli O6 GN=ppiA]	K.APVSVQNFVD(282.2056)YVNSGFYNNTTFHR.V	3	3.74945	0.38695	100	3058.517	-0.575	6.424553	2359510	1	49.3	1	6.09E-10	2.72E-10
[P0AG08 Ribulose-phosphate 3-epimerase OS=Escherichia coli O6 GN=rpe]	K.VNNIGEIAAAGAD(282.2056)M(15.9949)FVAGSAIFDQPDYK.K	3	3.1897	0.4542	100	3182.583	-3	6.794992	3451644	1	33.7	1	8.70E-10	3.77E-10
[P0AG31 Transcription termination factor Rho OS=Escherichia coli O6 GN=rho]	K.TMLLQNIAQSIAYNHPD(282.2056)CVLMVLLIDERPEEVTEMQR.L	5	5.0264	0.51065	100	4652.371	3.625	8.331747	1.40E+07	1	33.6	2	1.02E-04	1.99E-03
[P0AG56 50S ribosomal protein L6 OS=Escherichia coli O6 GN=rplF]	K.GNVINLSLGFSHPVD(282.2056)HQLPAGITAECPTQTEIVLK.G	4	6.562867	0.330733	99.7	4038.148	0.9	5.357041	1.79E+07	1	36.5	1	5.32E-10	2.72E-10
[P0AG68 30S ribosomal protein S1 OS=Escherichia coli O6 GN=rpsA]	K.AYED(282.2056)AETVTGVINGK.V	2	2.1989	0.4094	99.6	1848.97	2.15	7.788189	726610.8	1	55	1	9.35E-10	4.22E-10
	R.AVIESENSAERD(282.2056)QLLENLQEGMEVK.G	3	4.279333	0.447467	100	3113.578	-4.7	8.664146	1570020	1	33.7	2	7.42E-10	3.31E-10
[P0AGD4 Superoxide dismutase [Fe] OS=Escherichia coli O6 GN=sodB]	K.VAEAIAASFGSFAD(282.2056)FK.A	3	4.335625	0.525475	100	1913.017	-0.875	9.161053	2134886	1	46	2	1.11E-11	7.27E-12
[P60758 ATP phosphoribosyltransferase OS=Escherichia coli O6 GN=hisG]	R.AGLADAICD(282.2056)LVSTGATLEANGLREVEVIYR.S	4	4.0067	0.503483	99.2	3458.831	3.966667	7.204071	9157154	4	32.3	2	1.30E-10	3.95E-11
[P60907 Histidyl-tRNA synthetase OS=Escherichia coli O6 GN=hisS]	R.VLDSKNPEVQALLNDAPALGDYLD(282.2056)EESREHFAGLCK.L	5	4.17415	0.440467	99.4	4296.161	4.533333	6.84934	3.62E+07	1	32.7	1	1.33E-10	4.09E-11
[P61890 Malate dehydrogenase OS=Escherichia coli O6 GN=mdh]	K.GKQPGEVEVPVIGGHSGVTILPLLSQVPGVSFTEQEVAD(282.2056)LTKR.I	4	3.92275	0.27495	100	4750.614	-1.3	5.632754	2184913	1	25	1	7.56E-10	3.41E-10
	R.ALQGEQGVVECAYVEGD(282.2056)GQYAR.F	3	3.88982	0.5087	100	2681.299	-4.84	7.410256	1162259	1	36.2	1	5.00E-08	1.51E-06
[P62400 50S ribosomal protein L5 OS=Escherichia coli O6 GN=rplE]	K.LLD(282.2056)NAAADLAAISGQKPLITK.A	3	3.96532	0.38668	100	2405.413	-4.56	7.332753	2983623	1	52.5	1	0.006299	0.002033
[P62708 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Escherichia coli O6 GN=gpmA]	K.YLD(282.2056)NMSEEEILELNIPTGVPLVYEFDENFKPLKR.Y	4	4.189867	0.3218	100	4337.241	-3.13333	6.024743	1613360	1	20.8	2	9.79E-10	4.29E-10
	R.AIHTLWNVLD(282.2056)ELDQAWLPVEK.S	3	4.0967	0.310467	100	2772.508	-3.8	5.433195	3726383	1	45.8	1	1.01E-07	1.87E-05
[P63226 Phosphoheptose isomerase OS=Escherichia coli O6 GN=gmhA]	R.NELNEAAETLANFLKD(282.2056)DANIHAIQR.A	4	4.4025	0.4971	100	3092.612	-0.475	7.727639	2268951	1	29.3	1	0.004114	0.005093
[P68766 Cytosol aminopeptidase OS=Escherichia coli O6 GN=pepA]	K.GLTFDSGGISIKPSEGMD(282.2056)EMK.Y	2	3.5527	0.2932	100	2481.204	-0.675	7.613343	5762888	1	68.6	2	1.31E-06	7.38E-05
[P69777 Major outer membrane lipoprotein OS=Escherichia coli O6 GN=lpp]	K.IDQLSSD(282.2056)VQTLNAK.V	2	2.647967	0.432267	100	1814.002	-3.71667	7.747963	422734.3	1	40	1	9.09E-11	5.94E-11
[P69784 Glucose-specific phosphotransferase enzyme IIA component OS=Escherichia coli O6 GN=crr]	K.VGDTVIEFD(282.2056)LPLLEEK.A	2	3.3482	0.504938	100	2099.163	-1.325	9.107833	3072686	1	55.2	1	7.83E-11	5.12E-11
	K.DTGTIEIIAPLSGEIVNIEDVPD(282.2056)VVFAEK.I	3	3.0544	0.5425	100	3365.809	-1.9	8.284775	559221.6	1	21.8	3	3.80E-10	1.49E-10

Protein Descriptions	sequence	Charge State	XCorr	DeltCN	Conf%	Calc M+H+	ppm	Prob	TotalIntensity	SpR	IonProportion	Redundancy	globalFLR	localFLR
[Q8CVB3 ABC transporter Periplasmic binding protein ytfQ OS=Escherichia coli O6 GN=ytfQ]	R.SFVAQGVD(282.2056)AIFIAPVVATGWEPVLK.E	3	3.45915	0.39995	100	2896.634	-4.45	6.137115	2442318	1	41.1	1	7.26E-10	3.23E-10
[Q8CVJ7 D-ribose-binding periplasmic protein OS=Escherichia coli O6 GN=rbsB]	K.ELANVQD(282.2056)LTVR.G	2	2.882467	0.378067	99.5	1539.885	-4.39	7.285852	2542348	1	72.2	1	4.99E-11	3.26E-11
	K.MANQANIPVITLD(282.2056)R.Q	2	4.36659	0.49057	100	1838.032	-3.16	7.851164	611425.5	1	52.4	1	5.83E-05	1.12E-03
	K.D(282.2056)GAQKEADKLGYNLVVLDSQNNPAK.E	4	3.19175	0.3705	99.3	2969.569	-3.475	5.378007	2080427	1	29.8	1	0.009019	0.007221
	K.GLNVMQNLLTAHPD(282.2056)VQAVFAQNDEMALGALR.A	4	4.695629	0.512529	100	3618.888	-3.05714	7.681211	1.24E+07	1	28	1	1.12E-09	4.84E-10
	K.ILLINPTD(282.2056)SDAVGNAVK.M	2	2.757775	0.334325	100	2022.159	4.325	6.061663	5260906	1	48.3	1	0.00763	0.002931
	K.SD(282.2056)VMVVGFDGTPDGEKAVNDGK.L	3	4.1393	0.4297	100	2519.245	1.7	7.462507	2002832	1	46.8	1	9.56E-10	4.31E-10
[Q8CVS8 Glycine betaine-binding periplasmic protein OS=Escherichia coli O6 GN=proX]	K.LFAIMQLPVADINAQNAIMHD(282.2056)GK.A	3	4.1691	0.4701	100	2792.495	-1.25	7.879578	3242287	1	28.9	1	1.36E-05	6.31E-04
[Q8CVZ5 Protein yebF OS=Escherichia coli O6 GN=yebF]	K.IVGQAD(282.2056)PVAWVSLQDIQGKDDKWSVPLTVR.G	4			100	3602.969	2.1	6.816507	3347588	1	33.1	1	8.96E-10	3.84E-10
[Q8CW07 Putative uncharacterized protein ynhG OS=Escherichia coli O6 GN=ynhG]	R.YVEVHRPLSAEEQQNVQTMPYTLPAGFTQFKD(282.2056)NK.A	5	3.83755	0.3405	100	4248.155	-0.95	5.559866	2287705	1	30.3	1	3.44E-09	1.36E-09
[Q8CW44 Periplasmic oligopeptide-binding protein OS=Escherichia coli O6 GN=oppA]	K.WSDGTPVTAQD(282.2056)FVYSWQR.S	3	5.62112	0.59114	99.6	2425.194	-1.80286	6.932344	450633.2	1	15.8	1	5.32E-10	2.55E-10
	K.AEQQLD(282.2056)KDSAIVPVYYYVNAR.L	3	3.873971	0.386414	100	2724.436	-4.8	6.582139	1332939	1	40.3	1	0.002728	0.007778
[Q8CW76 Outer membrane protein A OS=Escherichia coli O6 GN=ompA]	K.ATLKPEGQAALD(282.2056)QLYSQLSNLDPK.D	3	3.68682	0.39846	100	2882.562	-3.94	7.445889	4747262	1	41.8	1	1.37E-03	2.99E-03
	R.GMGESNPVTGNTCD(282.2056)NVK.Q	2	2.7132	0.30345	99.9	2061.969	-1.175	6.168942	294063.8	1	34.6	1	1.06E-09	4.76E-10
[Q8CW78 Outer membrane protein F OS=Escherichia coli O6 GN=ompF]	K.YADVGSFD(282.2056)YGR.N	2	2.6079	0.5093	100	1531.754	3.4	10.40942	1864555	1	60	1	1.18E-10	3.59E-11
[Q8CWD1 Protease do OS=Escherichia coli O6 GN=htrA]	R.SGLNAENYENFIQTD(282.2056)AAINR.G	2	5.2299	0.6349	100	2522.263	-4.73333	12.25428	1002421	1	66.7	1	3.30E-11	1.01E-11
[Q8CXW0 Transcriptional Regulatory protein basR/pmrA OS=Escherichia coli O6 GN=basR]	R.MAEQSLEAGHYSLVVLD(282.2056)LGLPDEDGLHFLAR.I	4	4.3955	0.2993	100	3677.9	3.9	7.617318	5197688	1	35.5	1	8.18E-10	3.69E-10
[Q8FAE5 Mg(2+) transport ATPase, P-type 1 OS=Escherichia coli O6 GN=mgtA]	K.VCHEVGLD(282.2056)AGEVVIGSDIETLSDDELANLAQR.T	4	6.997056	0.395533	99.8	3706.859	4.877778	7.417605	2.05E+07	1	35.7	2	3.43E-03	2.67E-03
[Q8FAU3 Alpha-galactosidase OS=Escherichia coli O6 GN=melA]	R.NDGLIDNLPQGCCVEVACLVD(282.2056)ANGIQPTK.V	3	4.24408	0.36262	100	3452.697	-1.16	7.278889	6314490	1	34.1	3	1.17E-10	8.00E-11
	R.TIPHLWQICED(282.2056)MTEVCPDATMLNYVNPMAMNTWAMYAR.Y	4	5.15355	0.552867	100	4856.23	1.466667	6.126363	646954.9	1	11.6	1	1.33E-10	4.09E-11
[Q8FAV0 PhnB protein OS=Escherichia coli O6 GN=phnB]	K.SAQD(282.2056)SAENCPSGMQFPDTAIAHANVR.I	3	4.51475	0.49745	99.9	3056.431	3.15	9.05452	3508989	1	38.9	2	2.33E-04	4.72E-03
[Q8FB83 DNA-directed RNA polymerase subunit beta' OS=Escherichia coli O6 GN=rpoC]	K.AMMDNLQTETVINRD(282.2056)GQEEK.Q	3	3.615475	0.510175	99.6	2604.276	-0.325	7.112984	1.59E+07	1	47.5	1	4.36E-10	2.09E-10
	K.IVDAQGND(282.2056)VLIPGTDMPAQYFLPGK.A	3	3.69355	0.24555	99.8	2941.549	-4.3	5.116859	4394298	1	43.1	1	0.009944	0.002602
[Q8FBA9 Catalase-peroxidase OS=Escherichia coli O6 GN=katG]	R.FAPLNSWPD(282.2056)NVSLDK.A	2	2.720475	0.36325	100	1985.049	2.675	8.067015	2413244	1	64.3	1	1.06E-09	4.55E-10
[Q8FBC3 Glycerol kinase OS=Escherichia coli O6 GN=glpK]	K.YIVALD(282.2056)QGTTSSR.A	2	2.9998	0.4019	100	1692.928	-1.275	9.604556	1006605	1	61.9	1	4.40E-04	0.001219
[Q8FBV2 Tryptophanase OS=Escherichia coli O6 GN=tnaA]	K.MVAFSNYFFD(282.2056)TTQGHSQINGCTVR.N	3	4.26642	0.4187	100	3062.461	-0.99	8.47233	1311568	1	31	3	2.19E-03	2.89E-02
	R.IAQVQYLVD(282.2056)GLEEIGVVCQQAGGHAAFVDAGK.L	4	3.8859	0.2809	99.8	3624.884	-2.4	5.378563	3197558	1	35.9	1	1.09E-09	4.81E-10

Protein Descriptions	sequence	Charge State	XCorr	DeltCN	Conf%	Calc M+H+	ppm	Prob	TotalIntensity	SpR	IonProportion	Redundancy	globalFLR	localFLR
[Q8FCA1 2-amino-3-ketobutyrate coenzyme A ligase OS=Escherichia coli O6 GN=kbl]	R.YANND(282.2056)MQELEAR.L	2	2.6464	0.3583	99.9	1735.843	-4.68333	5.891358	1484420	1	18.4	1	1.36E-05	6.31E-04
[Q8FCA6 2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Escherichia coli O6 GN=gpmI]	K.TPVMDALWANRPHTLIDASGLEVGLPD(282.2056)RQMGNSEVGHVNLGAGR.I	5	5.682638	0.48555	99.8	4933.531	-0.0375	7.44647	3.26E+07	1	39.8	2	1.68E-08	8.58E-07
Protein Descriptions	sequence	Charge State	XCorr	DeltCN	Conf%	Calc M+H+	ppm	Prob	TotalIntensity	SpR	IonProportion	Redundancy	goballFLR	localFLR
[Q8FD87 Polyribonucleotide nucleotidyltransferase OS=Escherichia coli O6 GN=pnp]	R.VGYIND(282.2056)QYVLNPTQDELKESK.L	3	2.8745	0.3473	99.8	2735.425	-3.4	5.825948	1251774	1	42.4	1	1.08E-09	4.80E-10
[Q8FE38 Transketolase 1 OS=Escherichia coli O6 GN=tktA]	K.YGVERQD(282.2056)GPTALILSR.Q	3	5.786975	0.483025	99.8	2057.15	-1.875	6.492442	3850584	1	31.7	2	3.22E-10	1.57E-10
[Q8FE53 Fructose-bisphosphate aldolase class II OS=Escherichia coli O6 GN=fba]	K.ENNFALPAVNCVGTD(282.2056)SINAVLETAAK.V	3	3.775229	0.442629	99.6	3000.546	-1.61071	7.531749	2764233	1	29.5	4	3.06E-10	1.68E-10
[Q8FE67 Glycine dehydrogenase [decarboxylating] OS=Escherichia coli O6 GN=gcvP]	R.HIGPD(282.2056)AAQQQEMLNAVGAQSLNALTGQIVPK.D	3	5.176067	0.579967	100	3481.858	-4.8	10.67853	2192994	1	44.8	1	7.53E-10	3.35E-10
[Q8FF47 Peptidase B OS=Escherichia coli O6 GN=pepB]	K.ATYSINNDGITLHLNGAD(282.2056)DLGLIQR.A	3	4.28125	0.49045	100	2966.569	-4.4	9.339482	2719971	1	39.7	1	0.001012	0.008692
[Q8FF53 Nucleoside diphosphate kinase OS=Escherichia coli O6 GN=ndk]	R.ADYADSLTENGTHGSD(282.2056)SVESAAR.E	3	3.151833	0.518567	100	2635.223	-0.13333	7.769305	793592.5	1	32.9	2	1.03E-09	4.63E-10
[Q8FFB8 Cysteine synthase A OS=Escherichia coli O6 GN=cysK]	K.GKTDLISVAVEPTD(282.2056)SPVIAQALAGEEIKPGPHK.I	5	4.25485	0.3488	99.6	3650.016	-1.7	5.335237	6940755	1	32.8	1	9.59E-10	4.26E-10
[Q8FFI9 Phosphate acetyltransferase OS=Escherichia coli O6 GN=pta]	R.TGGDAPD(282.2056)QTTTIVR.A	2	2.6056	0.282	100	1713.913	-1.125	6.258899	983413.5	1	71.4	1	0.001174	0.00569
[Q8FFJ9 NADH-quinone oxidoreductase subunit G OS=Escherichia coli O6 GN=nuoG]	R.IAPYYHLFGSD(282.2056)ELSQR.A	3	2.5053	0.3855	99.7	2178.134	-4.975	5.690764	2414814	1	39.6	1	5.04E-10	1.97E-10
	R.RGDDFITLNAEQAMQGAAD(282.2056)ILR.Q	3	4.08415	0.3534	100	2687.393	-4.45	6.043969	3717534	1	44.6	1	3.64E-08	4.29E-06
[Q8FFX8 Methionyl-tRNA synthetase OS=Escherichia coli O6 GN=metG]	K.AQQLGITPEQMIGEMSQEHQTD(282.2056)FAGFNISYDNYHSTHSEENR.Q	5	3.0945	0.3595	99.4	5122.333	-3.8	5.700945	1766296	1	15.9	1	2.84E-09	3.70E-07
[Q8FFY8 D-tagatose-1,6-bisphosphate aldolase subunit gatZ OS=Escherichia coli O6 GN=gatZ]	R.ERIILGGDHLGPNCWQQENAD(282.2056)AAMEK.S	3	3.62525	0.52015	100	3234.578	3.3	7.646817	4719584	1	30.7	1	3.32E-04	9.02E-03
	R.IILGGD(282.2056)HLGPNCWQQENADAAMEK.S	3	4.6503	0.383813	99.7	2949.435	2.825	6.593102	1.90E+07	1	48.6	3	1.20E-10	6.39E-11
[Q8FG44 6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli O6 GN=gnd]	K.IAAVAED(282.2056)GEPCVTYIGADGAGHYVK.M	3	4.04575	0.507875	99.8	2845.419	3.625	8.237231	6376046	2	35.6	2	1.02E-04	1.99E-03
[Q8FH20 6-phosphofructokinase isozyme 2 OS=Escherichia coli O6 GN=pfkB]	R.CIVD(282.2056)SSGEALSAALAIGNIELVKPNQK.E	3	5.574733	0.596367	100	3079.682	3.766667	9.053409	1.09E+07	1	39.7	1	4.11E-10	2.24E-10
[Q8FHS5 Phage shock protein A OS=Escherichia coli O6 GN=pspA]	K.SLDD(282.2056)QFAELKADDAISEQLAQLK.A	3	4.0881	0.327333	100	2830.483	-3.46667	5.995772	3819777	1	58.7	1	1.50E-04	0.001821
[Q8FHX2 Aldehyde-alcohol dehydrogenase OS=Escherichia coli O6 GN=adhE]	K.LVAMGGIGHTSCLYTD(282.2056)QDNQPAR.V	3	4.943375	0.521625	100	2786.371	-0.65	8.825508	1.95E+07	1	41.4	3	0.005678	0.004265
	K.SLCAFGGLD(282.2056)AVTHAMEAYVSVLASEFSDGQALQALK.L	4	5.0106	0.528038	99.7	4039.03	2.275	8.15414	1552235	1	14	3	0.000638	0.007105
[Q8FJ96 Aminopeptidase N OS=Escherichia coli O6 GN=pepN]	K.GGHPVNSVLNVTQAEQTFVFD(282.2056)NVYFQPVPALLCEFSAPVKLEYK.W	4	5.7337	0.4293	100	5234.702	-0.43333	6.72245	1.20E+07	1	30.2	1	3.78E-10	2.06E-10
[Q8FJM0 DNA protection during starvation protein OS=Escherichia coli O6 GN=dps]	R.TALIDHLD(282.2056)TMAER.A	2	5.5297	0.453425	100	1767.942	-0.96	7.157894	1.57E+07	1	37.5	2	1.91E-10	9.65E-11
[Q8FJT8 Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Escherichia coli O6 GN=sucB]	R.QQASLEEQNND(282.2056)ALSPAIRR.L	3	3.3541	0.4164	100	2422.28	-1.05	6.314877	2095966	1	43.1	1	1.20E-10	3.65E-11
[Q8FKM7 Xanthine phosphoribosyltransferase OS=Escherichia coli O6 GN=gpt]	R.HVD(282.2056)TVCISSYDHDNQR.E	3	2.828833	0.509067	100	2228.051	4.033333	9.495481	1714041	1	53.5	1	0.002092	0.001527
[Q8FL41 Aconitate hydratase 2 OS=Escherichia coli O6 GN=acnB]	R.MLLPDTVGTGGD(282.2056)SHTRFPIGISFPAGSGLVAFAAATGVMPLDMPESVLVR.F	4	3.479	0.3104	100	5337.784	-1.7	5.712161	1980895	1	15.5	1	0.001989	0.001699
[Q8FL43 Pyruvate dehydrogenase E1 component OS=Escherichia coli O6 GN=aceE]	K.LIQLMNETVDGD(282.2056)YQTFK.S	2	7.711014	0.534243	100	2297.185	-1.825	8.58541	5.94E+07	1	24	2	2.19E-04	6.29E-03
[Q8FLD1 Transaldolase B OS=Escherichia coli O6 GN=talB]	K.LYQPQD(282.2056)ATTNPSLILNAAQIPEYR.K	3	3.581475	0.358738	100	2998.6	-4.975	6.31171	4566406	1	42.9	1	3.23E-09	9.96E-10

	R.ITESEFLWQHNQD(282.2056)PMAVDK.L	3	3.8113	0.3	100	2570.271	-4.73333	5.470058	2261317	1	40.4	1	4.64E-05	2.03E-03

Supplementary Table S2 – TMT ratio without DBHA

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P17446	betI	0.3035108	HTH-type transcriptional regulator OS=Escherichia coli O6 GN=betI
P0AAD6	sdaC	0.3231478	Serine transporter OS=Escherichia coli O6 GN=sdaC
P28629	adiA	0.3376048	Biodegradative arginine decarboxylase OS=Escherichia coli O6 GN=adiA
W8ZQQ8	prfA	0.3504218	Peptide chain release factor 1 OS=Escherichia coli O6 GN=prfA
P0A8H6	yihI	0.3598991	Der GTPase-activating protein YihI OS=Escherichia coli O6 GN=yihI
P0AGK4	yhbY	0.3902801	RNA-binding protein YhbY OS=Escherichia coli O6 GN=yhbY
P76372	wzzB	0.395638	Chain length determinant protein OS=Escherichia coli O6 GN=wzzB
A0A0H2V5L9	c0952	0.4007883	Major capsid protein OS=Escherichia coli O6 GN=c0952
P08014	sdhB	0.4044381	Succinate dehydrogenase iron-sulfur protein OS=Escherichia coli O6 GN=sdhB
P0A9G6	aceA	0.4337789	Isocitrate lyase OS=Escherichia coli O6 GN=aceA
P43672	uup	0.4789615	ABC transporter ATP-binding protein uup OS=Escherichia coli O6 GN=uup
P02925	rbsB	0.4798012	D-ribose-binding periplasmic protein OS=Escherichia coli O6 GN=rbsB
A0A0H2VAK2	c2392	0.4896955	Putative P4-family integrase OS=Escherichia coli O6 GN=c2392
P69801	manY	0.5011332	Mannose permease IIC component OS=Escherichia coli O6 GN=manY
P0A7D7	purC	0.5087966	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Escherichia coli O6 GN=purC
P77454	glsA1	0.5136018	Glutaminase 1 OS=Escherichia coli O6 GN=glsA1
P77747	ompN	0.520146	Outer membrane protein N OS=Escherichia coli O6 GN=ompN
A0A0H2VGI6	c5432	0.5225545	Uncharacterized protein OS=Escherichia coli O6 GN=c5432
P77757	arnC	0.5251272	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase OS=Escherichia coli O6 GN=arnC
P0ADE2	ytfK	0.5388041	Uncharacterized protein ytfK OS=Escherichia coli O6 GN=ytfK
P69786	ptsG	0.5401173	PTS system glucose-specific EIICB component OS=Escherichia coli O6 GN=ptsG
P0AAG8	mglA	0.5526579	Galactose/methyl galactoside import ATP-binding protein MglA OS=Escherichia coli O6 GN=mglA
A0A0H2VE33	c4605	0.55382	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4605
P69428	tatA	0.5601959	Sec-independent protein translocase protein tatA OS=Escherichia coli O6 GN=tatA
A0A0H2VB35	c3819	0.5644768	Putative conserved protein OS=Escherichia coli O6 GN=c3819
Q8FCW0	c4155	0.5688288	Phosphoglycolate phosphatase OS=Escherichia coli O6 GN=c4155
P21151	fadA	0.5765341	3-ketoacyl-CoA thiolase OS=Escherichia coli O6 GN=fadA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P77348	mppA	0.5863075	Periplasmic murein peptide-binding protein OS=Escherichia coli O6 GN=mppA
A0A0H2VEB5	c4764	0.5921488	Carbamate kinase-like protein yahI OS=Escherichia coli O6 GN=c4764
P15639	putH	0.598546	Bifunctional purine biosynthesis protein purH OS=Escherichia coli O6 GN=purH
P76145	tam	0.607817	Trans-aconitate 2-methyltransferase OS=Escherichia coli O6 GN=tam
Q8FDI4	asst	0.6180655	Arylsulfate sulfotransferase OS=Escherichia coli O6 GN=asst
P0A8G3	uxaC	0.6196519	Uronate isomerase OS=Escherichia coli O6 GN=uxaC
P0AC30	ftsX	0.6208459	Cell division protein OS=Escherichia coli O6 GN=ftsX
Q93K97	nudF	0.6232125	ADP-ribose pyrophosphatase OS=Escherichia coli O6 GN=nudF
P77399	fadj	0.6309645	Fatty acid oxidation complex subunit alpha OS=Escherichia coli O6 GN=fadJ
P37685	aldB	0.6332423	Aldehyde dehydrogenase B OS=Escherichia coli O6 GN=aldB
P0A6E6	atpC	0.6404413	ATP synthase epsilon chain OS=Escherichia coli O6 GN=atpC
P0A759	nagB	0.6473125	Glucosamine-6-phosphate deaminase OS=Escherichia coli O6 GN=nagB
P0AE78	corC	0.6484594	Magnesium and cobalt efflux protein CorC OS=Escherichia coli O6 GN=corC
P0AES0	gsp	0.6505682	Glutathionylspermidine synthase OS=Escherichia coli O6 GN=gsp
P0ACU5	fabR	0.6515249	HTH-type transcriptional repressor fabR OS=Escherichia coli O6 GN=fabR
P69805	manZ	0.6529139	Mannose permease IID component OS=Escherichia coli O6 GN=manZ
P40120	mdoD	0.6590376	Glucans biosynthesis protein D OS=Escherichia coli O6 GN=mdoD
P61887	rffH	0.6607092	Glucose-1-phosphate thymidylyltransferase OS=Escherichia coli O6 GN=rffH
P15254	purL	0.6619524	Phosphoribosylformylglycinamidine synthase OS=Escherichia coli O6 GN=purL
P0A8Z3	ybgC	0.6646533	Acyl-CoA thioester hydrolase YbgC OS=Escherichia coli O6 GN=ybgC
P02931	ompF	0.668287	Outer membrane protein F OS=Escherichia coli O6 GN=ompF
P00490	malP	0.6726271	Maltodextrin phosphorylase OS=Escherichia coli O6 GN=malP
P0AG27	yibN	0.6743906	Uncharacterized protein yibN OS=Escherichia coli O6 GN=yibN
W9AHZ8	yfbT	0.6758105	Protein yfbT OS=Escherichia coli O6 GN=yfbT
P76045	ompG	0.6775701	Outer membrane protein G OS=Escherichia coli O6 GN=ompG
P0ACK2	agaR	0.680078	Putative aga operon transcriptional repressor OS=Escherichia coli O6 GN=agaR
P0AC19	folX	0.6805175	D-erythro-7,8-dihydroneopterin triphosphate epimerase OS=Escherichia coli O6 GN=folX
P23830	pssA	0.6825318	CDP-diacylglycerol--serine O-phosphatidyltransferase OS=Escherichia coli O6 GN=pssA
P0A8F0	upp	0.6849994	Uracil phosphoribosyltransferase OS=Escherichia coli O6 GN=upp

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P77376	ydgJ	0.6888543	Hypothetical oxidoreductase ydgJ OS=Escherichia coli O6 GN=ydgJ
P68187	malK	0.6894906	Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli O6 GN=malK
P75914	ycdX	0.6955932	Putative hydrolase ycdX OS=Escherichia coli O6 GN=ycdX
P75864	rlmI	0.6970101	Ribosomal RNA large subunit methyltransferase K/L OS=Escherichia coli O6 GN=rlmI
P04993	recD	0.6985757	Exodeoxyribonuclease V alpha chain OS=Escherichia coli O6 GN=recD
P0A853	tnaA	0.7013516	Tryptophanase OS=Escherichia coli O6 GN=tnaA
P0ABV6	tolR	0.7044193	Protein tolR OS=Escherichia coli O6 GN=tolR
P0AGE9	sucD	0.7056318	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Escherichia coli O6 GN=sucD
P08997	aceB	0.7073828	Malate synthase A OS=Escherichia coli O6 GN=aceB
P0A6Y8	dnaK	0.7074224	Chaperone protein dnaK OS=Escherichia coli O6 GN=dnaK
P39377	iadA	0.7075718	Isoaspartyl dipeptidase OS=Escherichia coli O6 GN=iadA
P16681	phnB	0.7083605	PhnB protein OS=Escherichia coli O6 GN=phnB
P00803	lepB	0.7103782	Signal peptidase I OS=Escherichia coli O6 GN=lepB
P60785	lepA	0.7108197	Elongation factor 4 OS=Escherichia coli O6 GN=lepA
F8LVU1	rpiL	0.7135127	50S ribosomal protein L7/L12 OS=Escherichia coli O6 GN=rpiL
P04982	rbsD	0.7154137	D-ribose pyranase OS=Escherichia coli O6 GN=rbsD
Q54GJ2	purD	0.7173813	Phosphoribosylamine--glycine ligase OS=Escherichia coli O6 GN=purD
P0AFZ3	sspB	0.7195922	Stringent starvation protein B OS=Escherichia coli O6 GN=sspB
P0AG93	secF	0.7212695	Protein-export membrane protein secF OS=Escherichia coli O6 GN=secF
P0ADT5	ygiC	0.7236345	Uncharacterized protein ygiC OS=Escherichia coli O6 GN=ygiC
P37330	glcB	0.7283577	Malate synthase G OS=Escherichia coli O6 GN=glcB
P0AB61	yciN	0.7309509	Protein yciN OS=Escherichia coli O6 GN=yciN
A0A0H2V9S6	c2461	0.7318841	Uncharacterized protein OS=Escherichia coli O6 GN=c2461
P0ACW6	ydcH	0.737812	Putative uncharacterized protein ydcH OS=Escherichia coli O6 GN=ydcH
P00946	manA	0.7386313	Mannose-6-phosphate isomerase OS=Escherichia coli O6 GN=manA
W9ALX3	yibP	0.7386596	Putative uncharacterized protein yibP OS=Escherichia coli O6 GN=yibP
P41407	azoR	0.7387319	FMN-dependent NADH-azoreductase OS=Escherichia coli O6 GN=azoR
A0A0H2V625	c1249	0.7390671	Uncharacterized protein OS=Escherichia coli O6 GN=c1249
P05042	fumC	0.7405291	Fumarate hydratase class II OS=Escherichia coli O6 GN=fumC

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P12008	aroC	0.7413628	Chorismate synthase OS=Escherichia coli O6 GN=aroC
A0A0H2V8R4	c2514	0.741502	Uncharacterized protein OS=Escherichia coli O6 GN=c2514
P22256	gabT	0.7417741	4-aminobutyrate aminotransferase OS=Escherichia coli O6 GN=gabT
P0A9J6	rbsK	0.742538	Ribokinase OS=Escherichia coli O6 GN=rbsK
W8ZSQ1	ytfR	0.7432493	Putative ATP-binding component of a transport system OS=Escherichia coli O6 GN=ytfR
P0AAB8	uspD	0.7434233	Universal stress protein D OS=Escherichia coli O6 GN=uspD
P0ADC1	lptE	0.7435898	LPS-assembly lipoprotein lptE OS=Escherichia coli O6 GN=lptE
P0A6Y5	hslO	0.7462018	33 kDa chaperonin OS=Escherichia coli O6 GN=hslO
W9AEC6	ycgK	0.7475444	Protein ycgK OS=Escherichia coli O6 GN=ycgK
P0A8N5	lysU	0.7488918	Lysyl-tRNA synthetase, heat inducible OS=Escherichia coli O6 GN=lysU
P0ABS5	dnaG	0.7499411	DNA primase OS=Escherichia coli O6 GN=dnaG
P0A6F5	groL	0.7523511	60 kDa chaperonin OS=Escherichia coli O6 GN=groL
P27306	sthA	0.7547843	Soluble pyridine nucleotide transhydrogenase OS=Escherichia coli O6 GN=sthA
P0ABH9	clpA	0.7549316	ATP-dependent Clp protease ATP-binding subunit ClpA OS=Escherichia coli O6 GN=clpA
P76346	mtfA	0.7549486	Protein mtfA OS=Escherichia coli O6 GN=mtfA
P0A7B8	hslV	0.7553135	ATP-dependent protease subunit HslV OS=Escherichia coli O6 GN=hslV
P27550	acs	0.7568972	Acetyl-coenzyme A synthetase OS=Escherichia coli O6 GN=acs
P0A836	sucC	0.7615993	Succinate--CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O6 GN=sucC
P0A790	panD	0.7650979	Aspartate 1-decarboxylase OS=Escherichia coli O6 GN=panD
Q8FDS2	c3666	0.7652051	UPF0401 protein c3666 OS=Escherichia coli O6 GN=c3666
P0AFY8	seqA	0.7654819	Protein seqA OS=Escherichia coli O6 GN=seqA
P671714	ribH	0.7656628	6,7-dimethyl-8-ribityllumazine synthase OS=Escherichia coli O6 GN=ribH
P0AEG6	dsbC	0.7669683	Thiol:disulfide interchange protein dsbC OS=Escherichia coli O6 GN=dsbC
P0A870	talB	0.7719801	Transaldolase B OS=Escherichia coli O6 GN=talB
P0A8W2	slyA	0.7728412	Transcriptional regulator slyA OS=Escherichia coli O6 GN=slyA
P37692	rfaF	0.7749071	ADP-heptose--LPS heptosyltransferase II OS=Escherichia coli O6 GN=rfaF
P0AC38	aspA	0.7772054	Aspartate ammonia-lyase OS=Escherichia coli O6 GN=aspA
P37636	mdtE	0.7846701	Multidrug resistance protein mdtE OS=Escherichia coli O6 GN=mdtE
P37637	mdtF	0.7849003	Multidrug resistance protein MdtF OS=Escherichia coli O6 GN=mdtF

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P06710	dnaZ	0.7916178	DNA polymerase III subunit tau OS=Escherichia coli O6 GN=dnaZ
P07623	metA	0.7927514	Homoserine O-succinyltransferase OS=Escherichia coli O6 GN=metA
P68206	yjbJ	0.7928615	UPF0337 protein yjbJ OS=Escherichia coli O6 GN=yjbJ
P0AG40	ribF	0.7929873	Riboflavin biosynthesis protein ribF OS=Escherichia coli O6 GN=ribF
P25748	galS	0.7953068	Mgl repressor and galactose ultrainduction factor OS=Escherichia coli O6 GN=galS
P0AEL6	fepB	0.7954509	Ferrienterobactin-binding periplasmic protein OS=Escherichia coli O6 GN=fepB
P0AFI2	parC	0.79637	Topoisomerase IV subunit A OS=Escherichia coli O6 GN=parC
P0AF12	mtnN	0.7973573	methylthioadenosine/S-adenosylhomocysteine nucleosidase OS=Escherichia coli O6 GN=mtnN
P0ADG4	suhB	0.7975179	Inositol-1-monophosphatase OS=Escherichia coli O6 GN=suhB
P76187	ydhF	0.7999398	Hypothetical oxidoreductase ydhF OS=Escherichia coli O6 GN=ydhF
P0AFC3	nuoA	0.8001767	NADH-quinone oxidoreductase subunit A OS=Escherichia coli O6 GN=nuoA
A0A0H2VGG0	c5375	0.8004717	Putative uncharacterized protein OS=Escherichia coli O6 GN=c5375
P23872	aes	0.8009381	Acetyl esterase OS=Escherichia coli O6 GN=aes
P0A8N3	lysS	0.8015215	Lysyl-tRNA synthetase OS=Escherichia coli O6 GN=lysS
W8ZIS6	yebH	0.8020247	Ribosomal RNA large subunit methyltransferase A OS=Escherichia coli O6 GN=yebH
P0AD83	pyrI	0.8025645	Aspartate carbamoyltransferase regulatory chain OS=Escherichia coli O6 GN=pyrI
P31437	yicI	0.8042744	Uncharacterized inner membrane transporter OS=Escherichia coli O6 GN=yicI
P75942	flgJ	0.8050922	Peptidoglycan hydrolase flgJ OS=Escherichia coli O6 GN=flgJ
P17117	mdaA	0.8054687	Oxygen-insensitive NADPH nitroreductase OS=Escherichia coli O6 GN=mdaA
P0AGH8	pstC	0.8103661	Phosphate transport system permease protein pstC OS=Escherichia coli O6 GN=pstC
P0AFG3	sucA	0.8109479	2-oxoglutarate dehydrogenase E1 component OS=Escherichia coli O6 GN=sucA
P27431	ycfD	0.8111712	Putative uncharacterized protein ycfD OS=Escherichia coli O6 GN=ycfD
A0A0H2VDS3	c5349	0.813702	Carbamate kinase OS=Escherichia coli O6 GN=c5349
P28248	dcd	0.8151751	Deoxycytidine triphosphate deaminase OS=Escherichia coli O6 GN=dcd
P21170	speA	0.815756	Biosynthetic arginine decarboxylase OS=Escherichia coli O6 GN=speA
P04951	kdsB	0.81582	3-deoxy-manno-octulosonate cytidylyltransferase OS=Escherichia coli O6 GN=kdsB
P0ABQ4	folA	0.8160549	Dihydrofolate reductase OS=Escherichia coli O6 GN=folA
P0A6P5	der	0.8192091	GTPase Der OS=Escherichia coli O6 GN=der
A0A0H2V9M3	c2399	0.8197371	Uncharacterized protein OS=Escherichia coli O6 GN=c2399

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0AB65	yccX	0.820717	Acylphosphatase OS=Escherichia coli O6 GN=yccX
P0AFG6	sucB	0.8213714	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Escherichia coli O6 GN=sucB
A0A0H2V7A8	c1765	0.8219571	Partial Putative outer membrane channel protein OS=Escherichia coli O6 GN=c1765
P36553	hemF	0.8220539	Coproporphyrinogen-III oxidase, aerobic OS=Escherichia coli O6 GN=hemF
P0A6Z3	htpG	0.8224283	Chaperone protein htpG OS=Escherichia coli O6 GN=htpG
P0ACR4	yeiE	0.8242372	Uncharacterized HTH-type transcriptional regulator yeiE OS=Escherichia coli O6 GN=yeiE
P0A7DA	purA	0.8273174	Adenylosuccinate synthetase OS=Escherichia coli O6 GN=purA
Q46927	ygdL	0.8276668	Putative uncharacterized protein ygdL OS=Escherichia coli O6 GN=ygdL
P0ABK2	cydB	0.8280925	Cytochrome d ubiquinol oxidase subunit 2 OS=Escherichia coli O6 GN=cydB
P27833	wecE	0.8290551	Lipopolysaccharide biosynthesis protein rffA OS=Escherichia coli O6 GN=wecE
P21179	katE	0.8290757	Catalase HPII OS=Escherichia coli O6 GN=katE
P0ABQ2	garR	0.8295932	2-hydroxy-3-oxopropionate reductase OS=Escherichia coli O6 GN=garR
P0AE12	amn	0.8305317	AMP nucleosidase OS=Escherichia coli O6 GN=amn
P37440	ucpA	0.8310599	Oxidoreductase ucpA OS=Escherichia coli O6 GN=ucpA
P0AG00	wzzE	0.8349676	Lipopolysaccharide biosynthesis protein wzzE OS=Escherichia coli O6 GN=wzzE
P0ACP7	purR	0.8351157	HTH-type transcriptional repressor purR OS=Escherichia coli O6 GN=purR
A0A0H2VF72	c5312	0.8365224	Putative conserved protein OS=Escherichia coli O6 GN=c5312
P77150	pdxY	0.8368369	Pyridoxamine kinase OS=Escherichia coli O6 GN=pdxY
A0A0H2V5Y8	c1138	0.8370507	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1138
P02924	araF	0.8374721	L-arabinose-binding periplasmic protein OS=Escherichia coli O6 GN=araF
P21165	pepQ	0.8378954	Xaa-Pro dipeptidase OS=Escherichia coli O6 GN=pepQ
P0AFM6	pspA	0.8385626	Phage shock protein A OS=Escherichia coli O6 GN=pspA
P39199	yfcB	0.8387841	Hypothetical adenine-specific methylase yfcB OS=Escherichia coli O6 GN=yfcB
P0AF20	nagC	0.839116	N-acetylglucosamine repressor OS=Escherichia coli O6 GN=nagC
P0AA25	trxA	0.8407472	Thioredoxin-1 OS=Escherichia coli O6 GN=trxA
P0ABF1	pcnB	0.8415398	Poly(A) polymerase OS=Escherichia coli O6 GN=pcnB
P0A784	orn	0.843318	Oligoribonuclease OS=Escherichia coli O6 GN=orn
P08390	usg	0.8433327	USG-1 protein OS=Escherichia coli O6 GN=usg

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P69776	lpp	0.8447712	Major outer membrane lipoprotein OS=Escherichia coli O6 GN=lpp
P06715	gor	0.845186	Glutathione reductase OS=Escherichia coli O6 GN=gor
P36659	cbpA	0.846235	Curved DNA-binding protein OS=Escherichia coli O6 GN=cbpA
P0A7L3	rplT	0.8471887	50S ribosomal protein L20 OS=Escherichia coli O6 GN=rplT
P08192	folC	0.8477285	FolC bifunctional protein OS=Escherichia coli O6 GN=folC
P0ACB2	hemB	0.8488563	Delta-aminolevulinic acid dehydratase OS=Escherichia coli O6 GN=hemB
P0A7M6	rpmC	0.8493525	50S ribosomal protein L29 OS=Escherichia coli O6 GN=rpmC
P0AC41	sdhA	0.8501422	Succinate dehydrogenase flavoprotein subunit OS=Escherichia coli O6 GN=sdhA
P13029	katG	0.853388	Catalase-peroxidase OS=Escherichia coli O6 GN=katG
A0A0H2V701	c1248	0.8539515	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1248
Q8FD60	nanK1	0.8540907	N-acetylmannosamine kinase OS=Escherichia coli O6 GN=nanK1
P0DMC5	rcsC	0.8559814	Sensor histidine kinase rcsC OS=Escherichia coli O6 GN=rcsC
P0A884	thyA	0.8566369	Thymidylate synthase OS=Escherichia coli O6 GN=thyA
P0AF50	yjbR	0.8584167	Uncharacterized protein OS=Escherichia coli O6 GN=yjbR
P10100	rlpA	0.859582	Rare lipoprotein A OS=Escherichia coli O6 GN=rlpA
A0A0H2V9V5	c2496	0.8604387	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2496
P28249	dgt	0.8607062	Deoxyguanosinetriphosphate triphosphohydrolase OS=Escherichia coli O6 GN=dgt
P63020	nfuA	0.8619257	Fe/S biogenesis protein nfuA OS=Escherichia coli O6 GN=nfuA
W8ZQ81	icdA	0.862156	Isocitrate dehydrogenase (NADP) OS=Escherichia coli O6 GN=icdA
P0A8C4	ygfB	0.862836	UPF0149 protein ygfB OS=Escherichia coli O6 GN=ygfB
P39177	uspG	0.864485	Universal stress protein G OS=Escherichia coli O6 GN=uspG
P0A805	frr	0.8655674	Ribosome-recycling factor OS=Escherichia coli O6 GN=frr
P12994	ybhB	0.8669044	Protein ybhB OS=Escherichia coli O6 GN=ybhB
P0DP64	ybeM	0.8670979	Putative amidase OS=Escherichia coli O6 GN=ybeM
P22186	mraZ	0.8671283	Protein MraZ OS=Escherichia coli O6 GN=mraZ
P77756	queC	0.8675475	7-cyano-7-deazaguanine synthase OS=Escherichia coli O6 GN=queC
P0A9K9	slyD	0.8705743	FKBP-type peptidyl-prolyl cis-trans isomerase slyD OS=Escherichia coli O6 GN=slyD
P16659	proS	0.8730212	Prolyl-tRNA synthetase OS=Escherichia coli O6 GN=proS
P25526	gabD	0.8730911	Succinate-semialdehyde dehydrogenase (NADP+) OS=Escherichia coli O6 GN=gabD

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A749	murA	0.8737785	UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Escherichia coli O6 GN=murA
P0A7K6	rplS	0.8738765	50S ribosomal protein L19 OS=Escherichia coli O6 GN=rplS
P0A800	rpoZ	0.8739955	DNA-directed RNA polymerase subunit omega OS=Escherichia coli O6 GN=rpoZ
P36771	lrhA	0.8740274	Probable transcriptional regulator lrhA OS=Escherichia coli O6 GN=lrhA
P33354	yehR	0.874531	Hypothetical lipoprotein yehR OS=Escherichia coli O6 GN=yehR
A0A0H2VDX6	c5447	0.8757431	Putative uncharacterized protein OS=Escherichia coli O6 GN=c5447
P0A9B2	gapA	0.8781931	Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli O6 GN=gapA
A0A0H2V8L8	c2458	0.8788131	Putative peptide synthetase OS=Escherichia coli O6 GN=c2458
P0AFX4	rsd	0.8802881	Regulator of sigma D OS=Escherichia coli O6 GN=rsd
P0ACJ8	crp	0.8813287	Catabolite gene activator OS=Escherichia coli O6 GN=crp
P0A7M9	rpmE	0.8817148	50S ribosomal protein L31 OS=Escherichia coli O6 GN=rpmE
P19926	agp	0.8817427	Glucose-1-phosphatase OS=Escherichia coli O6 GN=agp
W8ZXJ1	yhbH	0.8841731	Probable sigma-54 modulation protein OS=Escherichia coli O6 GN=yhbH
P0A7A9	ppa	0.8843632	Inorganic pyrophosphatase OS=Escherichia coli O6 GN=ppa
P0A7K2	rplL	0.8849573	50S ribosomal protein L7/L12 OS=Escherichia coli O6 GN=rplL
P09424	mtlD	0.8858564	Mannitol-1-phosphate 5-dehydrogenase OS=Escherichia coli O6 GN=mtlD
P0ADN2	yifE	0.8875468	UPF0438 protein yifE OS=Escherichia coli O6 GN=yifE
P32131	hemN	0.8877272	Oxygen-independent coproporphyrinogen III oxidase OS=Escherichia coli O6 GN=hemN
P64506	yebY	0.8884845	Uncharacterized protein OS=Escherichia coli O6 GN=yebY
P0ABT2	dps	0.8902183	DNA protection during starvation protein OS=Escherichia coli O6 GN=dps
P0A6H5	hslU	0.8918183	ATP-dependent protease ATPase subunit HslU OS=Escherichia coli O6 GN=hslU
P39300	ulaG	0.8921955	Probable L-ascorbate-6-phosphate lactonase ulaG OS=Escherichia coli O6 GN=ulaG
P0A744	msrA	0.892828	Peptide methionine sulfoxide reductase msrA OS=Escherichia coli O6 GN=msrA
P0AGG4	trxC	0.8934964	Thioredoxin 2 OS=Escherichia coli O6 GN=trxC
W9ALK8	yhiR	0.8935003	Putative uncharacterized protein yhiR OS=Escherichia coli O6 GN=yhiR
P0AD61	pykF	0.8936632	Pyruvate kinase I OS=Escherichia coli O6 GN=pykF
P17169	glmS	0.8940766	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Escherichia coli O6 GN=glmS
P0A6F9	grosS	0.8953768	10 kDa chaperonin OS=Escherichia coli O6 GN=grosS
P75746	ybgl	0.8960229	UPF0271 protein ybgL OS=Escherichia coli O6 GN=ybgL

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
Q46920	queF	0.8961411	NADPH-dependent 7-cyano-7-deazaguanine reductase OS=Escherichia coli O6 GN=queF
P25714	yajC	0.8965712	UPF0092 membrane protein yajC OS=Escherichia coli O6 GN=yajC
P0ABA0	atpF	0.8976695	ATP synthase subunit b OS=Escherichia coli O6 GN=atpF
P0AEW4	icc	0.8987035	Icc protein OS=Escherichia coli O6 GN=icc
P0AE52	bcp	0.9004762	Putative peroxiredoxin bcp OS=Escherichia coli O6 GN=bcp
P37689	gpmI	0.9005146	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Escherichia coli O6 GN=gpmI
Q46845	yghU	0.9007078	Hypothetical GST-like protein yghU OS=Escherichia coli O6 GN=yghU
P04805	gltX	0.903203	Glutamyl-tRNA synthetase OS=Escherichia coli O6 GN=gltX
P0ABD8	argB	0.9037436	Acetylglutamate kinase OS=Escherichia coli O6 GN=argB
P22564	rihC	0.9054682	Non-specific ribonucleoside hydrolase rihC OS=Escherichia coli O6 GN=rihC
P07862	ddlB	0.9058561	D-alanine--D-alanine ligase B OS=Escherichia coli O6 GN=ddlB
A0A0H2VAP3	c2895	0.9059055	YapH homolog OS=Escherichia coli O6 GN=c2895
P0A6X3	hfq	0.9062833	RNA-binding protein hfq OS=Escherichia coli O6 GN=hfq
P0AGE0	ssb	0.9065669	Single-stranded DNA-binding protein OS=Escherichia coli O6 GN=ssb
P21367	ycaC	0.9068393	Protein ycaC OS=Escherichia coli O6 GN=ycaC
P0A8A2	yeeN	0.9091156	UPF0082 protein yeeN OS=Escherichia coli O6 GN=yeeN
P0ADU2	ygiN	0.910486	Protein ygiN OS=Escherichia coli O6 GN=ygiN
P00968	carB	0.9107106	Carbamoyl-phosphate synthase large chain OS=Escherichia coli O6 GN=carB
P0AB77	kbl	0.9128605	2-amino-3-ketobutyrate coenzyme A ligase OS=Escherichia coli O6 GN=kbl
P0A720	tmk	0.9135802	Thymidylate kinase OS=Escherichia coli O6 GN=tmk
P24215	uxuA	0.9145486	Mannonate dehydratase OS=Escherichia coli O6 GN=uxuA
W8ZSB0	yjdB	0.9146416	Putative uncharacterized protein yjdB OS=Escherichia coli O6 GN=yjdB
W9ALV3	yibH	0.9148805	Putative uncharacterized protein yibH OS=Escherichia coli O6 GN=yibH
P0A8Z0	yciA	0.9153877	Acyl-CoA thioester hydrolase YciA OS=Escherichia coli O6 GN=yciA
P0ADZ0	rplW	0.9155898	50S ribosomal protein L23 OS=Escherichia coli O6 GN=rplW
P61517	yadF	0.9157022	Protein yadF OS=Escherichia coli O6 GN=yadF
P0ABP8	deoD	0.918489	Purine nucleoside phosphorylase deoD-type OS=Escherichia coli O6 GN=deoD
P0A7L8	rpmA	0.918672	50S ribosomal protein L27 OS=Escherichia coli O6 GN=rpmA
P0AE01	trmJ	0.9202312	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ OS=Escherichia coli O6 GN=trmJ

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P28250	phrB	0.9202729	Deoxyribodipyrimidine photolyase OS=Escherichia coli O6 GN=phrB
P0A6S7	gpsA	0.9206434	Glycerol-3-phosphate dehydrogenase [NAD(P)+] OS=Escherichia coli O6 GN=gpsA
A0A0H2VDJ1	c5314	0.9212071	Protein ytfJ OS=Escherichia coli O6 GN=c5314
A0A0H2VBF4	c2791	0.9220318	CinA-like protein OS=Escherichia coli O6 GN=c2791
P0ADA5	yajG	0.9229028	Uncharacterized lipoprotein yajG OS=Escherichia coli O6 GN=yajG
P21889	aspS	0.9229835	Aspartyl-tRNA synthetase OS=Escherichia coli O6 GN=aspS
P61889	mdh	0.9236081	Malate dehydrogenase OS=Escherichia coli O6 GN=mdh
P63284	clpB	0.9241559	Chaperone protein ClpB OS=Escherichia coli O6 GN=clpB
P00370	gdhA	0.9248307	NADP-specific glutamate dehydrogenase OS=Escherichia coli O6 GN=gdhA
P0A8J4	ybeD	0.9250576	UPF0250 protein ybeD OS=Escherichia coli O6 GN=ybeD
P0ACU7	yjdC	0.9257843	HTH-type transcriptional regulator yjdC OS=Escherichia coli O6 GN=yjdC
P30125	leuB	0.9258521	3-isopropylmalate dehydrogenase OS=Escherichia coli O6 GN=leuB
P76402	yegP	0.9267111	UPF0339 protein YegP OS=Escherichia coli O6 GN=yegP
Q8FD58	nanA1	0.9274534	N-acetylneuraminate lyase 1 OS=Escherichia coli O6 GN=nanA1
P0AD49	raiA	0.9277487	Ribosome-associated inhibitor A OS=Escherichia coli O6 GN=raiA
P0A6I3	coaA	0.9281533	Pantothenate kinase OS=Escherichia coli O6 GN=coaA
P28904	treC	0.9281884	Trehalose-6-phosphate hydrolase OS=Escherichia coli O6 GN=treC
P65298	yqhH	0.9282297	Uncharacterized lipoprotein YqhH OS=Escherichia coli O6 GN=yqhH
P04983	rbsA	0.929674	Ribose import ATP-binding protein RbsA OS=Escherichia coli O6 GN=rbsA
P33607	nuoI	0.9305735	NADH-quinone oxidoreductase subunit L OS=Escherichia coli O6 GN=nuoI
P07012	prfB	0.9313501	Peptide chain release factor 2 OS=Escherichia coli O6 GN=prfB
P0AG30	rho	0.9314694	Transcription termination factor Rho OS=Escherichia coli O6 GN=rho
P0AAX8	ybiS	0.9322858	Probable L,D-transpeptidase YbiS OS=Escherichia coli O6 GN=ybiS
P0A6T5	folE	0.932733	GTP cyclohydrolase 1 OS=Escherichia coli O6 GN=folE
P05020	pyrC	0.9343897	Dihydroorotase OS=Escherichia coli O6 GN=pyrC
P24175	manB	0.9352568	Phosphomannomutase OS=Escherichia coli O6 GN=manB
P0A7R1	rplI	0.9363161	50S ribosomal protein L9 OS=Escherichia coli O6 GN=rplI
P69451	fadD	0.936644	Long-chain-fatty-acid--CoA ligase OS=Escherichia coli O6 GN=fadD
P27434	rodZ	0.936823	Cytoskeleton protein rodZ OS=Escherichia coli O6 GN=rodZ

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P25519	hflX	0.9377653	GTP-binding protein hflX OS=Escherichia coli O6 GN=hflX
P06986	ruvA	0.9384372	Holliday junction ATP-dependent DNA helicase ruvA OS=Escherichia coli O6 GN=ruvA
P0A7Z0	rpiA	0.9386511	Ribose-5-phosphate isomerase A OS=Escherichia coli O6 GN=rpiA
P0AFI7	pdxH	0.9392393	Pyridoxine/pyridoxamine 5'-phosphate oxidase OS=Escherichia coli O6 GN=pdxH
P0AF08	mrp	0.9392424	Protein mrp OS=Escherichia coli O6 GN=mrp
P0A9J8	pheA	0.9400605	P-protein OS=Escherichia coli O6 GN=pheA
P0A7D1	pth	0.9418367	Peptidyl-tRNA hydrolase OS=Escherichia coli O6 GN=pth
P0A877	trpA	0.9420978	Tryptophan synthase alpha chain OS=Escherichia coli O6 GN=trpA
P60757	hisG	0.9430731	ATP phosphoribosyltransferase OS=Escherichia coli O6 GN=hisG
P0AAI5	fabF	0.9440827	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Escherichia coli O6 GN=fabF
P33352	yehP	0.9441816	Uncharacterized protein YehP OS=Escherichia coli O6 GN=yehP
P0AG51	rpmD	0.9447352	50S ribosomal protein L30 OS=Escherichia coli O6 GN=rpmD
P00954	trpS	0.9447805	Tryptophanyl-tRNA synthetase OS=Escherichia coli O6 GN=trpS
W8ZWJ4	speC	0.9452055	Ornithine decarboxylase, constitutive OS=Escherichia coli O6 GN=speC
P27828	wecB	0.9462001	UDP-N-acetylglucosamine 2-epimerase OS=Escherichia coli O6 GN=wecB
P76008	ldcA	0.9473117	Murein tetrapeptide carboxypeptidase OS=Escherichia coli O6 GN=ldcA
P0A9H5	btuR	0.9474857	Cob(I)yrinic acid a,c-diamide adenosyltransferase OS=Escherichia coli O6 GN=btuR
P0AC53	zwf	0.9485207	Glucose-6-phosphate 1-dehydrogenase OS=Escherichia coli O6 GN=zwf
P0A7C6	pepE	0.9486179	Peptidase E OS=Escherichia coli O6 GN=pepE
P36938	pgm	0.949223	Phosphoglucomutase OS=Escherichia coli O6 GN=pgm
A0A0H2VBP8	c4265	0.9494482	DcrB protein OS=Escherichia coli O6 GN=c4265
P0ADZ4	rpsO	0.9509459	30S ribosomal protein S15 OS=Escherichia coli O6 GN=rpsO
A0A0H2V6Q3	c1549	0.9511294	Putative replication protein O of bacteriophage OS=Escherichia coli O6 GN=c1549
P0AA10	rplM	0.9515223	50S ribosomal protein L13 OS=Escherichia coli O6 GN=rplM
P0AD57	ispB	0.9515437	Octaprenyl-diphosphate synthase OS=Escherichia coli O6 GN=ispB
P0A8P3	yggX	0.9516683	Probable Fe(2+)-trafficking protein OS=Escherichia coli O6 GN=yggX
P02943	lamB	0.9525443	Maltoporin OS=Escherichia coli O6 GN=lamB
P0A6L9	hscB	0.9530138	Co-chaperone protein hscB OS=Escherichia coli O6 GN=hscB
W8ZUT7	yfiQ	0.9531328	Putative uncharacterized protein yfiQ OS=Escherichia coli O6 GN=yfiQ

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P04968	ilvA	0.9531419	Threonine dehydratase biosynthetic OS=Escherichia coli O6 GN=ilvA
P28635	yaeC	0.9534414	D-methionine-binding lipoprotein metQ OS=Escherichia coli O6 GN=yaeC
P09372	grpE	0.9535396	Protein grpE OS=Escherichia coli O6 GN=grpE
P23893	hemL	0.9539492	Glutamate-1-semialdehyde 2,1-aminomutase OS=Escherichia coli O6 GN=hemL
A0A0H2V646	c1234	0.9546149	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1234
P0AFQ7	ycfH	0.954654	Uncharacterized deoxyribonuclease ycfH OS=Escherichia coli O6 GN=ycfH
P61714	ribE	0.9552366	Riboflavin synthase alpha chain OS=Escherichia coli O6 GN=ribE
Q47622	sapA	0.9552916	Peptide transport periplasmic protein sapA OS=Escherichia coli O6 GN=sapA
P0A8K1	psd	0.9557835	Phosphatidylserine decarboxylase proenzyme OS=Escherichia coli O6 GN=psd
P00509	aspC	0.9561746	Aspartate aminotransferase OS=Escherichia coli O6 GN=aspC
P0A9M5	gpt	0.9564491	Xanthine phosphoribosyltransferase OS=Escherichia coli O6 GN=gpt
P0AG44	rplQ	0.9564511	50S ribosomal protein L17 OS=Escherichia coli O6 GN=rplQ
P02929	tonB	0.9570335	Protein TonB OS=Escherichia coli O6 GN=tonB
A0A0H2V8P3	c1468	0.9574397	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1468
P0A7E9	pyrH	0.9580057	Uridylate kinase OS=Escherichia coli O6 GN=pyrH
P52697	pgl	0.9594797	6-phosphogluconolactonase OS=Escherichia coli O6 GN=pgl
P24171	dcp	0.9599525	Peptidyl-dipeptidase dcp OS=Escherichia coli O6 GN=dcp
P0A6L2	dapA	0.9600044	Dihydrodipicolinate synthase OS=Escherichia coli O6 GN=dapA
W8ZRS2	yiiM	0.9606998	Putative uncharacterized protein yiiM OS=Escherichia coli O6 GN=yiiM
A0A0H2V970	c2909	0.9614035	Probable oxalyl-CoA decarboxylase OS=Escherichia coli O6 GN=c2909
A0A0H2VAZ0	kpsD	0.961729	KpsD protein OS=Escherichia coli O6 GN=kpsD
P0A6A8	acpP	0.9618343	Acyl carrier protein OS=Escherichia coli O6 GN=acpP
P42632	tdcE	0.9622552	Keto-acid formate acetyltransferase OS=Escherichia coli O6 GN=tdcE
P0AG67	rpsA	0.9623354	30S ribosomal protein S1 OS=Escherichia coli O6 GN=rpsA
P60651	speB	0.9626448	Agmatinase OS=Escherichia coli O6 GN=speB
A0A0H2VD08	c5040	0.962946	Putative c4-dicarboxylate transport transcriptional Regulatory protein OS=Escherichia coli O6 GN=c5040
P0ABB4	atpD	0.9636745	ATP synthase subunit beta OS=Escherichia coli O6 GN=atpD
P0A7L0	rplA	0.9650644	50S ribosomal protein L1 OS=Escherichia coli O6 GN=rplA
P24183	fdnG	0.9651743	Formate dehydrogenase, nitrate-inducible, major subunit OS=Escherichia coli O6 GN=fdnG

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P76658	hldE	0.9652517	Bifunctional protein hldE OS=Escherichia coli O6 GN=hldE
Q46938	kduI	0.9657202	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase OS=Escherichia coli O6 GN=kduI
P0ACQ4	oxyR	0.9657913	Hydrogen peroxide-inducible genes activator OS=Escherichia coli O6 GN=oxyR
P62399	rplE	0.9662233	50S ribosomal protein L5 OS=Escherichia coli O6 GN=rplE
P0A847	tgt	0.9666707	Queuine tRNA-ribosyltransferase OS=Escherichia coli O6 GN=tgt
P0A7F6	speD	0.9673098	S-adenosylmethionine decarboxylase proenzyme OS=Escherichia coli O6 GN=speD
P0A7C2	lexA	0.9676618	LexA repressor OS=Escherichia coli O6 GN=lexA
P38489	nfnB	0.9703126	Oxygen-insensitive NAD(P)H nitroreductase OS=Escherichia coli O6 GN=nfnB
P16689	phnM	0.971306	PhnM protein OS=Escherichia coli O6 GN=phnM
P0AE88	cpxR	0.972232	Transcriptional Regulatory protein cpxR OS=Escherichia coli O6 GN=cpxR
P0ABB0	atpA	0.9724777	ATP synthase subunit alpha OS=Escherichia coli O6 GN=atpA
P0A6X7	ihfA	0.9726279	Integration host factor subunit alpha OS=Escherichia coli O6 GN=ihfA
P0AET8	hdhA	0.9735078	7-alpha-hydroxysteroid dehydrogenase OS=Escherichia coli O6 GN=hdhA
P77360	yphC	0.975089	Hypothetical zinc-type alcohol dehydrogenase-like protein yphC OS=Escherichia coli O6 GN=yphC
P0ACS7	rpiR	0.9752966	HTH-type transcriptional regulator rpiR OS=Escherichia coli O6 GN=rpiR
P0ABA6	atpG	0.9753356	ATP synthase gamma chain OS=Escherichia coli O6 GN=atpG
P0A8M6	yeeX	0.9779334	UPF0265 protein yeeX OS=Escherichia coli O6 GN=yeeX
P00926	dsdA	0.9787521	D-serine dehydratase OS=Escherichia coli O6 GN=dsdA
P0AF36	zapB	0.9787733	Cell division protein ZapB OS=Escherichia coli O6 GN=zapB
P0A8E7	yajQ	0.9789294	UPF0234 protein yajQ OS=Escherichia coli O6 GN=yajQ
P39099	degQ	0.9793609	Protease degQ OS=Escherichia coli O6 GN=degQ
P0AC02	yfiO	0.9796315	UPF0169 lipoprotein yfiO OS=Escherichia coli O6 GN=yfiO
P69222	infA	0.9802739	Translation initiation factor IF-1 OS=Escherichia coli O6 GN=infA
P30850	rnb	0.9804949	Exoribonuclease 2 OS=Escherichia coli O6 GN=rnb
P39173	yeaD	0.9824176	Putative uncharacterized protein yeaD OS=Escherichia coli O6 GN=yeaD
Q47147	yafJ	0.9826329	Putative uncharacterized protein yafJ OS=Escherichia coli O6 GN=yafJ
A0A0H2V689	c0290	0.9831164	Putative uncharacterized protein OS=Escherichia coli O6 GN=c0290
P33355	yehS	0.9864611	Putative uncharacterized protein yehS OS=Escherichia coli O6 GN=yehS
P45464	yraM	0.9867478	Putative uncharacterized protein yraM OS=Escherichia coli O6 GN=yraM

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P11454	entF	0.987505	Enterobactin synthetase component F OS=Escherichia coli O6 GN=entF
P0AFG8	aceE	0.9875818	Pyruvate dehydrogenase E1 component OS=Escherichia coli O6 GN=aceE
A0A0H2V9J3	c2988	0.9878307	NADP-dependent malic enzyme OS=Escherichia coli O6 GN=c2988
P0A8A8	rimP	0.9879622	Ribosome maturation factor rimP OS=Escherichia coli O6 GN=rimP
P75919	ymdC	0.9880804	Putative uncharacterized protein ymdC OS=Escherichia coli O6 GN=ymdC
P37194	slp	0.988227	Outer membrane protein slp OS=Escherichia coli O6 GN=slp
P0AFK0	pmbA	0.9884799	PmbA protein OS=Escherichia coli O6 GN=pmbA
P07762	glgB	0.9894007	1,4-alpha-glucan-branching enzyme OS=Escherichia coli O6 GN=glgB
P29217	yceH	0.9911307	UPF0502 protein yceH OS=Escherichia coli O6 GN=yceH
P0ABC7	hflK	0.9915433	HflK protein OS=Escherichia coli O6 GN=hflK
W8ZMC2	yggE	0.9926496	Putative uncharacterized protein yggE OS=Escherichia coli O6 GN=yggE
P0A7V0	rpsB	0.9935321	30S ribosomal protein S2 OS=Escherichia coli O6 GN=rpsB
P0A7P5	rpmH	0.9935931	50S ribosomal protein L34 OS=Escherichia coli O6 GN=rpmH
O07813	leuS	0.995003	Leucyl-tRNA synthetase OS=Escherichia coli O6 GN=leuS
P33195	gcvP	0.9950919	Glycine dehydrogenase [decarboxylating] OS=Escherichia coli O6 GN=gcvP
P30745	moaA	0.9951691	GTP 3',8-cyclase OS=Escherichia coli O6 GN=moaA
P36562	cobT	0.9956986	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase OS=Escherichia coli O6 GN=cobT
P0ABS1	dksA	0.9960705	DnaK suppressor protein OS=Escherichia coli O6 GN=dksA
P07001	pntA	0.9961597	NAD(P) transhydrogenase subunit alpha OS=Escherichia coli O6 GN=pntA
P0AEA8	cysG	0.9967812	Siroheme synthase OS=Escherichia coli O6 GN=cysG
P0AFJ1	phnA	0.9968022	Protein PhnA OS=Escherichia coli O6 GN=phnA
P77433	ykgG	0.9979899	Uncharacterized protein YkgG OS=Escherichia coli O6 GN=ykgG
P0AB71	fba	0.9982909	Fructose-bisphosphate aldolase class 2 OS=Escherichia coli O6 GN=fba
P68567	yhiQ	0.9985352	Ribosomal RNA small subunit methyltransferase J OS=Escherichia coli O6 GN=yhiQ
P30860	artJ	0.9988543	Arginine-binding periplasmic protein 2 OS=Escherichia coli O6 GN=artJ
P0A955	eda	0.9993178	KHG/KDPG aldolase OS=Escherichia coli O6 GN=eda
P0C0L2	osmC	0.9993726	Osmotically inducible protein C OS=Escherichia coli O6 GN=osmC
P0A9P0	lpdA	0.9993731	Dihydrolipoyl dehydrogenase OS=Escherichia coli O6 GN=lpdA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0AAK7	nrfC	0.9998052	NrfC protein OS=Escherichia coli O6 GN=nrfC
Q46829	bglA	1.000338	6-phospho-beta-glucosidase bglA OS=Escherichia coli O6 GN=bglA
P00561	thrA	1.000779	Aspartokinase I OS=Escherichia coli O6 GN=thrA
P0A7U3	rpsS	1.000943	30S ribosomal protein S19 OS=Escherichia coli O6 GN=rpsS
P24192	hypD	1.001229	Hydrogenase isoenzymes formation protein hypD OS=Escherichia coli O6 GN=hypD
W8ZN03	yghZ	1.002298	Putative uncharacterized protein yghZ OS=Escherichia coli O6 GN=yghZ
P0A799	pgk	1.00238	Phosphoglycerate kinase OS=Escherichia coli O6 GN=pgk
Q7WTI7	iroC	1.002481	IroC OS=Escherichia coli O6 GN=iroC
P02359	rpsG	1.002843	30S ribosomal protein S7 OS=Escherichia coli O6 GN=rpsG
P0A7Z4	rpoA	1.002946	DNA-directed RNA polymerase subunit alpha OS=Escherichia coli O6 GN=rpoA
P69783	crr	1.003248	Glucose-specific phosphotransferase enzyme IIA component OS=Escherichia coli O6 GN=crr
P0AGG2	tesB	1.006661	Acyl-CoA thioesterase II OS=Escherichia coli O6 GN=tesB
P15288	pepD	1.00708	Aminoacyl-histidine dipeptidase OS=Escherichia coli O6 GN=pepD
P0A780	nusB	1.009435	N utilization substance protein B OS=Escherichia coli O6 GN=nusB
A0A0H2VC65	c4537	1.009762	Putative conserved protein OS=Escherichia coli O6 GN=c4537
P0A7J7	rplK	1.010151	50S ribosomal protein L11 OS=Escherichia coli O6 GN=rplK
P0A8T7	rpoC	1.010286	DNA-directed RNA polymerase subunit beta' OS=Escherichia coli O6 GN=rpoC
P0A7J3	rplJ	1.010336	50S ribosomal protein L10 OS=Escherichia coli O6 GN=rplJ
P60595	hisH	1.011038	Imidazole glycerol phosphate synthase subunit hisH OS=Escherichia coli O6 GN=hisH
P0AFC7	nuoB	1.01114	NADH-quinone oxidoreductase subunit B OS=Escherichia coli O6 GN=nuoB
P37095	pepB	1.011572	Peptidase B OS=Escherichia coli O6 GN=pepB
P22524	mukE	1.011988	Chromosome partition protein mukE OS=Escherichia coli O6 GN=mukE
P0A858	tpiA	1.012311	Triosephosphate isomerase OS=Escherichia coli O6 GN=tpiA
P31979	nuoF	1.013231	NADH dehydrogenase I chain F OS=Escherichia coli O6 GN=nuoF
P0A6M8	fusA	1.013397	Elongation factor G OS=Escherichia coli O6 GN=fusA
P76513	yfdQ	1.013453	Uncharacterized protein YfdQ OS=Escherichia coli O6 GN=yfdQ
P60472	uppS	1.014031	Ditrans,polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific) OS=Escherichia coli O6 GN=uppS
P05825	fepA	1.015013	Ferrienterobactin receptor OS=Escherichia coli O6 GN=fepA

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P76352	yeeO	1.016193	Probable FMN/FAD exporter YeeO OS=Escherichia coli O6 GN=yeeO
P0AG14	sohB	1.017327	Possible protease sohB OS=Escherichia coli O6 GN=sohB
P00963	asnA	1.017754	Aspartate--ammonia ligase OS=Escherichia coli O6 GN=asnA
P0ABH7	gltA	1.018132	Citrate synthase OS=Escherichia coli O6 GN=gltA
P0AC51	yjbK	1.019932	Zinc uptake regulation protein OS=Escherichia coli O6 GN=yjbK
P08373	murB	1.020373	UDP-N-acetylenolpyruvoylglucosamine reductase OS=Escherichia coli O6 GN=murB
P0AA43	rsuA	1.020647	Ribosomal small subunit pseudouridine synthase A OS=Escherichia coli O6 GN=rsuA
P46853	yhhX	1.021371	Putative oxidoreductase yhhX OS=Escherichia coli O6 GN=yhhX
P0A6P9	eno	1.022036	Enolase OS=Escherichia coli O6 GN=eno
P05194	aroD	1.022712	3-dehydroquinate dehydratase OS=Escherichia coli O6 GN=aroD
P67910	hldD	1.02317	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Escherichia coli O6 GN=hldD
P30863	yafB	1.024608	2,5-diketo-D-gluconic acid reductase B OS=Escherichia coli O6 GN=yafB
P0A9A9	fur	1.024614	Ferric uptake regulation protein OS=Escherichia coli O6 GN=fur
W8ZP03	ygiF	1.025591	Putative uncharacterized protein ygiF OS=Escherichia coli O6 GN=ygiF
P13024	fdhE	1.026033	Protein fdhE OS=Escherichia coli O6 GN=fdhE
P21599	pykA	1.026892	Pyruvate kinase II OS=Escherichia coli O6 GN=pykA
P21338	rna	1.026926	Ribonuclease I OS=Escherichia coli O6 GN=rna
P08395	sppA	1.027265	Protease IV OS=Escherichia coli O6 GN=sppA
P64596	yraP	1.027496	Uncharacterized protein yraP OS=Escherichia coli O6 GN=yraP
A0A0H2V851	c2236	1.029304	Transcriptional regulator kdgR OS=Escherichia coli O6 GN=c2236
P0A8C1	ybjQ	1.030667	UPF0145 protein ybjQ OS=Escherichia coli O6 GN=ybjQ
P0ACC7	glmU	1.031011	Bifunctional protein glmU OS=Escherichia coli O6 GN=glmU
P0A7N9	rpmG	1.031347	50S ribosomal protein L33 OS=Escherichia coli O6 GN=rpmG
P0A7M2	rpmB	1.032219	50S ribosomal protein L28 OS=Escherichia coli O6 GN=rpmB
P36767	rdgC	1.032622	Recombination-associated protein rdgC OS=Escherichia coli O6 GN=rdgC
P08394	recB	1.032864	RecBCD enzyme subunit RecB OS=Escherichia coli O6 GN=recB
P0AEP3	galU	1.032924	UTP--glucose-1-phosphate uridylyltransferase OS=Escherichia coli O6 GN=galU
P0A7T3	rpsP	1.033175	30S ribosomal protein S16 OS=Escherichia coli O6 GN=rpsP
P0AB52	ychN	1.033363	Putative uncharacterized protein ychN OS=Escherichia coli O6 GN=ychN

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P17443	murG	1.033831	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase OS=Escherichia coli O6 GN=murG
P0AG82	pstS	1.034186	Phosphate-binding periplasmic protein OS=Escherichia coli O6 GN=pstS
P0AGA2	secY	1.035125	Preprotein translocase subunit secY OS=Escherichia coli O6 GN=secY
P0AGG0	thiL	1.036655	Thiamine-monophosphate kinase OS=Escherichia coli O6 GN=thiL
P30147	gip	1.037622	Hydroxypyruvate isomerase OS=Escherichia coli O6 GN=gip
A0A0H2V9W2	c2059	1.037638	Protein ydhR OS=Escherichia coli O6 GN=c2059
P0A8V2	rpoB	1.038204	DNA-directed RNA polymerase subunit beta OS=Escherichia coli O6 GN=rpoB
P0AFX9	rseB	1.038478	Sigma-E factor Regulatory protein rseB OS=Escherichia coli O6 GN=rseB
P00962	glnS	1.039784	Glutaminyl-tRNA synthetase OS=Escherichia coli O6 GN=glnS
P60438	rplC	1.04011	50S ribosomal protein L3 OS=Escherichia coli O6 GN=rplC
P07395	pheT	1.04108	Phenylalanyl-tRNA synthetase beta chain OS=Escherichia coli O6 GN=pheT
P37665	yiaD	1.041735	Hypothetical lipoprotein yiaD OS=Escherichia coli O6 GN=yiaD
P37051	purU	1.041763	Formyltetrahydrofolate deformylase OS=Escherichia coli O6 GN=purU
P0AB91	aroG	1.04224	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Escherichia coli O6 GN=aroG
P0A738	moaC	1.042307	Molybdenum cofactor biosynthesis protein C OS=Escherichia coli O6 GN=moaC
P60624	rplX	1.042644	50S ribosomal protein L24 OS=Escherichia coli O6 GN=rplX
P02358	rpsF	1.044547	30S ribosomal protein S6 OS=Escherichia coli O6 GN=rpsF
P0A6I6	coaD	1.044693	hosphopantetheine adenylyltransferase OS=Escherichia coli O6 GN=coaD
P0AEG4	dsbA	1.044778	Thiol:disulfide interchange protein DsbA OS=Escherichia coli O6 GN=dsbA
P39411	yjjX	1.044846	UPF0244 protein yjjX OS=Escherichia coli O6 GN=yjjX
P00961	glyS	1.04491	Glycyl-tRNA synthetase beta subunit OS=Escherichia coli O6 GN=glyS
P40874	solA	1.045326	N-methyl-L-tryptophan oxidase OS=Escherichia coli O6 GN=solA
P0ADR8	ygdH	1.046533	LOG family protein ygdH OS=Escherichia coli O6 GN=ygdH
P45578	luxS	1.046935	S-ribosylhomocysteine lyase OS=Escherichia coli O6 GN=luxS
W8ZXI3	yrbD	1.04724	Putative uncharacterized protein yrbD OS=Escherichia coli O6 GN=yrbD
P0A8F4	udk	1.047392	Uridine kinase OS=Escherichia coli O6 GN=udk
P0A9L3	fklB	1.04798	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase OS=Escherichia coli O6 GN=fklB
A0A0H2V8E0	c2429	1.048265	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2429

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P38038	cysJ	1.048593	Sulfite reductase [NADPH] flavoprotein alpha-component OS=Escherichia coli O6 GN=cysJ
P0AC69	grxD	1.048671	Glutaredoxin-4 OS=Escherichia coli O6 GN=grxD
P0A817	metK	1.049621	S-adenosylmethionine synthase OS=Escherichia coli O6 GN=metK
P77690	arnB	1.049685	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase OS=Escherichia coli O6 GN=arnB
P04425	gshB	1.049705	Glutathione synthetase OS=Escherichia coli O6 GN=gshB
P07363	cheA	1.049767	Chemotaxis protein CheA OS=Escherichia coli O6 GN=cheA
P0A6L0	deoC	1.050971	Deoxyribose-phosphate aldolase OS=Escherichia coli O6 GN=deoC
Q8FKW2	c0279	1.051066	UPF0401 protein c0279 OS=Escherichia coli O6 GN=c0279
P0AAB4	ubiD	1.051195	3-octaprenyl-4-hydroxybenzoate carboxy-lyase OS=Escherichia coli O6 GN=ubiD
A0A0H2V8B3	c2426	1.051447	Putative peptide synthetase OS=Escherichia coli O6 GN=c2426
A0A0H2V9L8	c3143	1.051549	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3143
A0A0H2V572	c0719	1.053788	Putative uncharacterized protein OS=Escherichia coli O6 GN=c0719
P0A8T1	prmA	1.055215	Ribosomal protein L11 methyltransferase OS=Escherichia coli O6 GN=prmA
A0A0H2V615	c1236	1.056102	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1236
P75726	citF	1.056185	Citrate lyase alpha chain OS=Escherichia coli O6 GN=citF
P37188	gatB	1.058128	Galactitol-specific phosphotransferase enzyme IIB component OS=Escherichia coli O6 GN=gatB
P76423	thiM	1.058314	Hydroxyethylthiazole kinase OS=Escherichia coli O6 GN=thiM
P0CE47	tufA	1.0588	Elongation factor Tu OS=Escherichia coli O6 GN=tufA
P0A8E5	yacL	1.059336	UPF0231 protein yacL OS=Escherichia coli O6 GN=yacL
P0ACC3	erpA	1.059463	Iron-sulfur cluster insertion protein erpA OS=Escherichia coli O6 GN=erpA
P0AB89	purB	1.059559	Adenylosuccinate lyase OS=Escherichia coli O6 GN=purB
P0A862	tpx	1.059629	Thiol peroxidase OS=Escherichia coli O6 GN=tpx
P77806	ybdL	1.060194	Hypothetical aminotransferase ybdL OS=Escherichia coli O6 GN=ybdL
P0ACF8	hns	1.06043	DNA-binding protein H-NS OS=Escherichia coli O6 GN=hns
P0AG55	rplF	1.060962	50S ribosomal protein L6 OS=Escherichia coli O6 GN=rplF
W8ZFB1	ybiK	1.061754	Putative L-asparaginase OS=Escherichia coli O6 GN=ybiK
P31828	pqqL	1.062115	Probable zinc protease pqqL OS=Escherichia coli O6 GN=pqqL
P69913	csrA	1.062781	Carbon storage regulator OS=Escherichia coli O6 GN=csrA
W8ZNS8	ybgI	1.06447	UPF0135 protein ybgI OS=Escherichia coli O6 GN=ybgI

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
W8ZP39	ybiP	1.064792	Putative uncharacterized protein ybiP OS=Escherichia coli O6 GN=ybiP
P0A7I4	prfC	1.065258	Peptide chain release factor 3 OS=Escherichia coli O6 GN=prfC
Q46822	idi	1.065561	Isopentenyl-diphosphate Delta-isomerase OS=Escherichia coli O6 GN=idi
P0A715	kdsA	1.065768	2-dehydro-3-deoxyphosphooctonate aldolase OS=Escherichia coli O6 GN=kdsA
P75863	ycbX	1.065866	Putative uncharacterized protein ycbX OS=Escherichia coli O6 GN=ycbX
P0A8M0	asnS	1.065981	Asparaginyl-tRNA synthetase OS=Escherichia coli O6 GN=asnS
P27838	cyaY	1.066646	Protein CyaY OS=Escherichia coli O6 GN=cyaY
P75745	ybgK	1.066665	Putative uncharacterized protein ybgK OS=Escherichia coli O6 GN=ybgK
P68919	rplY	1.066972	50S ribosomal protein L25 OS=Escherichia coli O6 GN=rplY
	rpsJ	1.068099	30S ribosomal protein S10 OS=Escherichia coli O6 GN=rpsJ
P22259	pckA	1.068528	Phosphoenolpyruvate carboxykinase [ATP] OS=Escherichia coli O6 GN=pckA
P33359	yehW	1.068725	Hypothetical ABC transporter permease protein yehW OS=Escherichia coli O6 GN=yehW
P11875	argS	1.069213	Arginyl-tRNA synthetase OS=Escherichia coli O6 GN=argS
P0AGI8	trkA	1.070045	Trk system potassium uptake protein trkA OS=Escherichia coli O6 GN=trkA
P39325	ytfQ	1.070552	ABC transporter Periplasmic binding protein ytfQ OS=Escherichia coli O6 GN=ytfQ
W9ALF0	yhhM	1.070663	Putative uncharacterized protein yhhM OS=Escherichia coli O6 GN=yhhM
P00956	ileS	1.072313	Isoleucyl-tRNA synthetase OS=Escherichia coli O6 GN=ileS
P0A8W0	nanR	1.073396	Transcriptional regulator nanR OS=Escherichia coli O6 GN=nanR
P10378	entE	1.073636	Enterobactin synthetase component E OS=Escherichia coli O6 GN=entE
P23869	ppiB	1.074067	Peptidyl-prolyl cis-trans isomerase B OS=Escherichia coli O6 GN=ppiB
P0A6F3	glpK	1.074904	Glycerol kinase OS=Escherichia coli O6 GN=glpK
P0ADY7	rplP	1.075982	50S ribosomal protein L16 OS=Escherichia coli O6 GN=rplP
P0A8R0	rraA	1.076421	Regulator of ribonuclease activity A OS=Escherichia coli O6 GN=rraA
P37652	yhjN	1.076549	Cyclic di-GMP binding protein OS=Escherichia coli O6 GN=yhjN
P77570	anmK	1.07656	Anhydro-N-acetylmuramic acid kinase OS=Escherichia coli O6 GN=anmK
W8ZXV8	yhiD	1.076794	Putative uncharacterized protein yhiD OS=Escherichia coli O6 GN=yhiD
P77581	astC	1.078005	Succinylornithine transaminase OS=Escherichia coli O6 GN=astC
P75777	ybhG	1.078174	UPF0194 membrane protein ybhG OS=Escherichia coli O6 GN=ybhG
P0AAC0	uspE	1.078219	Universal stress protein E OS=Escherichia coli O6 GN=uspE

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A8J8	rhlB	1.078666	ATP-dependent RNA helicase rhlB OS=Escherichia coli O6 GN=rhlB
P26616	maeA	1.079274	NAD-dependent malic enzyme OS=Escherichia coli O6 GN=maeA
P0A6P1	tsf	1.079572	Elongation factor Ts OS=Escherichia coli O6 GN=tsf
P0A794	pdxJ	1.080652	Pyridoxine 5'-phosphate synthase OS=Escherichia coli O6 GN=pdxJ
P0AG07	rpe	1.080952	Ribulose-phosphate 3-epimerase OS=Escherichia coli O6 GN=rpe
C3SLK2	oxaA	1.081851	Inner membrane protein oxaA OS=Escherichia coli O6 GN=oxaA
P0A8K5	yaeP	1.081936	UPF0253 protein YaeP OS=Escherichia coli O6 GN=yaeP
W8ZG87	ybiC	1.082376	Hypothetical oxidoreductase ybiC OS=Escherichia coli O6 GN=ybiC
P63224	gmhA	1.082456	Phosphoheptose isomerase OS=Escherichia coli O6 GN=gmhA
A0A0H2V833	c1187	1.082744	3-oxoacyl-[acyl-carrier protein] reductase OS=Escherichia coli O6 GN=c1187
P0A7H6	recR	1.084068	Recombination protein recR OS=Escherichia coli O6 GN=recR
P0A825	glyA	1.084298	Serine hydroxymethyltransferase OS=Escherichia coli O6 GN=glyA
P0AE06	acrA	1.084587	Acriflavine resistance protein A OS=Escherichia coli O6 GN=acrA
P39172	yebL	1.084718	High-affinity zinc uptake system protein znuA OS=Escherichia coli O6 GN=yebL
P33643	rluD	1.084925	Ribosomal large subunit pseudouridine synthase D OS=Escherichia coli O6 GN=rluD
P0AFF6	nusA	1.085855	Transcription elongation protein nusA OS=Escherichia coli O6 GN=nusA
W8ZS03	infC	1.086249	Translation initiation factor IF-3 OS=Escherichia coli O6 GN=infC
P77674	prr	1.086311	Gamma-aminobutyraldehyde dehydrogenase OS=Escherichia coli O6 GN=prr
P0AFR4	yciO	1.086363	Uncharacterized protein yciO OS=Escherichia coli O6 GN=yciO
W8ZLT0	ypdB	1.086601	Uncharacterized response regulatory protein ypdB OS=Escherichia coli O6 GN=ypdB
P0A7W1	rpsE	1.08721	30S ribosomal protein S5 OS=Escherichia coli O6 GN=rpsE
P61175	rplV	1.088563	50S ribosomal protein L22 OS=Escherichia coli O6 GN=rplV
P0ADI4	entB	1.088849	Isochorismatase OS=Escherichia coli O6 GN=entB
P04128	fimA	1.088853	Type-1 fimbrial protein, A chain OS=Escherichia coli O6 GN=fimA
P0A761	nanE	1.089632	Putative N-acetylmannosamine-6-phosphate 2-epimerase OS=Escherichia coli O6 GN=nanE
P30011	nadC	1.090122	Nicotinate-nucleotide pyrophosphorylase (Carboxylating) OS=Escherichia coli O6 GN=nadC
P77398	arnA	1.090493	Bifunctional polymyxin resistance protein ArnA OS=Escherichia coli O6 GN=arnA
W8ZRB2	hemX	1.092957	Putative uroporphyrin-III C-methyltransferase OS=Escherichia coli O6 GN=hemX
	hemE	1.093113	Uroporphyrinogen decarboxylase OS=Escherichia coli O6 GN=hemE

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P05459	pdxB	1.093956	Erythronate-4-phosphate dehydrogenase OS=Escherichia coli O6 GN=pdxB
P62768	yaeH	1.094182	UPF0325 protein yaeH OS=Escherichia coli O6 GN=yaeH
P0ACY1	ydjA	1.094292	Protein ydjA OS=Escherichia coli O6 GN=ydjA
P0AC33	fumA	1.095063	Fumarate hydratase class I, aerobic OS=Escherichia coli O6 GN=fumA
P22255	cysQ	1.095153	bisphosphate nucleotidase CysQ OS=Escherichia coli O6 GN=cysQ
P0AF93	yjgF	1.095426	RutC family protein yjgF OS=Escherichia coli O6 GN=yjgF
P67603	yqfB	1.095504	UPF0267 protein yqfB OS=Escherichia coli O6 GN=yqfB
P0A6D3	aroA	1.095866	3-phosphoshikimate 1-carboxyvinyltransferase OS=Escherichia coli O6 GN=aroA
P0AG63	rpsQ	1.096361	30S ribosomal protein S17 OS=Escherichia coli O6 GN=rpsQ
P37903	uspF	1.09639	Universal stress protein F OS=Escherichia coli O6 GN=uspF
P0A6W9	gshA	1.096569	Glutamate--cysteine ligase OS=Escherichia coli O6 GN=gshA
P0A7U7	rpsT	1.096679	30S ribosomal protein S20 OS=Escherichia coli O6 GN=rpsT
P0A6F1	carA	1.097403	Carbamoyl-phosphate synthase small chain OS=Escherichia coli O6 GN=carA
P77309	yneJ	1.097415	Hypothetical transcriptional regulator yneJ OS=Escherichia coli O6 GN=yneJ
P39274	yjdJ	1.098526	Putative uncharacterized protein yjdJ OS=Escherichia coli O6 GN=yjdJ
P0A7I7	ribA	1.098539	GTP cyclohydrolase-2 OS=Escherichia coli O6 GN=ribA
P09394	glpQ	1.099142	Glycerophosphoryl diester phosphodiesterase, periplasmic OS=Escherichia coli O6 GN=glpQ
P0ADP9	yihD	1.099772	Protein YihD OS=Escherichia coli O6 GN=yihD
P04995	sbcB	1.100482	Exodeoxyribonuclease I OS=Escherichia coli O6 GN=sbcB
P06983	hemC	1.100783	Porphobilinogen deaminase OS=Escherichia coli O6 GN=hemC
P15877	gcd	1.101268	Glucose dehydrogenase OS=Escherichia coli O6 GN=gcd
P0A8I3	yaaA	1.101879	UPF0246 protein yaaA OS=Escherichia coli O6 GN=yaaA
P0A959	yfbQ	1.102828	Uncharacterized aminotransferase YfbQ OS=Escherichia coli O6 GN=yfbQ
P06987	hisB	1.103002	Histidine biosynthesis bifunctional protein hisB OS=Escherichia coli O6 GN=hisB
P0ABF6	cdd	1.103053	Cytidine deaminase OS=Escherichia coli O6 GN=cdd
P0ADF8	ilvN	1.103363	Acetolactate synthase isozyme 1 small subunit OS=Escherichia coli O6 GN=ilvN
P07604	tyrR	1.104144	Transcriptional Regulatory protein tyrR OS=Escherichia coli O6 GN=tyrR
P77211	cusC	1.105049	Cation efflux system protein CusC OS=Escherichia coli O6 GN=cusC
P35340	ahpF	1.105074	Alkyl hydroperoxide reductase subunit F OS=Escherichia coli O6 GN=ahpF

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P05852	ygjD	1.105206	Uncharacterized protein yqjD OS=Escherichia coli O6 GN=yqjD
P03024	galR	1.105312	Galactose operon repressor OS=Escherichia coli O6 GN=galR
P75800	yliE	1.108933	Probable cyclic di-GMP phosphodiesterase PdeI OS=Escherichia coli O6 GN=yliE
P12281	moeA	1.110251	Molybdopterin biosynthesis protein moeA OS=Escherichia coli O6 GN=moeA
P76177	ydgH	1.110875	Protein ydgH OS=Escherichia coli O6 GN=ydgH
Q06902	pepA	1.1113	Cytosol aminopeptidase OS=Escherichia coli O6 GN=pepA
P0A7B5	proB	1.111713	Glutamate 5-kinase OS=Escherichia coli O6 GN=proB
P24232	hmp	1.112264	Flavohemoprotein OS=Escherichia coli O6 GN=hmp
P30136	thiC	1.112511	Phosphomethylpyrimidine synthase OS=Escherichia coli O6 GN=thiC
P0AA04	ptsH	1.112659	Phosphocarrier protein HPr OS=Escherichia coli O6 GN=ptsH
P69441	adk	1.112747	Adenylate kinase OS=Escherichia coli O6 GN=adk
P0A998	ftnA	1.11423	Ferritin-1 OS=Escherichia coli O6 GN=ftnA
P0AES4	gyrA	1.114238	DNA gyrase subunit A OS=Escherichia coli O6 GN=gyrA
P10408	secA	1.114365	Protein translocase subunit secA OS=Escherichia coli O6 GN=secA
W9AKJ9	yhbW	1.11509	Uncharacterized protein yhbW OS=Escherichia coli O6 GN=yhbW
P0AB55	yciI	1.11588	Protein YciI OS=Escherichia coli O6 GN=yciI
P0A6V1	glgC	1.116047	Glucose-1-phosphate adenylyltransferase OS=Escherichia coli O6 GN=glgC
P60340	truB	1.116356	tRNA pseudouridine synthase B OS=Escherichia coli O6 GN=truB
P77775	yfcH	1.116978	Putative uncharacterized protein yfcH OS=Escherichia coli O6 GN=yfcH
P23839	yicC	1.117005	Protein yicC OS=Escherichia coli O6 GN=yicC
P0A7W7	rpsH	1.117131	30S ribosomal protein S8 OS=Escherichia coli O6 GN=rpsH
P0ADG7	guaB	1.117774	Inosine-monophosphate dehydrogenase OS=Escherichia coli O6 GN=guaB
P0A763	ndk	1.117834	Nucleoside diphosphate kinase OS=Escherichia coli O6 GN=ndk
P02919	mrcB	1.118215	Penicillin-binding protein 1B OS=Escherichia coli O6 GN=mrcB
P0C0V0	htrA	1.118292	Protease do OS=Escherichia coli O6 GN=htrA
P60723	rplD	1.120333	50S ribosomal protein L4 OS=Escherichia coli O6 GN=rplD
P0AF90	yjgD	1.120366	Regulator of ribonuclease activity B OS=Escherichia coli O6 GN=yjgD
A0A0H2VDQ9	c4509	1.121019	Uncharacterized protein OS=Escherichia coli O6 GN=c4509
P0ABJ9	cydA	1.121611	Cytochrome d ubiquinol oxidase subunit 1 OS=Escherichia coli O6 GN=cydA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0AED7	dapE	1.121888	Succinyl-diaminopimelate desuccinylase OS=Escherichia coli O6 GN=dapE
P0AE37	astA	1.122658	Arginine N-succinyltransferase OS=Escherichia coli O6 GN=astA
P0C018	rplR	1.122888	50S ribosomal protein L18 OS=Escherichia coli O6 GN=rplR
P0A8L1	serS	1.123384	Seryl-tRNA synthetase OS=Escherichia coli O6 GN=serS
P76196	ydil	1.124408	Uncharacterized protein YdiL OS=Escherichia coli O6 GN=ydiL
P18956	ggt	1.124709	Gamma-glutamyltranspeptidase OS=Escherichia coli O6 GN=ggt
P0A6N4	efp	1.124754	Elongation factor P OS=Escherichia coli O6 GN=efp
P0ACL2	exuR	1.125229	Exu regulon transcriptional regulator OS=Escherichia coli O6 GN=exuR
P0A6P5	era	1.126303	GTPase Era OS=Escherichia coli O6 GN=era
A0A0H2V703	c1764	1.126994	Efflux pump membrane transporter OS=Escherichia coli O6 GN=c1764
P0AEZ9	moaB	1.127976	Molybdenum cofactor biosynthesis protein B OS=Escherichia coli O6 GN=moaB
P04152	umuC	1.129749	UmuC protein OS=Escherichia coli O6 GN=umuC
P32669	fsaB	1.130068	Fructose-6-phosphate aldolase 2 OS=Escherichia coli O6 GN=fsaB
P77215	rhmD	1.130189	L-rhamnonate dehydratase OS=Escherichia coli O6 GN=rhmD
P00350	gnd	1.130491	6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli O6 GN=gnd
P33018	yeiG	1.1305	S-formylglutathione hydrolase yeiG OS=Escherichia coli O6 GN=yeiG
	dnaN	1.13099	DNA polymerase III subunit beta OS=Escherichia coli O6 GN=dnaN
P27302	tktA	1.131936	Transketolase 1 OS=Escherichia coli O6 GN=tktA
P15977	malQ	1.132076	4-alpha-glucanotransferase OS=Escherichia coli O6 GN=malQ
P08312	pheS	1.132501	Phenylalanyl-tRNA synthetase alpha chain OS=Escherichia coli O6 GN=pheS
P0AEM0	fkpB	1.134328	FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase OS=Escherichia coli O6 GN=fkpB
P00959	metG	1.134364	Methionyl-tRNA synthetase OS=Escherichia coli O6 GN=metG
P76290	cmoA	1.13467	tRNA (cmo5U34)-methyltransferase OS=Escherichia coli O6 GN=cmoA
P68679	rpsU	1.134843	30S ribosomal protein S21 OS=Escherichia coli O6 GN=rpsU
W8ZG19	tolB	1.135853	Protein tolB OS=Escherichia coli O6 GN=tolB
P0A991	fbaB	1.137699	Fructose-bisphosphate aldolase class 1 OS=Escherichia coli O6 GN=fbaB
P39831	ydfG	1.138356	NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG OS=Escherichia coli O6 GN=ydfG
A0A0H2V6P0	c1102	1.138976	Protein yccU OS=Escherichia coli O6 GN=c1102
P00448	sodA	1.139105	Superoxide dismutase [Mn] OS=Escherichia coli O6 GN=sodA

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
W9AII4	yfgM	1.139441	Putative uncharacterized protein yfgM OS=Escherichia coli O6 GN=yfgM
P0AEY5	mdaB	1.13949	Modulator of drug activity B OS=Escherichia coli O6 GN=mdaB
P0A6Q3	fabA	1.140044	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Escherichia coli O6 GN=fabA
P11447	argH	1.14052	Argininosuccinate lyase OS=Escherichia coli O6 GN=argH
P0AAI9	fabD	1.140805	Malonyl CoA-acyl carrier protein transacylase OS=Escherichia coli O6 GN=fabD
W8ZWX3	yhbL	1.141907	Enhancing lycopene biosynthesis protein 2 OS=Escherichia coli O6 GN=yhbL
P0A717	prs	1.142131	Ribose-phosphate pyrophosphokinase OS=Escherichia coli O6 GN=prs
P0A6B7	iscS	1.142489	Cysteine desulfurase OS=Escherichia coli O6 GN=iscS
P25736	endA	1.142936	Endonuclease I OS=Escherichia coli O6 GN=endA
P0AE08	ahpC	1.142982	Alkyl hydroperoxide reductase subunit C OS=Escherichia coli O6 GN=ahpC
P32719	yjcU	1.143309	D-allulose-6-phosphate 3-epimerase OS=Escherichia coli O6 GN=yjcU
P55135	rumA	1.143374	23S rRNA (uracil-5-)-methyltransferase RumA OS=Escherichia coli O6 GN=rumA
P0A6U8	glgA	1.14419	Glycogen synthase OS=Escherichia coli O6 GN=glgA
P33602	nuoG	1.144719	NADH-quinone oxidoreductase subunit G OS=Escherichia coli O6 GN=nuoG
P23836	phoP	1.145272	Transcriptional regulatory protein phoP OS=Escherichia coli O6 GN=phoP
P0A786	pyrB	1.145314	Aspartate carbamoyltransferase catalytic chain OS=Escherichia coli O6 GN=pyrB
P0A796	pfkA	1.14593	6-phosphofructokinase OS=Escherichia coli O6 GN=pfkA
P0A929	yrdA	1.146146	Protein yrdA OS=Escherichia coli O6 GN=yrdA
P0AGG0	thiL	1.146351	Thiamine-monophosphate kinase OS=Escherichia coli O6 GN=thiL
P0ADX1	yhfA	1.146737	Protein yhfA OS=Escherichia coli O6 GN=yhfA
Q57261	truD	1.146835	tRNA pseudouridine synthase D OS=Escherichia coli O6 GN=truD
A0A0H2V8T3	c2669	1.14696	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2669
P0A6K3	def	1.147634	Peptide deformylase OS=Escherichia coli O6 GN=def
P0A7R9	rpsK	1.149278	30S ribosomal protein S11 OS=Escherichia coli O6 GN=rpsK
P29208	menC	1.149376	o-succinylbenzoate synthase OS=Escherichia coli O6 GN=menC
P0A850	tig	1.149662	Trigger factor OS=Escherichia coli O6 GN=tig
P16095	sdaA	1.150126	L-serine dehydratase 1 OS=Escherichia coli O6 GN=sdaA
P27298	prlC	1.15051	Oligopeptidase A OS=Escherichia coli O6 GN=prlC

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A7T7	rpsR	1.151487	30S ribosomal protein S18 OS=Escherichia coli O6 GN=rpsR
P64423	zntB	1.15178	Zinc transport protein ZntB OS=Escherichia coli O6 GN=zntB
P0A9X4	mreB	1.15197	Rod shape-determining protein mreB OS=Escherichia coli O6 GN=mreB
P0ACJ0	lrp	1.15294	Leucine-responsive regulatory protein OS=Escherichia coli O6 GN=lrp
P09099	xylB	1.153143	Xylulose kinase OS=Escherichia coli O6 GN=xylB
P0AG86	secB	1.154735	Protein-export protein secB OS=Escherichia coli O6 GN=secB
A0A0H2V889	c2318	1.155308	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2318
P0A9S5	gldA	1.156055	Glycerol dehydrogenase OS=Escherichia coli O6 GN=gldA
P31435	yicJ	1.157609	Hypothetical symporter yicJ OS=Escherichia coli O6 GN=yicJ
A0A0H2V8I8	c2422	1.157827	Putative inner membrane ABC-transporter OS=Escherichia coli O6 GN=c2422
P24238	yebB	1.157932	Uncharacterized protein YebB OS=Escherichia coli O6 GN=yebB
P41409	rihA	1.158274	Pyrimidine-specific ribonucleoside hydrolase rihA OS=Escherichia coli O6 GN=rihA
P15034	pepP	1.158573	Xaa-Pro aminopeptidase OS=Escherichia coli O6 GN=pepP
P0ACA7	yliJ	1.158819	Uncharacterized GST-like protein yliJ OS=Escherichia coli O6 GN=yliJ
P0ADK8	yibL	1.159166	Uncharacterized protein YibL OS=Escherichia coli O6 GN=yibL
P33920	yejK	1.159236	Nucleoid-associated protein YejK OS=Escherichia coli O6 GN=yejK
P21513	rne	1.159379	Ribonuclease E OS=Escherichia coli O6 GN=rne
P0AE18	map	1.160135	Methionine aminopeptidase OS=Escherichia coli O6 GN=map
P0ACE0	hybC	1.161246	Hydrogenase-2 large chain OS=Escherichia coli O6 GN=hybC
P0ADD8	yjjQ	1.161667	Putative uncharacterized protein yjjQ OS=Escherichia coli O6 GN=yjjQ
P0A7A7	plsB	1.162488	Glycerol-3-phosphate acyltransferase OS=Escherichia coli O6 GN=plsB
P25522	mnmE	1.163005	tRNA modification GTPase mnmE OS=Escherichia coli O6 GN=mnmE
P27829	wecC	1.163718	UDP-N-acetyl-D-mannosamine dehydrogenase OS=Escherichia coli O6 GN=wecC
P0A7A5	pcm	1.163887	Protein-L-isoaspartate O-methyltransferase OS=Escherichia coli O6 GN=pcm
A0A0H2VE33	c4605	1.165339	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4605
P0A7X3	rpsI	1.165523	30S ribosomal protein S9 OS=Escherichia coli O6 GN=rpsI
P76403	yegQ	1.165662	Putative protease yegQ OS=Escherichia coli O6 GN=yegQ
P23538	ppsA	1.166867	Phosphoenolpyruvate synthase OS=Escherichia coli O6 GN=ppsA
P0AFL3	ppiA	1.167872	Peptidyl-prolyl cis-trans isomerase A OS=Escherichia coli O6 GN=ppiA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A6T9	gcvH	1.168323	Glycine cleavage system H protein OS=Escherichia coli O6 GN=gcvH
P07913	tdh	1.169996	L-threonine 3-dehydrogenase OS=Escherichia coli O6 GN=tdh
P0AF18	nagA	1.170052	N-acetylglucosamine-6-phosphate deacetylase OS=Escherichia coli O6 GN=nagA
P0A722	lpxA	1.170414	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase OS=Escherichia coli O6 GN=lpxA
P0ADQ7	ygaM	1.171468	Uncharacterized protein ygaM OS=Escherichia coli O6 GN=ygaM
P0ACE7	ycfF	1.171494	Purine nucleoside phosphoramidase OS=Escherichia coli O6 GN=ycfF
P0A8S1	iciA	1.17334	HTH-type transcriptional regulator ArgP OS=Escherichia coli O6 GN=iciA
P63386	mlaF	1.173459	Probable phospholipid import ATP-binding protein MlaF OS=Escherichia coli O6 GN=mlaF
P75797	gsiB	1.174009	Glutathione-binding protein gsiB OS=Escherichia coli O6 GN=gsiB
P24182	accC	1.174015	Biotin carboxylase OS=Escherichia coli O6 GN=accC
P22634	murI	1.17427	Glutamate racemase OS=Escherichia coli O6 GN=murI
P61949	fldA	1.176475	Flavodoxin-1 OS=Escherichia coli O6 GN=fldA
P37666	ghrB	1.177537	Glyoxylate/hydroxypyruvate reductase B OS=Escherichia coli O6 GN=ghrB
P31142	sseA	1.177901	3-mercaptopyruvate sulfurtransferase OS=Escherichia coli O6 GN=sseA
P0AC62	grxC	1.178054	Glutaredoxin 3 OS=Escherichia coli O6 GN=grxC
P36683	acnB	1.178928	Aconitate hydratase 2 OS=Escherichia coli O6 GN=acnB
P52645	ydbH	1.179145	Uncharacterized protein YdbH OS=Escherichia coli O6 GN=ydbH
P0A894	yhbJ	1.179795	RNase adapter protein RapZ OS=Escherichia coli O6 GN=yhbJ
P63417	yhbS	1.180021	Uncharacterized N-acetyltransferase YhbS OS=Escherichia coli O6 GN=yhbS
P18335	argD	1.181758	Acetylornithine/succinyldiaminopimelate aminotransferase OS=Escherichia coli O6 GN=argD
P0ABK5	cysK	1.182222	Cysteine synthase A OS=Escherichia coli O6 GN=cysK
P37672	dlgD	1.18307	2,3-diketo-L-gulonate reductase OS=Escherichia coli O6 GN=dlgD
P0A8M3	thrS	1.183955	Threonyl-tRNA synthetase OS=Escherichia coli O6 GN=thrS
P77258	nemA	1.184469	N-ethylmaleimide reductase OS=Escherichia coli O6 GN=nemA
P0AAQ6	ybaA	1.184783	Uncharacterized protein YbaA OS=Escherichia coli O6 GN=ybaA
P0A9Q5	accD	1.184792	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Escherichia coli O6 GN=accD
P0ADF6	edd	1.185886	Phosphogluconate dehydratase OS=Escherichia coli O6 GN=edd
A0A0H2V9I5	c2973	1.186909	Ethanolamine utilization protein eutL OS=Escherichia coli O6 GN=c2973
P0ABA4	atpH	1.187175	ATP synthase subunit delta OS=Escherichia coli O6 GN=atpH

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A8Y5	yidA	1.187928	Phosphatase YidA OS=Escherichia coli O6 GN=yidA
P00934	thrC	1.187996	Threonine synthase OS=Escherichia coli O6 GN=thrC
P23908	argE	1.188715	Acetylornithine deacetylase OS=Escherichia coli O6 GN=argE
P0A9M8	pta	1.190442	Phosphate acetyltransferase OS=Escherichia coli O6 GN=pta
W8ZP84	ybeJ	1.190696	Glutamate/aspartate Periplasmic binding protein OS=Escherichia coli O6 GN=ybeJ
P52096	yaeR	1.190842	Putative uncharacterized protein yaeR OS=Escherichia coli O6 GN=yaeR
P05055	pnp	1.191431	Polyribonucleotide nucleotidyltransferase OS=Escherichia coli O6 GN=pnp
P63284	clpP	1.191971	ATP-dependent Clp protease proteolytic subunit OS=Escherichia coli O6 GN=clpP
W8ZYW0	yicH	1.192701	Putative uncharacterized protein yicH OS=Escherichia coli O6 GN=yicH
W8ZLP7	ygaD	1.193633	Protein YgaD OS=Escherichia coli O6 GN=ygaD
P04949	fliC	1.193662	Flagellin OS=Escherichia coli O6 GN=fliC
P42911	agaD	1.193898	N-acetylgalactosamine permease IID component OS=Escherichia coli O6 GN=agaD
P33599	nuoC	1.194087	NADH-quinone oxidoreductase subunit C/D OS=Escherichia coli O6 GN=nuoC
Q46939	yqeF	1.194413	Probable acetyl-CoA acetyltransferase OS=Escherichia coli O6 GN=yqeF
P07004	proA	1.194579	Gamma-glutamyl phosphate reductase OS=Escherichia coli O6 GN=proA
A0A0H2V7Y9	c2225	1.194989	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2225
P77552	ydhQ	1.195271	Putative uncharacterized protein ydhQ OS=Escherichia coli O6 GN=ydhQ
P0A7E5	pyrG	1.198143	CTP synthase OS=Escherichia coli O6 GN=pyrG
P11880	murF	1.199559	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase OS=Escherichia coli O6 GN=murF
P0AEX5	prkB	1.199564	Probable phosphoribulokinase OS=Escherichia coli O6 GN=prkB
P0A7V8	rpsD	1.200204	30S ribosomal protein S4 OS=Escherichia coli O6 GN=rpsD
P77374	ynfE	1.20059	Putative dimethyl sulfoxide reductase chain ynfE OS=Escherichia coli O6 GN=ynfE
Q47679	yafV	1.200676	Putative uncharacterized protein yafV OS=Escherichia coli O6 GN=yafV
P29012	dadX	1.206196	Alanine racemase, catabolic OS=Escherichia coli O6 GN=dadX
P0AAR3	ybaK	1.207305	Protein ybaK OS=Escherichia coli O6 GN=ybaK
P76186	ydhK	1.207768	Putative uncharacterized protein ydhK OS=Escherichia coli O6 GN=ydhK
P23721	serC	1.208949	Phosphoserine aminotransferase OS=Escherichia coli O6 GN=serC
P64503	yebV	1.210019	Uncharacterized protein YebV OS=Escherichia coli O6 GN=yebV

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0A9N4	pflA	1.210969	Pyruvate formate-lyase 1-activating enzyme OS=Escherichia coli O6 GN=pflA
P0A6A3	ackA	1.211255	Acetate kinase OS=Escherichia coli O6 GN=ackA
P0ABD5	accA	1.211524	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Escherichia coli O6 GN=accA
P69797	manX	1.212378	PTS system mannose-specific EIIAB component OS=Escherichia coli O6 GN=manX
P27830	rffG	1.21327	dTDP-glucose 4,6-dehydratase OS=Escherichia coli O6 GN=rffG
P25740	rfaG	1.213473	Lipopolysaccharide core biosynthesis protein rfaG OS=Escherichia coli O6 GN=rfaG
P0A734	minE	1.213935	Cell division topological specificity factor OS=Escherichia coli O6 GN=minE
P0AAN1	hybE	1.214734	Hydrogenase-2 operon protein hybE OS=Escherichia coli O6 GN=hybE
P31663	panC	1.215604	Pantothenate synthetase OS=Escherichia coli O6 GN=panC
P23877	fepG	1.216387	Ferric enterobactin transport system permease protein fepG OS=Escherichia coli O6 GN=fepG
P07024	ushA	1.216622	Protein ushA OS=Escherichia coli O6 GN=ushA
P0A6Y1	ihfB	1.217281	Integration host factor subunit beta OS=Escherichia coli O6 GN=ihfB
P0A6V8	glk	1.218293	Glucokinase OS=Escherichia coli O6 GN=glk
P0AGJ7	trmL	1.219719	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmL OS=Escherichia coli O6 GN=trmL
P21499	vacB	1.220614	Ribonuclease R OS=Escherichia coli O6 GN=vacB
P0A7G2	rbfA	1.222842	Ribosome-binding factor A OS=Escherichia coli O6 GN=rbfA
P45395	kdsD	1.222858	Arabinose 5-phosphate isomerase OS=Escherichia coli O6 GN=kdsD
W8ZMW8	yahK	1.223448	Hypothetical zinc-type alcohol dehydrogenase-like protein yahK OS=Escherichia coli O6 GN=yahK
P0A867	talA	1.224714	Transaldolase A OS=Escherichia coli O6 GN=talA
P21513	rne	1.225304	Ribonuclease E OS=Escherichia coli O6 GN=rne
P04693	tyrB	1.226196	Aromatic-amino-acid aminotransferase OS=Escherichia coli O6 GN=tyrB
P0A7S9	rpsM	1.226236	30S ribosomal protein S13 OS=Escherichia coli O6 GN=rpsM
P76216	astB	1.226237	N-succinylarginine dihydrolase OS=Escherichia coli O6 GN=astB
P45577	proQ	1.226584	ProP effector OS=Escherichia coli O6 GN=proQ
Q46893	ispD	1.228449	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase OS=Escherichia coli O6 GN=ispD
P0ADW3	yhcB	1.228627	Putative cytochrome d ubiquinol oxidase subunit 3 OS=Escherichia coli O6 GN=yhcB
P0AG59	rpsN	1.228678	30S ribosomal protein S14 OS=Escherichia coli O6 GN=rpsN
P30014	rnt	1.2299	Ribonuclease T OS=Escherichia coli O6 GN=rnt
P52643	ldhA	1.230077	D-lactate dehydrogenase OS=Escherichia coli O6 GN=ldhA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
W8ZUA4	yegE	1.231653	Putative sensor-type protein OS=Escherichia coli O6 GN=yegE
P09323	nagE	1.23356	PTS system, N-acetylglucosamine-specific IIABC component OS=Escherichia coli O6 GN=nagE
P0A8B5	ybaB	1.233723	Nucleoid-associated protein YbaB OS=Escherichia coli O6 GN=ybaB
P19642	malX	1.234494	PTS system, maltose and glucose-specific IIABC component OS=Escherichia coli O6 GN=malX
W8ZPA8	yrbA	1.234786	Uncharacterized protein OS=Escherichia coli O6 GN=yrbA
W8ZKZ6	yfeX	1.236289	Putative uncharacterized protein yfeX OS=Escherichia coli O6 GN=yfeX
P18843	nadE	1.23704	NH(3)-dependent NAD(+) synthetase OS=Escherichia coli O6 GN=nadE
P77395	ybbN	1.23759	Putative uncharacterized protein ybbN OS=Escherichia coli O6 GN=ybbN
P66817	diaA	1.237814	DnaA initiator-associating protein diaA OS=Escherichia coli O6 GN=diaA
P0ACL0	glpR	1.239169	Glycerol-3-phosphate regulon repressor OS=Escherichia coli O6 GN=glpR
P0ADX9	rsmD	1.239825	Ribosomal RNA small subunit methyltransferase D OS=Escherichia coli O6 GN=rsmD
P22188	murE	1.239868	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase OS=Escherichia coli O6 GN=murE
P17952	murC	1.241578	UDP-N-acetylmuramate--L-alanine ligase OS=Escherichia coli O6 GN=murC
P05707	srlD	1.242243	Sorbitol-6-phosphate 2-dehydrogenase OS=Escherichia coli O6 GN=srlD
P0A9Q7	adhE	1.243191	Aldehyde-alcohol dehydrogenase OS=Escherichia coli O6 GN=adhE
P04825	pepN	1.24338	Aminopeptidase N OS=Escherichia coli O6 GN=pepN
P37686	yiaY	1.243879	Probable alcohol dehydrogenase OS=Escherichia coli O6 GN=yiaY
P33232	lldD	1.247728	L-lactate dehydrogenase [cytochrome] OS=Escherichia coli O6 GN=lldD
P0AEK4	fabI	1.24824	Enoyl-[acyl-carrier-protein] reductase (NADH) OS=Escherichia coli O6 GN=fabI
P0A9Q9	asd	1.248588	Aspartate-semialdehyde dehydrogenase OS=Escherichia coli O6 GN=asd
P0A7E3	pyrE	1.249236	Orotate phosphoribosyltransferase OS=Escherichia coli O6 GN=pyrE
P0ADS2	zapA	1.249298	Cell division protein ZapA OS=Escherichia coli O6 GN=zapA
W8ZR79	ycgC	1.249572	Putative uncharacterized protein ycgC OS=Escherichia coli O6 GN=ycgC
A0A0H2V8N1	c2473	1.253008	Transposase OS=Escherichia coli O6 GN=c2473
P0AC44	sdhD	1.254979	Succinate dehydrogenase hydrophobic membrane anchor subunit OS=Escherichia coli O6 GN=sdhD
P0A9S3	gatD	1.255962	Galactitol-1-phosphate 5-dehydrogenase OS=Escherichia coli O6 GN=gatD
P0A7G6	recA	1.256429	Protein recA OS=Escherichia coli O6 GN=recA
P33136	mdoG	1.256652	Glucans biosynthesis protein G OS=Escherichia coli O6 GN=mdoG

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0A9R4	fdx	1.258939	2Fe-2S ferredoxin OS=Escherichia coli O6 GN=fdx
P76194	sufE	1.259857	Cysteine desulfuration protein SufE OS=Escherichia coli O6 GN=sufE
P0AB43	ycgL	1.260165	UPF0745 protein YcgL OS=Escherichia coli O6 GN=ycgL
A0A0H2V847	c1695	1.260738	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1695
P09546	putA	1.261709	PutA protein OS=Escherichia coli O6 GN=putA
P0A6S0	flgH	1.262982	Flagellar L-ring protein OS=Escherichia coli O6 GN=flgH
P02413	rplO	1.263445	50S ribosomal protein L15 OS=Escherichia coli O6 GN=rplO
P0AC84	gloB	1.264032	Hydroxyacylglutathione hydrolase OS=Escherichia coli O6 GN=gloB
P42593	ygjL	1.264131	2,4-dienoyl-CoA reductase (NADPH) OS=Escherichia coli O6 GN=ygjL
P21645	lpxD	1.264885	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase OS=Escherichia coli O6 GN=lpxD
A0A0H2VCE3	c3292	1.265016	Potential molybdenum-pterin-binding-protein OS=Escherichia coli O6 GN=c3292
P0A7V3	rpsC	1.265216	30S ribosomal protein S3 OS=Escherichia coli O6 GN=rpsC
P02930	tolC	1.266728	Outer membrane protein tolC OS=Escherichia coli O6 GN=tolC
A0A0H2V793	c1886	1.268021	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1886
P0AAT9	ybeL	1.272086	Uncharacterized protein YbeL OS=Escherichia coli O6 GN=ybeL
P0A6K6	deoB	1.272934	Phosphopentomutase OS=Escherichia coli O6 GN=deoB
W8ZGW3	ycbL	1.273903	Putative uncharacterized protein ycbL OS=Escherichia coli O6 GN=ycbL
P45523	fkpA	1.274308	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA OS=Escherichia coli O6 GN=fkpA
P60390	rsmH	1.274361	Ribosomal RNA small subunit methyltransferase H OS=Escherichia coli O6 GN=rsmH
L4VBF4	spr	1.275835	Lipoprotein spr OS=Escherichia coli O6 GN=spr
P77499	ynhD	1.276281	Probable ATP-dependent transporter sufC OS=Escherichia coli O6 GN=ynhD
P30859	artI	1.277649	Putative ABC transporter arginine-binding protein 2 OS=Escherichia coli O6 GN=artI
P69829	ptsN	1.277817	Nitrogen regulatory IIA protein OS=Escherichia coli O6 GN=ptsN
P0A993	fbp	1.277999	Fructose-1,6-bisphosphatase class 1 OS=Escherichia coli O6 GN=fbp
P0A9J4	apbA	1.278071	2-dehydropantoate 2-reductase OS=Escherichia coli O6 GN=apbA
P0AFH8	osmY	1.278411	Osmotically-inducible protein Y OS=Escherichia coli O6 GN=osmY
P33353	yehQ	1.278431	Putative uncharacterized protein yehQ OS=Escherichia coli O6 GN=yehQ
P0A705	infB	1.279896	Translation initiation factor IF-2 OS=Escherichia coli O6 GN=infB
P00864	ppc	1.280004	Phosphoenolpyruvate carboxylase OS=Escherichia coli O6 GN=ppc

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
A0A0H2VAT6	c3736	1.280805	Putative enzyme OS=Escherichia coli O6 GN=c3736
P77671	allB	1.280875	Allantoinase OS=Escherichia coli O6 GN=allB
P32132	typA	1.280967	GTP-binding protein TypA/BipA OS=Escherichia coli O6 GN=typA
P64451	ydcL	1.281165	Hypothetical lipoprotein ydcL OS=Escherichia coli O6 GN=ydcL
P00452	nrdA	1.283296	Ribonucleoside-diphosphate reductase 1 alpha chain OS=Escherichia coli O6 GN=nrdA
P69902	frc	1.283538	Formyl-coenzyme A transferase OS=Escherichia coli O6 GN=frc
P0A9D4	cysE	1.288026	Serine acetyltransferase OS=Escherichia coli O6 GN=cysE
P66948	yfgC	1.28836	Putative uncharacterized protein yfgC OS=Escherichia coli O6 GN=yfgC
P69913	csrA	1.288463	Carbon storage regulator OS=Escherichia coli O6 GN=csrA
P12758	udp	1.290515	Uridine phosphorylase OS=Escherichia coli O6 GN=udp
P0A901	yjeI	1.290691	Outer membrane lipoprotein Blc OS=Escherichia coli O6 GN=yjeI
P0A887	ubiE	1.291403	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE OS=Escherichia coli O6 GN=ubiE
P0ADE8	ygfZ	1.291554	tRNA-modifying protein ygfZ OS=Escherichia coli O6 GN=ygfZ
P24255	rpoN	1.294366	RNA polymerase sigma-54 factor OS=Escherichia coli O6 GN=rpoN
P0A9Q1	arcA	1.294492	Arginine deiminase OS=Escherichia coli O6 GN=arcA
P33346	yehI	1.295019	Uncharacterized protein YehI OS=Escherichia coli O6 GN=yehI
P0AED0	uspA	1.297646	Universal stress protein A OS=Escherichia coli O6 GN=uspA
P0A840	surE	1.29954	Multifunctional protein surE OS=Escherichia coli O6 GN=surE
P28251	dut	1.300371	Deoxyuridine-triphosphate nucleotidohydrolase OS=Escherichia coli O6 GN=dut
P0A6E4	argG	1.30113	Argininosuccinate synthase OS=Escherichia coli O6 GN=argG
A0A0H2V6C1	c0936	1.301635	Uncharacterized protein OS=Escherichia coli O6 GN=c0936
W8ZP71	ybjK	1.302742	Putative uncharacterized protein ybjK OS=Escherichia coli O6 GN=ybjK
P52647	ydbK	1.305904	Pyruvate-flavodoxin oxidoreductase OS=Escherichia coli O6 GN=ydbK
P76193	ynhG	1.305918	Putative uncharacterized protein ynhG OS=Escherichia coli O6 GN=ynhG
P0AEQ3	glnH	1.306649	Glutamine-binding periplasmic protein OS=Escherichia coli O6 GN=glnH
P31057	panB	1.307914	3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Escherichia coli O6 GN=panB
P0A904	trxB	1.308071	Thioredoxin reductase OS=Escherichia coli O6 GN=trxB
P77634	ybcM	1.308804	Hypothetical transcriptional regulator ybcM OS=Escherichia coli O6 GN=ybcM
P27248	gcvT	1.309362	Aminomethyltransferase OS=Escherichia coli O6 GN=gcvT

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0ADB7	ecnB	1.310748	Entericidin B OS=Escherichia coli O6 GN=ecnB
P77504	ybbP	1.310811	Putative uncharacterized protein ybbP OS=Escherichia coli O6 GN=ybbP
P0AAZ4	rarA	1.310985	Replication-associated recombination protein A OS=Escherichia coli O6 GN=rarA
P0AGD3	sodB	1.312954	Superoxide dismutase [Fe] OS=Escherichia coli O6 GN=sodB
P0A6M4	dtd	1.313401	D-tyrosyl-tRNA(Tyr) deacylase OS=Escherichia coli O6 GN=dtd
P62620	ispG	1.313625	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase OS=Escherichia coli O6 GN=ispG
P0A6Q6	fabZ	1.31567	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Escherichia coli O6 GN=fabZ
P0A746	msrB	1.316546	3Peptide methionine sulfoxide reductase MsrB OS=Escherichia coli O6 GN=msrB
P33012	sbmC	1.320809	DNA gyrase inhibitor OS=Escherichia coli O6 GN=sbmC
P08839	ptsI	1.320954	Phosphoenolpyruvate-protein phosphotransferase OS=Escherichia coli O6 GN=ptsI
P75949	nagZ	1.321606	Beta-hexosaminidase OS=Escherichia coli O6 GN=nagZ
W8ZQQ4	ychM	1.324028	Putative sulfate transporter ychM OS=Escherichia coli O6 GN=ychM
W8ZNB1	yhaK	1.324565	Putative uncharacterized protein yhaK OS=Escherichia coli O6 GN=yhaK
P0ABU9	tolQ	1.324787	TolQ protein OS=Escherichia coli O6 GN=tolQ
P77239	cusB	1.325191	Cation efflux system protein CusB OS=Escherichia coli O6 GN=cusB
P77791	ylaD	1.325319	Maltose O-acetyltransferase OS=Escherichia coli O6 GN=ylaD
P0A9A6	ftsZ	1.328389	Cell division protein ftsZ OS=Escherichia coli O6 GN=ftsZ
A0A0H2VAF4	c3429	1.328467	Tas protein OS=Escherichia coli O6 GN=c3429
P77739	yniA	1.331175	Putative uncharacterized protein yniA OS=Escherichia coli O6 GN=yniA
P07118	valS	1.33267	Valyl-tRNA synthetase OS=Escherichia coli O6 GN=valS
P37648	yhjJ	1.333822	Protein yhjJ OS=Escherichia coli O6 GN=yhjJ
A0A0H2VCI8	c3381	1.335038	Cysteine sulfinate desulfinase OS=Escherichia coli O6 GN=c3381
P16384	miaA	1.336343	tRNA dimethylallyltransferase OS=Escherichia coli O6 GN=miaA
A0A0H2V6Z7	focD	1.336568	F1C fimbrial usher OS=Escherichia coli O6 GN=focD
W9ABI4	yagU	1.336706	Putative uncharacterized protein yagU OS=Escherichia coli O6 GN=yagU
P0A6W5	greA	1.337047	Transcription elongation factor greA OS=Escherichia coli O6 GN=greA
P25772	ligB	1.337095	DNA ligase B OS=Escherichia coli O6 GN=ligB
P75736	ybfF	1.33797	Esterase YbfF OS=Escherichia coli O6 GN=ybfF
P00935	metB	1.339266	Cystathionine gamma-synthase OS=Escherichia coli O6 GN=metB

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P67080	yggS	1.341277	UPF0001 protein yggS OS=Escherichia coli O6 GN=yggS
P0AEW9	fruK	1.341515	1-phosphofructokinase OS=Escherichia coli O6 GN=fruK
P67087	yraL	1.342746	Putative uncharacterized protein yraL OS=Escherichia coli O6 GN=yraL
P0AFK9	potD	1.343717	Spermidine/putrescine-binding periplasmic protein OS=Escherichia coli O6 GN=potD
P39404	bglJ	1.344093	Transcriptional activator protein bglJ OS=Escherichia coli O6 GN=bglJ
P52076	ygiX	1.345141	Transcriptional regulatory protein QseB OS=Escherichia coli O6 GN=ygiX
P0ABU2	ychF	1.346048	Probable GTP-binding protein ychF OS=Escherichia coli O6 GN=ychF
P00722	lacZ	1.346539	Beta-galactosidase OS=Escherichia coli O6 GN=lacZ
P0AGB0	serB	1.347928	Phosphoserine phosphatase OS=Escherichia coli O6 GN=serB
P0AF48	yjbQ	1.348469	Putative uncharacterized protein yjbQ OS=Escherichia coli O6 GN=yjbQ
P0A6I0	cmk	1.348632	Cytidylate kinase OS=Escherichia coli O6 GN=cmk
P75746	ybgL	1.349771	UPF0271 protein ybgL OS=Escherichia coli O6 GN=ybgL
P0AGJ9	tyrS	1.350251	Tyrosyl-tRNA synthetase OS=Escherichia coli O6 GN=tyrS
P0A9U3	ybiT	1.353573	Uncharacterized ABC transporter ATP-binding protein YbiT OS=Escherichia coli O6 GN=ybiT
P0ACD4	nifU	1.354075	Iron-sulfur cluster assembly scaffold protein IscU OS=Escherichia coli O6 GN=nifU
P0A953	fabB	1.354455	3-oxoacyl-[acyl-carrier-protein] synthase 1 OS=Escherichia coli O6 GN=fabB
P0AFG0	nusG	1.356579	Transcription antitermination protein nusG OS=Escherichia coli O6 GN=nusG
P04079	guaA	1.359249	GMP synthase [glutamine-hydrolyzing] OS=Escherichia coli O6 GN=guaA
W8ZL69	yfgL	1.360055	Putative uncharacterized protein yfgL OS=Escherichia coli O6 GN=yfgL
P68066	grcA	1.360693	Autonomous glycyl radical cofactor OS=Escherichia coli O6 GN=grcA
P10346	glnQ	1.361506	Glutamine transport ATP-binding protein glnQ OS=Escherichia coli O6 GN=glnQ
P0A6N8	yeiP	1.36644	Elongation factor P-like protein OS=Escherichia coli O6 GN=yeiP
P0ACN7	cytR	1.367648	HTH-type transcriptional repressor CytR OS=Escherichia coli O6 GN=cytR
Q46861	ygiQ	1.369128	UPF0313 protein ygiQ OS=Escherichia coli O6 GN=ygiQ
P63177	rlmB	1.371113	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB OS=Escherichia coli O6 GN=rlmB
P0AES2	ygcX	1.373371	Glucarate dehydratase OS=Escherichia coli O6 GN=ygcX
P0ACF4	hupB	1.373881	DNA-binding protein HU-beta OS=Escherichia coli O6 GN=hupB
P0ABQ0	coaBC	1.374398	Coenzyme A biosynthesis bifunctional protein CoaBC OS=Escherichia coli O6 GN=coaBC
P68191	sra	1.374723	Stationary-phase-induced ribosome-associated protein OS=Escherichia coli O6 GN=sra

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P69811	fruB	1.375646	Multiphosphoryl transfer protein OS=Escherichia coli O6 GN=fruB
A0A0H2V8T6	c2543	1.377561	Protein yeeZ OS=Escherichia coli O6 GN=c2543
A0A0H2VEC0	c4769	1.37882	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4769
W8ZII7	ydaL	1.379916	Putative uncharacterized protein ydaL OS=Escherichia coli O6 GN=ydaL
P63883	amiC	1.383293	N-acetylmuramoyl-L-alanine amidase AmiC OS=Escherichia coli O6 GN=amiC
P0A7X6	rimM	1.384862	Ribosome maturation factor rimM OS=Escherichia coli O6 GN=rimM
P0ADY3	rplN	1.38617	50S ribosomal protein L14 OS=Escherichia coli O6 GN=rplN
W8ZPZ2	ybjU	1.387078	Low-specificity L-threonine aldolase OS=Escherichia coli O6 GN=ybjU
P0A9C5	glnA	1.388835	Glutamine synthetase OS=Escherichia coli O6 GN=glnA
P0A6D7	aroK	1.38938	Shikimate kinase 1 OS=Escherichia coli O6 GN=aroK
P15770	aroE	1.391816	Shikimate dehydrogenase OS=Escherichia coli O6 GN=aroE
P06999	pfkB	1.392738	6-phosphofructokinase isozyme 2 OS=Escherichia coli O6 GN=pfkB
P0AEM9	fliY	1.393008	Cystine-binding periplasmic protein OS=Escherichia coli O6 GN=fliY
P62707	gpmA	1.395053	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Escherichia coli O6 GN=gpmA
P06961	cca	1.395464	Multifunctional CCA protein OS=Escherichia coli O6 GN=cca
W9AJ41	ygcF	1.396647	Putative uncharacterized protein ygcF OS=Escherichia coli O6 GN=ygcF
P0AGK8	iscR	1.396979	HTH-type transcriptional regulator iscR OS=Escherichia coli O6 GN=iscR
P0AB38	ycfM	1.39711	Putative uncharacterized protein ycfM OS=Escherichia coli O6 GN=ycfM
P0A6J5	dadA	1.399433	D-amino acid dehydrogenase small subunit OS=Escherichia coli O6 GN=dadA
P0A698	uvrA	1.402656	UvrABC system protein A OS=Escherichia coli O6 GN=uvrA
P23003	trmA	1.404254	tRNA (uracil-5-)-methyltransferase OS=Escherichia coli O6 GN=trmA
P60546	gmk	1.40619	Guanylate kinase OS=Escherichia coli O6 GN=gmk
P37028	btuF	1.40886	Vitamin B12-binding protein OS=Escherichia coli O6 GN=btuF
P0A6Z6	nikR	1.409182	Nickel-responsive regulator OS=Escherichia coli O6 GN=nikR
P40191	pdxK	1.410998	Pyridoxine kinase OS=Escherichia coli O6 GN=pdxK
P0C8J6	gatY	1.41118	D-tagatose-1,6-bisphosphate aldolase subunit GatY OS=Escherichia coli O6 GN=gatY
P0A8A0	yebC	1.41245	UPF0082 protein yebC OS=Escherichia coli O6 GN=yebC
W9AJE7	ygfM	1.41446	Putative uncharacterized protein ygfM OS=Escherichia coli O6 GN=ygfM
P0ACC1	hemK	1.414952	Protein methyltransferase hemK OS=Escherichia coli O6 GN=hemK

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P10908	ugpQ	1.415743	Glycerophosphoryl diester phosphodiesterase OS=Escherichia coli O6 GN=ugpQ
P0A9W3	yjjK	1.418371	ABC transporter ATP-binding protein yjjK OS=Escherichia coli O6 GN=yjjK
P0AC59	grxB	1.418403	Glutaredoxin-2 OS=Escherichia coli O6 GN=grxB
P0A6RO	fabH	1.420316	3-oxoacyl-[acyl-carrier-protein] synthase 3 OS=Escherichia coli O6 GN=fabH
A0A0H2VEC0	c4769	1.421322	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4769
P0AEI1	miaB	1.421824	(Dimethylallyl)adenosine tRNA methylthiotransferase miaB OS=Escherichia coli O6 GN=miaB
P0A8W5	yqgE	1.422301	UPF0301 protein yqgE OS=Escherichia coli O6 GN=yqgE
W8ZVD2	hisS	1.423476	Histidyl-tRNA synthetase OS=Escherichia coli O6 GN=hisS
P77735	yajO	1.424961	Hypothetical oxidoreductase yajO OS=Escherichia coli O6 GN=yajO
W9AI84	yfeA	1.428871	Putative uncharacterized protein yfeA OS=Escherichia coli O6 GN=yfeA
P0ADV7	yrbC	1.430464	Protein yrbC OS=Escherichia coli O6 GN=yrbC
P0AF24	nagD	1.430486	NagD protein OS=Escherichia coli O6 GN=nagD
W8ZPV7	yrfB	1.434637	Putative uncharacterized protein yrfB OS=Escherichia coli O6 GN=yrfB
P0AG84	yghA	1.435492	Hypothetical oxidoreductase yghA OS=Escherichia coli O6 GN=yghA
P06846	ebgR	1.436109	Ebg operon repressor OS=Escherichia coli O6 GN=ebgR
P0AE91	creA	1.438591	Protein CreA OS=Escherichia coli O6 GN=creA
P0AB14	yccJ	1.439155	Uncharacterized protein YccJ OS=Escherichia coli O6 GN=yccJ
P0A6J8	ddlA	1.441091	D-alanine--D-alanine ligase A OS=Escherichia coli O6 GN=ddlA
P0A9D8	dapD	1.442104	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Escherichia coli O6 GN=dapD
P45565	ais	1.443028	Lipopolysaccharide core heptose(II)-phosphate phosphatase OS=Escherichia coli O6 GN=ais
P0ABH0	ftsA	1.443857	Cell division protein ftsA OS=Escherichia coli O6 GN=ftsA
P0AA16	ompR	1.444594	Transcriptional regulatory protein ompR OS=Escherichia coli O6 GN=ompR
P0A9H1	mug	1.445757	G/U mismatch-specific DNA glycosylase OS=Escherichia coli O6 GN=mug
P75913	ghrA	1.446013	Glyoxylate/hydroxypyruvate reductase A OS=Escherichia coli O6 GN=ghrA
W8ZS32	yniC	1.448375	Putative uncharacterized protein yniC OS=Escherichia coli O6 GN=yniC
P0AG80	ugpB	1.450434	sn-glycerol-3-phosphate-binding periplasmic protein ugpB OS=Escherichia coli O6 GN=ugpB
P76422	thiD	1.451837	Phosphomethylpyrimidine kinase OS=Escherichia coli O6 GN=thiD
P0AGJ5	yfiF	1.45571	Hypothetical tRNA/rRNA methyltransferase yfiF OS=Escherichia coli O6 GN=yfiF
P0A910	ompA	1.456037	Outer membrane protein A OS=Escherichia coli O6 GN=ompA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P08178	purM	1.457155	Phosphoribosylformylglycinamidine cyclo-ligase OS=Escherichia coli O6 GN=purM
Q46832	yghD	1.458186	Hypothetical oxidoreductase yqhD OS=Escherichia coli O6 GN=yqhD
P29131	ftsN	1.459202	Cell division protein ftsN OS=Escherichia coli O6 GN=ftsN
P0A9T0	serA	1.460658	D-3-phosphoglycerate dehydrogenase OS=Escherichia coli O6 GN=serA
P76397	mdtA	1.461621	Multidrug resistance protein mdtA OS=Escherichia coli O6 GN=mdtA
P0AFW4	rnk	1.463566	Regulator of nucleoside diphosphate kinase OS=Escherichia coli O6 GN=rnk
P46889	ftsK	1.464028	DNA translocase FtsK OS=Escherichia coli O6 GN=ftsK
P0ABD3	bfr	1.466521	Bacterioferritin OS=Escherichia coli O6 GN=bfr
P77717	ybaY	1.468245	Putative uncharacterized protein ybaY OS=Escherichia coli O6 GN=ybaY
P25665	metE	1.468901	5-methyltetrahydrofolate--homocysteine methyltransferase OS=Escherichia coli O6 GN=metE
A0A0H2V8I2	c2513	1.470402	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2513
P31808	yciK	1.471095	Hypothetical oxidoreductase yciK OS=Escherichia coli O6 GN=yciK
P0A8W8	yfbU	1.473925	UPF0304 protein yfbU OS=Escherichia coli O6 GN=yfbU
P39451	adhP	1.474855	Alcohol dehydrogenase, propanol-preferring OS=Escherichia coli O6 GN=adhP
P02918	mrcA	1.475872	Penicillin-binding protein 1A OS=Escherichia coli O6 GN=mrcA
P77252	ykgE	1.477294	Putative uncharacterized protein ykgE OS=Escherichia coli O6 GN=ykgE
P0C054	ibpA	1.478542	Small heat shock protein ibpA OS=Escherichia coli O6 GN=ibpA
P0ABZ6	surA	1.478682	Chaperone surA OS=Escherichia coli O6 GN=surA
P21888	cysS	1.481785	Cysteinyl-tRNA synthetase OS=Escherichia coli O6 GN=cysS
P07110	papC	1.483284	PapC protein OS=Escherichia coli O6 GN=papC
W8ZMK5	tbpA	1.483872	Thiamine-binding periplasmic protein OS=Escherichia coli O6 GN=tbpA
P0ACP5	gntR	1.484143	THTH-type transcriptional regulator GntR OS=Escherichia coli O6 GN=gntR
P75915	ycdY	1.484654	Putative uncharacterized protein ycdY OS=Escherichia coli O6 GN=ycdY
P77396	ypdC	1.488372	Uncharacterized HTH-type transcriptional regulator YpdC OS=Escherichia coli O6 GN=ypdC
P0AFB8	glnG	1.489792	Nitrogen regulation protein NR(I) OS=Escherichia coli O6 GN=glnG
W8ZIR5	gcp	1.491963	Probable O-sialoglycoprotein endopeptidase OS=Escherichia coli O6 GN=gcp
Q2M7R5	yibT	1.493778	Uncharacterized protein YibT OS=Escherichia coli O6 GN=yibT
P33644	yfiH	1.49407	Putative uncharacterized protein yfiH OS=Escherichia coli O6 GN=yfiH
P45759	yheG	1.497546	Probable general secretion pathway protein E OS=Escherichia coli O6 GN=yheG

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0ABD8	accB	1.503883	Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli O6 GN=accB
P17854	cysH	1.504469	Phosphoadenosine phosphosulfate reductase OS=Escherichia coli O6 GN=cysH
P0A8E1	ycfP	1.505455	UPF0227 protein ycfP OS=Escherichia coli O6 GN=ycfP
P28905	holC	1.507262	DNA polymerase III, chi subunit OS=Escherichia coli O6 GN=holC
P10371	hisA	1.508388	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Escherichia coli O6 GN=hisA
P16700	cysP	1.51001	Thiosulfate-binding protein OS=Escherichia coli O6 GN=cysP
Q46871	yqjH	1.519048	Putative uncharacterized protein yqjH OS=Escherichia coli O6 GN=yqjH
P76015	ycgT	1.520604	Putative uncharacterized protein ycgT OS=Escherichia coli O6 GN=ycgT
P0A9D2	gst	1.52125	Glutathione S-transferase OS=Escherichia coli O6 GN=gst
P0AEN8	fucU	1.522184	L-fucose mutarotase OS=Escherichia coli O6 GN=fucU
P0A8U0	syd	1.5273	Protein syd OS=Escherichia coli O6 GN=syd
P75957	lolD	1.533036	Lipoprotein-releasing system ATP-binding protein LolD OS=Escherichia coli O6 GN=lolD
P0A731	mgsA	1.538828	Methylglyoxal synthase OS=Escherichia coli O6 GN=mgsA
P33030	yeiR	1.539312	Putative uncharacterized protein yeiR OS=Escherichia coli O6 GN=yeiR
P34209	ydcF	1.540229	Protein ydcF OS=Escherichia coli O6 GN=ydcF
P39160	uxuB	1.543703	D-mannonate oxidoreductase OS=Escherichia coli O6 GN=uxuB
P0A8U6	metJ	1.546534	Met repressor OS=Escherichia coli O6 GN=metJ
P75764	ybhJ	1.549114	Uncharacterized protein YbhJ OS=Escherichia coli O6 GN=ybhJ
P0A6B4	alr	1.550508	Alanine racemase, biosynthetic OS=Escherichia coli O6 GN=alr
P0AF28	narL	1.551944	Nitrate/nitrite response regulator protein narL OS=Escherichia coli O6 GN=narL
P76329	yedp	1.552543	Putative mannosyl-3-phosphoglycerate phosphatase OS=Escherichia coli O6 GN=yedP
P60716	lipA	1.55359	Lipoyl synthase OS=Escherichia coli O6 GN=lipA
A0A0H2VDG6	c3746	1.557971	2,5-diketo-D-gluconic acid reductase A OS=Escherichia coli O6 GN=c3746
A0A0H2V775	c0690	1.559977	Putative uncharacterized protein OS=Escherichia coli O6 GN=c0690
P05458	ptrA	1.560493	Protease 3 OS=Escherichia coli O6 GN=ptrA
P0A823	sfsA	1.561515	Sugar fermentation stimulation protein A OS=Escherichia coli O6 GN=sfsA
W8ZH73	htrB	1.56334	Lipid A biosynthesis lauroyl acyltransferase OS=Escherichia coli O6 GN=htrB
P25536	yhdE	1.564288	Maf-like protein YhdE OS=Escherichia coli O6 GN=yhdE

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0ABM9	ccmH	1.56494	Cytochrome c-type biogenesis protein ccmH OS=Escherichia coli O6 GN=ccmH
A0A0H2VCZ2	c4771	1.564984	Putative carboxymethylenebutenolidase OS=Escherichia coli O6 GN=c4771
P29745	pepT	1.565437	Peptidase T OS=Escherichia coli O6 GN=pepT
A0A0H2VB71	c3153	1.56837	Putative outer membrane protein of prophage OS=Escherichia coli O6 GN=c3153
W8ZQC2	ycbB	1.568643	Putative uncharacterized protein ycbB OS=Escherichia coli O6 GN=ycbB
P05041	pabB	1.579002	Para-aminobenzoate synthase component I OS=Escherichia coli O6 GN=pabB
P39286	rsgA	1.579288	Putative ribosome biogenesis GTPase RsgA OS=Escherichia coli O6 GN=rsgA
P22523	mukB	1.581502	Chromosome partition protein MukB OS=Escherichia coli O6 GN=mukB
P16703	cysM	1.582228	Cysteine synthase B OS=Escherichia coli O6 GN=cysM
P0ACF0	hupA	1.589989	DNA-binding protein HU-alpha OS=Escherichia coli O6 GN=hupA
P0A8I8	rlmH	1.593265	Ribosomal RNA large subunit methyltransferase H OS=Escherichia coli O6 GN=rlmH
P0AEU7	skp	1.594686	Chaperone protein skp OS=Escherichia coli O6 GN=skp
P0A7S3	rpsL	1.595968	30S ribosomal protein S12 OS=Escherichia coli O6 GN=rpsL
P25553	aldA	1.596495	Aldehyde dehydrogenase A OS=Escherichia coli O6 GN=aldA
W9AMQ8	yigP	1.601843	Putative uncharacterized protein yigP OS=Escherichia coli O6 GN=yigP
P77488	dxs	1.611799	1-deoxy-D-xylulose-5-phosphate synthase OS=Escherichia coli O6 GN=dxs
P0ADA1	tesA	1.61266	Thioesterase 1/protease 1/lysophospholipase L1 OS=Escherichia coli O6 GN=tesA
P17315	cirA	1.617483	Colicin I receptor OS=Escherichia coli O6 GN=cirA
P0AEE5	mglB	1.617527	D-galactose-binding periplasmic protein OS=Escherichia coli O6 GN=mglB
P25516	acnA	1.622036	Aconitate hydratase 1 OS=Escherichia coli O6 GN=acnA
P0ADB1	osmE	1.626253	Osmotically-inducible putative lipoprotein OsmE OS=Escherichia coli O6 GN=osmE
A0A0H2VCJ9	c3794	1.628393	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3794
A0A0H2V525	c0327	1.62877	Putative uncharacterized protein OS=Escherichia coli O6 GN=c0327
A0A0H2VAA8	c3459	1.629308	Possible hypoxanthine oxidase xdhD OS=Escherichia coli O6 GN=c3459
A0A0H2VAR6	c2459	1.631923	Putative peptide synthetase OS=Escherichia coli O6 GN=c2459
A0A0H2VBM9	c3363	1.634285	Uncharacterized protein OS=Escherichia coli O6 GN=c3363
P0ADI7	yecD	1.639736	Hypothetical isochorismatase family protein yecD OS=Escherichia coli O6 GN=yecD
P76138	yneI	1.639998	Aldehyde-dehydrogenase like protein yneI OS=Escherichia coli O6 GN=yneI
P30177	ybiB	1.640596	Putative uncharacterized protein ybiB OS=Escherichia coli O6 GN=ybiB

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P07650	deoA	1.641398	Thymidine phosphorylase OS=Escherichia coli O6 GN=deoA
P0A8G6	wrbA	1.645332	Flavoprotein wrbA OS=Escherichia coli O6 GN=wrbA
A0A0H2V8N2	c1937	1.648014	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1937
P76034	yciT	1.65254	Hypothetical transcriptional regulator yciT OS=Escherichia coli O6 GN=yciT
P04391	argI	1.652644	Ornithine carbamoyltransferase OS=Escherichia coli O6 GN=argI
P0A7E1	pyrD	1.653228	Dihydroorotate dehydrogenase OS=Escherichia coli O6 GN=pyrD
P10384	fadL	1.65659	Long-chain fatty acid transport protein OS=Escherichia coli O6 GN=fadL
A0A0H2V9S7	c3224	1.658399	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3224
A0A0H2V9H7	c1846	1.662737	Putative conserved protein OS=Escherichia coli O6 GN=c1846
P62617	ispF	1.665632	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase OS=Escherichia coli O6 GN=ispF
P29018	cydD	1.666266	Transport ATP-binding protein cydD OS=Escherichia coli O6 GN=cydD
A0A0H2V7F1	c0823	1.668707	Putative conserved protein OS=Escherichia coli O6 GN=c0823
P0A7Y0	rnc	1.669847	Ribonuclease 3 OS=Escherichia coli O6 GN=rnc
P12282	moeB	1.67597	Molybdopterin-synthase adenylyltransferase OS=Escherichia coli O6 GN=moeB
P22939	ispA	1.678048	Geranyltranstransferase OS=Escherichia coli O6 GN=ispA
P0AEN1	fre	1.679035	NAD(P)H-flavin reductase OS=Escherichia coli O6 GN=fre
A0A0H2V8F6	c2383	1.689652	Outer membrane protein N OS=Escherichia coli O6 GN=c2383
P0AEH5	elaB	1.699446	Protein elaB OS=Escherichia coli O6 GN=elaB
P08142	ilvB	1.706019	Acetolactate synthase isozyme I large subunit OS=Escherichia coli O6 GN=ilvB
P0AEC8	dcuS	1.713664	Sensor protein dcuS OS=Escherichia coli O6 GN=dcuS
P46859	gntK	1.714286	Thermoresistant gluconokinase OS=Escherichia coli O6 GN=gntK
A0A0H2V4M9	c0413	1.715948	Putative aldo/keto reductase OS=Escherichia coli O6 GN=c0413
A0A0H2VBV9	c3029	1.72093	RatA homolog OS=Escherichia coli O6 GN=c3029
A0A0H2VBF0	c3892	1.720975	Putative N-acetylgalctosamine-6-phosphate deacetylase OS=Escherichia coli O6 GN=c3892
P37613	yhhK	1.730718	PanD regulatory factor OS=Escherichia coli O6 GN=yhhK
P0AF67	yjeE	1.73081	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE OS=Escherichia coli O6 GN=yjeE
P03007	dnaQ	1.735573	DNA polymerase III, epsilon chain OS=Escherichia coli O6 GN=dnaQ
P09030	xthA	1.736467	Exodeoxyribonuclease III OS=Escherichia coli O6 GN=xthA
A0A0H2V5K7	c0959	1.739775	Putative Regulatory protein OS=Escherichia coli O6 GN=c0959

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P69828	gatA	1.751035	PTS system galactitol-specific EIIA component OS=Escherichia coli O6 GN=gatA
P05793	ilvC	1.751529	Ketol-acid reductoisomerase OS=Escherichia coli O6 GN=ilvC
P0A9P6	deaD	1.755402	Cold-shock DEAD box protein A OS=Escherichia coli O6 GN=deaD
P0AB80	ilvE	1.771877	Branched-chain-amino-acid aminotransferase OS=Escherichia coli O6 GN=ilvE
P0A729	yceF	1.772595	Maf-like protein yceF OS=Escherichia coli O6 GN=yceF
P0ADU5	ygiW	1.774341	Protein YgiW OS=Escherichia coli O6 GN=ygiW
A0A0H2VCZ6	c4776	1.774804	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4776
P21507	srmB	1.776175	ATP-dependent RNA helicase srmB OS=Escherichia coli O6 GN=srmB
P06986	hisC	1.786947	Histidinol-phosphate aminotransferase OS=Escherichia coli O6 GN=hisC
P25397	tehB	1.787562	Tellurite resistance protein tehB OS=Escherichia coli O6 GN=tehB
P0A9C9	glpX	1.794526	Fructose-1,6-bisphosphatase class 2 OS=Escherichia coli O6 GN=glpX
P76585	yphG	1.801449	Putative uncharacterized protein yphG OS=Escherichia coli O6 GN=yphG
P77269	yphF	1.812474	ABC transporter Periplasmic binding protein yphF OS=Escherichia coli O6 GN=yphF
P60422	rplB	1.814917	50S ribosomal protein L2 OS=Escherichia coli O6 GN=rplB
A0A0H2V9V0	c3206	1.816159	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3206
P0A940	yaeT	1.835757	Outer membrane protein assembly factor yaeT OS=Escherichia coli O6 GN=yaeT
A0A0H2VAQ8	c3692	1.839123	Uncharacterized protein OS=Escherichia coli O6 GN=c3692
P0A7Y4	rnhA	1.839621	Ribonuclease HI OS=Escherichia coli O6 GN=rnhA
P62522	ilvI	1.851141	Acetolactate synthase isozyme III large subunit OS=Escherichia coli O6 GN=ilvI
P0AFL9	pqiA	1.858456	Paraquat-inducible protein A OS=Escherichia coli O6 GN=pqiA
A0A0H2VAH8	c3470	1.859477	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3470
P76481	yfbK	1.861556	Putative uncharacterized protein yfbK OS=Escherichia coli O6 GN=yfbK
P0ADP0	yigB	1.867521	Putative uncharacterized protein yigB OS=Escherichia coli O6 GN=yigB
P77318	ydeN	1.871547	Putative sulfatase ydeN OS=Escherichia coli O6 GN=ydeN
P0AF18	nagA	1.877465	N-acetylglucosamine-6-phosphate deacetylase OS=Escherichia coli O6 GN=nagA
A0A0H2VBR0	c4113	1.885138	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4113
P0A9M2	hpt	1.886001	Hypoxanthine phosphoribosyltransferase OS=Escherichia coli O6 GN=hpt
P16456	selD	1.887084	Selenide, water dikinase OS=Escherichia coli O6 GN=selD
P32156	rhaM	1.891938	L-rhamnose mutarotase OS=Escherichia coli O6 GN=rhaM

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P13039	fes	1.893702	Enterochelin esterase OS=Escherichia coli O6 GN=fes
P05791	ilvD	1.89667	Dihydroxy-acid dehydratase OS=Escherichia coli O6 GN=ilvD
A0A0H2V801	c1628	1.908024	Protein ycgM OS=Escherichia coli O6 GN=c1628
P46837	yhgF	1.909524	Protein yhgF OS=Escherichia coli O6 GN=yhgF
P0ACM3	ydfH	1.910041	Uncharacterized HTH-type transcriptional regulator ydfH OS=Escherichia coli O6 GN=ydfH
A0A0H2VBY7	c4442	1.910362	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4442
P0ACG1	stpA	1.914269	DNA-binding protein stpA OS=Escherichia coli O6 GN=stpA
W9A0M2	yjeP	1.917462	Putative uncharacterized protein yjeP OS=Escherichia coli O6 GN=yjeP
P0AEI4	rimO	1.927379	Ribosomal protein S12 methylthiotransferase RimO OS=Escherichia coli O6 GN=rimO
P62623	ispH	1.939262	4-hydroxy-3-methylbut-2-enyl diphosphate reductase OS=Escherichia coli O6 GN=ispH
P0C8J8	gatZ	1.944344	D-tagatose-1,6-bisphosphate aldolase subunit gatZ OS=Escherichia coli O6 GN=gatZ
P23843	oppA	1.94598	Periplasmic oligopeptide-binding protein OS=Escherichia coli O6 GN=oppA
P0AGD1	sodC	1.957044	Superoxide dismutase [Cu-Zn] OS=Escherichia coli O6 GN=sodC
P0AEZ3	minD	1.973464	Septum site-determining protein minD OS=Escherichia coli O6 GN=minD
P30138	thiF	1.97431	Adenylyltransferase thiF OS=Escherichia coli O6 GN=thiF
A0A0H2V897	c1281	1.979874	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1281
P36649	yacK	1.9919	Blue copper oxidase cueO OS=Escherichia coli O6 GN=yacK
P0AEU0	hisJ	1.994402	Histidine-binding periplasmic protein OS=Escherichia coli O6 GN=hisJ
A0A0H2V9X5	c3240	2.010197	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3240
P0AEX9	malE	2.019326	Maltose-binding periplasmic protein OS=Escherichia coli O6 GN=malE
A0A0H2VCY9	c4920	2.020389	Starvation sensing protein rspA OS=Escherichia coli O6 GN=c4920
A0A0H2VAX4	c3016	2.022373	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3016
P25665	metE	2.024312	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Escherichia coli O6 GN=metE
P0A9Z1	glnB	2.037425	Nitrogen regulatory protein P-II 1 OS=Escherichia coli O6 GN=glnB
P76116	yncE	2.038899	Putative uncharacterized protein yncE OS=Escherichia coli O6 GN=yncE
W8ZF88	thiJ	2.052575	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis enzyme OS=Escherichia coli O6 GN=thiJ
P0ABG4	ftsW	2.05414	Cell division protein ftsW OS=Escherichia coli O6 GN=ftsW
A0A0H2VAD7	c3400	2.056738	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3400

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
A0A0H2VD31	c3611	2.060232	Transposase insD for insertion element IS2A/D/F/H/I/K OS=Escherichia coli O6 GN=c3611
P0A7B1	ppk	2.065085	Polyphosphate kinase OS=Escherichia coli O6 GN=ppk
P0AC81	gloA	2.07489	Lactoylglutathione lyase OS=Escherichia coli O6 GN=gloA
P16688	phnj	2.097749	PhnJ protein OS=Escherichia coli O6 GN=phnJ
P0A6C1	nfo	2.098401	Endonuclease 4 OS=Escherichia coli O6 GN=nfo
A0A0H2V6G6	c1466	2.103717	Putative tail component of prophage OS=Escherichia coli O6 GN=c1466
P09158	speE	2.10475	Polyamine aminopropyltransferase OS=Escherichia coli O6 GN=speE
P37340	mdtK	2.114023	Multidrug resistance protein MdtK OS=Escherichia coli O6 GN=mdtK
P76584	yphB	2.114579	Putative uncharacterized protein yphB OS=Escherichia coli O6 GN=yphB
W9AJR9	insl	2.117925	IS30 transposase OS=Escherichia coli O6 GN=insI
A0A0H2V942	c2723	2.125706	Uncharacterized protein OS=Escherichia coli O6 GN=c2723
P0AEL3	feoA	2.128162	Ferrous iron transport protein A OS=Escherichia coli O6 GN=feoA
P19636	eutC	2.130259	Ethanolamine ammonia-lyase light chain OS=Escherichia coli O6 GN=eutC
P27859	yigW	2.155711	3'-5' ssDNA/RNA exonuclease TatD OS=Escherichia coli O6 GN=yigW
P33362	yehZ	2.217292	Glycine betaine-binding protein YehZ OS=Escherichia coli O6 GN=yehZ
P16525	tus	2.21837	DNA replication terminus site-binding protein OS=Escherichia coli O6 GN=tus
P76535	murQ	2.220793	N-acetylmuramic acid 6-phosphate etherase OS=Escherichia coli O6 GN=murQ
P23524	yhaD	2.226358	Glycerate 2-kinase OS=Escherichia coli O6 GN=yhaD
P20099	bisC	2.23938	Biotin sulfoxide reductase OS=Escherichia coli O6 GN=bisC
A0A0H2V9V8	c3150	2.242608	Putative uncharacterized protein OS=Escherichia coli O6 GN=c3150
P0AC81	gloA	2.249559	Lactoylglutathione lyase OS=Escherichia coli O6 GN=gloA
P31447	yidj	2.253586	Putative sulfatase yidJ OS=Escherichia coli O6 GN=yidJ
P43341	lpxH	2.255644	UDP-2,3-diacylglucosamine hydrolase OS=Escherichia coli O6 GN=lpxH
P23827	eco	2.281326	Ecotin OS=Escherichia coli O6 GN=eco
P19317	narW	2.290047	Respiratory nitrate reductase 2 delta chain OS=Escherichia coli O6 GN=narW
P76154	ydfK	2.290511	Cold shock protein YdfK OS=Escherichia coli O6 GN=ydfK
P17846	cysl	2.300577	Sulfite reductase [NADPH] hemoprotein beta-component OS=Escherichia coli O6 GN=cysI
A0A0H2V728	c1804	2.307321	Uncharacterized protein OS=Escherichia coli O6 GN=c1804
P37650	yhjL	2.313274	Cellulose synthase operon protein C OS=Escherichia coli O6 GN=yhjL

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
A0A0H2V9Q2	c3187	2.321637	Uncharacterized protein OS=Escherichia coli O6 GN=c3187
P0A812	ruvB	2.338898	Holliday junction ATP-dependent DNA helicase ruvB OS=Escherichia coli O6 GN=ruvB
P09152	narG	2.354704	Respiratory nitrate reductase 1 alpha chain OS=Escherichia coli O6 GN=narG
W8ZQQ8	ycdO	2.368255	UPF0409 protein ycdO OS=Escherichia coli O6 GN=ycdO
P60293	mukF	2.373406	Chromosome partition protein mukF OS=Escherichia coli O6 GN=mukF
P30137	thiE	2.374841	Thiamine-phosphate pyrophosphorylase OS=Escherichia coli O6 GN=thiE
P0AAJ5	fdoH	2.378664	Formate dehydrogenase-O iron-sulfur subunit OS=Escherichia coli O6 GN=fdoH
P32718	yjcT	2.386942	D-allose kinase OS=Escherichia coli O6 GN=yjcT
P14375	hydG	2.446826	Transcriptional Regulatory protein zraR OS=Escherichia coli O6 GN=hydG
P03841	malM	2.531905	Maltose operon periplasmic protein OS=Escherichia coli O6 GN=malM
P42598	ygjQ	2.532874	Uncharacterized protein YgjQ OS=Escherichia coli O6 GN=ygjQ
A0A0H2VBV0	c3012	2.534806	Arsenate reductase OS=Escherichia coli O6 GN=c3012
W8ZWI3	yggM	2.552565	Putative uncharacterized protein yggM OS=Escherichia coli O6 GN=yggM
P06720	melA	2.698849	Alpha-galactosidase OS=Escherichia coli O6 GN=melA
P0AFP4	ybbO	2.722191	Uncharacterized oxidoreductase ybbO OS=Escherichia coli O6 GN=ybbO
W9AHM5	yeiT	2.729987	Hypothetical oxidoreductase yeiT OS=Escherichia coli O6 GN=yeiT
A0A0H2V731	c1273	2.745801	Antigen 43 OS=Escherichia coli O6 GN=c1273
P46122	yajI	2.816604	Uncharacterized lipoprotein YajI OS=Escherichia coli O6 GN=yajI
P08400	phoR	2.835813	Phosphate regulon sensor protein phoR OS=Escherichia coli O6 GN=phoR
P76108	ydcS	3.009163	Putative ABC transporter Periplasmic binding protein ydcS OS=Escherichia coli O6 GN=ydcS
A0A0H2V7S0	c0976	3.036425	Putative uncharacterized protein OS=Escherichia coli O6 GN=c0976
P31678	otsB	3.053632	Trehalose-phosphatase OS=Escherichia coli O6 GN=otsB
A0A0H2V8U3	c1522	3.085827	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1522
P0AEJ2	entC	3.113252	Isochorismate synthase entC OS=Escherichia coli O6 GN=entC
Q46904	ygcN	3.138707	Probable electron transfer flavoprotein-quinone oxidoreductase ygcN OS=Escherichia coli O6 GN=ygcN
P0ABC9	betT	3.335455	High-affinity choline transport protein OS=Escherichia coli O6 GN=betT
P0AA93	ypdA	3.338627	Sensor histidine kinase ypdA OS=Escherichia coli O6 GN=ypdA
P36943	eaeH	3.454658	Putative adhesin OS=Escherichia coli O6 GN=eaeH

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A976	cspF	3.459181	Cold shock-like protein CspF OS=Escherichia coli O6 GN=cspF
A0A0H2VAX2	c2526	3.481079	Putative uncharacterized protein OS=Escherichia coli O6 GN=c2526
P23847	dppA	3.504416	Periplasmic dipeptide transport protein OS=Escherichia coli O6 GN=dppA
P17445	betB	3.6345837	NAD/NADP-dependent betaine aldehyde dehydrogenase OS=Escherichia coli O6 GN=betB
P0AFM2	proX	3.653601	Glycine betaine-binding periplasmic protein OS=Escherichia coli O6 GN=proX
P36929	rsmB	3.67724	Ribosomal RNA small subunit methyltransferase B OS=Escherichia coli O6 GN=rsmB
P33937	napA	3.792738	Periplasmic nitrate reductase OS=Escherichia coli O6 GN=napA
A0A0H2VE10	c4566	3.862595	Hypothetical transcriptional regulator yfjR OS=Escherichia coli O6 GN=c4566
A0A0H2VED5	c4283	4.457541	Putative phosphocarrier protein OS=Escherichia coli O6 GN=c4283
P37351	rpiB	5.392922	Ribose 5-phosphate isomerase B OS=Escherichia coli O6 GN=rpiB

Supplementary Table S2 – TMT ratio with DBHA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P02931	ompF	0.366961442	Outer membrane protein F OS=Escherichia coli O6 GN=ompF
P39325	ytfQ	0.438457123	ABC transporter Periplasmic binding protein ytfQ OS=Escherichia coli O6 GN=ytfQ
P0A7A9	ppa	0.465958862	Inorganic pyrophosphatase OS=Escherichia coli O6 GN=ppa
P69783	crr	0.468220682	Glucose-specific phosphotransferase enzyme IIA component OS=Escherichia coli O6 GN=crr
P02413	rplO	0.477810021	50S ribosomal protein L15 OS=Escherichia coli O6 GN=rplO
P05804	uidA	0.483706167	Beta-glucuronidase OS=Escherichia coli O6 GN=uidA
P37661	yhjW	0.490896269	Membrane-protein yhjW OS=Escherichia coli O6 GN=yhjW
P0A7K2	rplL	0.494399527	50S ribosomal protein L7/L12 OS=Escherichia coli O6 GN=rplL
P0ABJ9	cydA	0.522692172	Cytochrome d ubiquinol oxidase subunit 1 OS=Escherichia coli O6 GN=cydA
P0A8G3	uxaC	0.526978468	Uronate isomerase OS=Escherichia coli O6 GN=uxaC
P0AC53	zwf	0.52921293	Glucose-6-phosphate 1-dehydrogenase OS=Escherichia coli O6 GN=zwf
P04983	rbsA	0.531094237	Ribose import ATP-binding protein RbsA OS=Escherichia coli O6 GN=rbsA
P66948	yfgC	0.532373868	Putative uncharacterized protein yfgC OS=Escherichia coli O6 GN=yfgC
P0A7U7	rpsT	0.53730558	30S ribosomal protein S20 OS=Escherichia coli O6 GN=rpsT
P0A862	tpx	0.538343988	Thiol peroxidase OS=Escherichia coli O6 GN=tpx

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A9Q7	adhE	0.53968755	Aldehyde-alcohol dehydrogenase OS=Escherichia coli O6 GN=adhE
P68919	rplY	0.540290112	50S ribosomal protein L25 OS=Escherichia coli O6 GN=rplY
P9AA25	trxA	0.541948454	Thioredoxin-1 OS=Escherichia coli O6 GN=trxA
P00490	malP	0.547823706	Maltodextrin phosphorylase OS=Escherichia coli O6 GN=malP
P37685	aldB	0.560893351	Aldehyde dehydrogenase B OS=Escherichia coli O6 GN=aldB
P0AG59	rpsN	0.564345119	30S ribosomal protein S14 OS=Escherichia coli O6 GN=rpsN
P0A8R0	rraA	0.568879571	Regulator of ribonuclease activity A OS=Escherichia coli O6 GN=rraA
P0A853	tnaA	0.568996121	Tryptophanase OS=Escherichia coli O6 GN=tnaA
P02925	rbsB	0.569184611	D-ribose-binding periplasmic protein OS=Escherichia coli O6 GN=rbsB
P0ADY7	rplP	0.580072108	50S ribosomal protein L16 OS=Escherichia coli O6 GN=rplP
P0ADV7	yrbC	0.581576	Protein yrbC OS=Escherichia coli O6 GN=yrbC
P17169	glmS	0.582251545	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Escherichia coli O6 GN=glmS
P0A8N5	lysU	0.58376284	Lysyl-tRNA synthetase, heat inducible OS=Escherichia coli O6 GN=lysU
P07913	tdh	0.589848018	L-threonine 3-dehydrogenase OS=Escherichia coli O6 GN=tdh
P04982	rbsD	0.590686958	D-ribose pyranase OS=Escherichia coli O6 GN=rbsD
P0A6T1	pgi	0.592483686	Glucose-6-phosphate isomerase OS=Escherichia coli O6 GN=pgi
P0AA10	rplM	0.59282381	50S ribosomal protein L13 OS=Escherichia coli O6 GN=rplM
P0AFG6	sucB	0.595179108	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Escherichia coli O6 GN=sucB
P0A8N3	lysS	0.595541468	Lysyl-tRNA synthetase OS=Escherichia coli O6 GN=lysS
P0ADZ0	rplW	0.59766627	50S ribosomal protein L23 OS=Escherichia coli O6 GN=rplW
P0AC38	aspA	0.599067963	Aspartate ammonia-lyase OS=Escherichia coli O6 GN=aspA
P00550	mtlA	0.603153145	PTS system, mannitol-specific IIABC component OS=Escherichia coli O6 GN=mtlA
P28629	adiA	0.60391285	Biodegradative arginine decarboxylase OS=Escherichia coli O6 GN=adiA
P0A6F3	glpK	0.607440805	Glycerol kinase OS=Escherichia coli O6 GN=glpK
P19926	agp	0.612156954	Glucose-1-phosphatase OS=Escherichia coli O6 GN=agp
P02359	rpsG	0.618532808	30S ribosomal protein S7 OS=Escherichia coli O6 GN=rpsG
P00350	gnd	0.619084082	6-phosphogluconate dehydrogenase, decarboxylating OS=Escherichia coli O6 GN=gnd
P0AG44	rplQ	0.619459508	50S ribosomal protein L17 OS=Escherichia coli O6 GN=rplQ

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0ABD8	accB	0.621883849	Biotin carboxyl carrier protein of acetyl-CoA carboxylase OS=Escherichia coli O6 GN=accB
P21507	srmB	0.621945928	ATP-dependent RNA helicase srmB OS=Escherichia coli O6 GN=srmB
P0A7X3	rpsI	0.622006972	30S ribosomal protein S9 OS=Escherichia coli O6 GN=rpsI
P0AG16	purF	0.6229395	Amidophosphoribosyltransferase OS=Escherichia coli O6 GN=purF
P25748	galS	0.624099279	Mgl repressor and galactose ultrainduction factor OS=Escherichia coli O6 GN=galS
P21338	rna	0.625285902	Ribonuclease I OS=Escherichia coli O6 GN=rna
P0AFX9	rseB	0.626054454	Sigma-E factor Regulatory protein rseB OS=Escherichia coli O6 GN=rseB
P0A7R9	rpsK	0.626878528	30S ribosomal protein S11 OS=Escherichia coli O6 GN=rpsK
P0ADT8	ygiM	0.627438586	Uncharacterized protein ygiM OS=Escherichia coli O6 GN=ygiM
P61175	rplV	0.630906626	50S ribosomal protein L22 OS=Escherichia coli O6 GN=rplV
P0ABH7	gltA	0.635481267	Citrate synthase OS=Escherichia coli O6 GN=gltA
P0A7U3	rpsS	0.637803671	30S ribosomal protein S19 OS=Escherichia coli O6 GN=rpsS
P0AE08	ahpC	0.638620185	Alkyl hydroperoxide reductase subunit C OS=Escherichia coli O6 GN=ahpC
P27302	tktA	0.638857725	Transketolase 1 OS=Escherichia coli O6 GN=tktA
P0A7V8	rpsD	0.642526009	30S ribosomal protein S4 OS=Escherichia coli O6 GN=rpsD
O07813	leuS	0.643824658	Leucyl-tRNA synthetase OS=Escherichia coli O6 GN=leuS
P0ADU2	ygiN	0.643856177	Protein ygiN OS=Escherichia coli O6 GN=ygiN
A0A0H2V9J3	c2988	0.647027441	NADP-dependent malic enzyme OS=Escherichia coli O6 GN=c2988
P0A6Y8	dnaK	0.648021908	Chaperone protein dnaK OS=Escherichia coli O6 GN=dnaK
P76585	yphG	0.650806481	Putative uncharacterized protein yphG OS=Escherichia coli O6 GN=yphG
P0AG55	rplF	0.656873919	50S ribosomal protein L6 OS=Escherichia coli O6 GN=rplF
P21170	speA	0.660402504	Biosynthetic arginine decarboxylase OS=Escherichia coli O6 GN=speA
P23538	ppsA	0.660661901	Phosphoenolpyruvate synthase OS=Escherichia coli O6 GN=ppsA
P0AEU7	skp	0.660950999	Chaperone protein skp OS=Escherichia coli O6 GN=skp
P13029	katG	0.670756615	Catalase-peroxidase OS=Escherichia coli O6 GN=katG
P60422	rplB	0.680953211	50S ribosomal protein L2 OS=Escherichia coli O6 GN=rplB
P09372	grpE	0.681984559	Protein grpE OS=Escherichia coli O6 GN=grpE
P0A6Z3	htpG	0.682302999	Chaperone protein htpG OS=Escherichia coli O6 GN=htpG
A0A0H2VAF4	c3429	0.684052632	Tas protein OS=Escherichia coli O6 GN=c3429

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A8M3	thrS	0.687479254	Threonyl-tRNA synthetase OS=Escherichia coli O6 GN=thrS
P77674	prr	0.689640304	Gamma-aminobutyraldehyde dehydrogenase OS=Escherichia coli O6 GN=prr
P0A7S3	rpsL	0.692856654	30S ribosomal protein S12 OS=Escherichia coli O6 GN=rpsL
P0A9G6	aceA	0.693271439	Isocitrate lyase OS=Escherichia coli O6 GN=aceA
P0A7W1	rpsE	0.694248544	30S ribosomal protein S5 OS=Escherichia coli O6 GN=rpsE
P07102	appA	0.694668215	Periplasmic appA protein OS=Escherichia coli O6 GN=appA
P0ABA0	atpF	0.699665616	ATP synthase subunit b OS=Escherichia coli O6 GN=atpF
P0A9M5	gpt	0.70138689	Xanthine phosphoribosyltransferase OS=Escherichia coli O6 GN=gpt
P00962	glnS	0.701862537	Glutaminyl-tRNA synthetase OS=Escherichia coli O6 GN=glnS
P76116	yncE	0.703267036	Putative uncharacterized protein yncE OS=Escherichia coli O6 GN=yncE
P0ABJ1	cyoA	0.703493686	Ubiquinol oxidase subunit 2 OS=Escherichia coli O6 GN=cyoA
P0C0V0	htrA	0.703965607	Protease do OS=Escherichia coli O6 GN=htrA
P06149	dld	0.706779871	D-lactate dehydrogenase OS=Escherichia coli O6 GN=dld
P27306	sthA	0.708286187	Soluble pyridine nucleotide transhydrogenase OS=Escherichia coli O6 GN=sthA
P0AEQ3	glnH	0.71017556	Glutamine-binding periplasmic protein OS=Escherichia coli O6 GN=glnH
P00968	carB	0.7104931	Carbamoyl-phosphate synthase large chain OS=Escherichia coli O6 GN=carB
P0AAB8	uspD	0.711926435	Universal stress protein D OS=Escherichia coli O6 GN=uspD
P0A8T7	rpoC	0.712613552	DNA-directed RNA polymerase subunit beta' OS=Escherichia coli O6 GN=rpoC
P05042	fumC	0.715274137	Fumarate hydratase class II OS=Escherichia coli O6 GN=fumC
P0ACJ8	crp	0.717747691	Catabolite gene activator OS=Escherichia coli O6 GN=crp
P0AEU0	hisJ	0.725252308	Histidine-binding periplasmic protein OS=Escherichia coli O6 GN=hisJ
P33195	gcvP	0.727304286	Glycine dehydrogenase [decarboxylating] OS=Escherichia coli O6 GN=gcvP
P0AFK9	potD	0.727939385	Spermidine/putrescine-binding periplasmic protein OS=Escherichia coli O6 GN=potD
P00959	metG	0.728299492	Methionyl-tRNA synthetase OS=Escherichia coli O6 GN=metG
P0AB89	purB	0.73003569	Adenylosuccinate lyase OS=Escherichia coli O6 GN=purB
P0AGD3	sodB	0.730390474	Superoxide dismutase [Fe] OS=Escherichia coli O6 GN=sodB
P04825	pepN	0.733199388	Aminopeptidase N OS=Escherichia coli O6 GN=pepN
P31979	nuoF	0.734633513	NADH dehydrogenase I chain F OS=Escherichia coli O6 GN=nuoF
P0AFG3	sucA	0.73556176	2-oxoglutarate dehydrogenase E1 component OS=Escherichia coli O6 GN=sucA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P10408	secA	0.7409409	Protein translocase subunit secA OS=Escherichia coli O6 GN=secA
P60723	rplD	0.74220412	50S ribosomal protein L4 OS=Escherichia coli O6 GN=rplD
P76193	ynhG	0.743256207	Putative uncharacterized protein ynhG OS=Escherichia coli O6 GN=ynhG
P21599	pykA	0.743297232	Pyruvate kinase II OS=Escherichia coli O6 GN=pykA
P0C018	rplR	0.746246012	50S ribosomal protein L18 OS=Escherichia coli O6 GN=rplR
P00926	dsdA	0.748758236	D-serine dehydratase OS=Escherichia coli O6 GN=dsdA
P11875	argS	0.751127857	Arginyl-tRNA synthetase OS=Escherichia coli O6 GN=argS
P67910	hldD	0.752979613	ADP-L-glycero-D-manno-heptose-6-epimerase OS=Escherichia coli O6 GN=hldD
P40120	mdoD	0.754877336	Glucans biosynthesis protein D OS=Escherichia coli O6 GN=mdoD
P15288	pepD	0.757459166	Aminoacyl-histidine dipeptidase OS=Escherichia coli O6 GN=pepD
P0A9J8	pheA	0.758013669	P-protein OS=Escherichia coli O6 GN=pheA
P00960	glyQ	0.759829126	Glycyl-tRNA synthetase alpha subunit OS=Escherichia coli O6 GN=glyQ
P24182	accC	0.760093446	Biotin carboxylase OS=Escherichia coli O6 GN=accC
Q06902	pepA	0.762522719	Cytosol aminopeptidase OS=Escherichia coli O6 GN=pepA
A0A0H2V5Y8	c1138	0.763337675	Putative uncharacterized protein OS=Escherichia coli O6 GN=c1138
P0A9D4	cysE	0.764669677	Serine acetyltransferase OS=Escherichia coli O6 GN=cysE
P39377	iadA	0.766158102	Isoaspartyl dipeptidase OS=Escherichia coli O6 GN=iadA
P21177	fadB	0.76634442	Fatty acid oxidation complex subunit alpha OS=Escherichia coli O6 GN=fadB
P0AES4	gyrA	0.769041633	DNA gyrase subunit A OS=Escherichia coli O6 GN=gyrA
P37773	yjfG	0.771496548	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase OS=Escherichia coli O6 GN=yjfG
P24215	uxuA	0.77243237	Mannonate dehydratase OS=Escherichia coli O6 GN=uxuA
P0A8V2	rpoB	0.772807268	DNA-directed RNA polymerase subunit beta OS=Escherichia coli O6 GN=rpoB
P63284	clpB	0.773016487	Chaperone protein ClpB OS=Escherichia coli O6 GN=clpB
P0A8W8	yfbU	0.773723193	UPF0304 protein yfbU OS=Escherichia coli O6 GN=yfbU
P77739	yniA	0.774007572	Putative uncharacterized protein yniA OS=Escherichia coli O6 GN=yniA
P25539	ribD	0.77563834	Riboflavin biosynthesis protein ribD OS=Escherichia coli O6 GN=ribD
P0A9B2	gapA	0.775683823	Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli O6 GN=gapA
P16659	proS	0.777056557	Prolyl-tRNA synthetase OS=Escherichia coli O6 GN=proS
P0ADY3	rplN	0.779454544	50S ribosomal protein L14 OS=Escherichia coli O6 GN=rplN

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P37648	yhjJ	0.77979622	Protein yhjJ OS=Escherichia coli O6 GN=yhjJ
P33570	tktB	0.781441342	Transketolase 2 OS=Escherichia coli O6 GN=tktB
P0AE06	acrA	0.781449646	Acriflavine resistance protein A OS=Escherichia coli O6 GN=acrA
P00956	ileS	0.783119014	Isoleucyl-tRNA synthetase OS=Escherichia coli O6 GN=ileS
P31120	glmM	0.783533716	Phosphoglucosamine mutase OS=Escherichia coli O6 GN=glmM
P25526	gabD	0.784688333	Succinate-semialdehyde dehydrogenase (NADP+) OS=Escherichia coli O6 GN=gabD
P0AG51	rpmD	0.785590525	50S ribosomal protein L30 OS=Escherichia coli O6 GN=rpmD
A0A0H2VF72	c5312	0.785798066	Putative conserved protein OS=Escherichia coli O6 GN=c5312
P21889	aspS	0.78715046	Aspartyl-tRNA synthetase OS=Escherichia coli O6 GN=aspS
P0A6T5	folE	0.787823323	GTP cyclohydrolase 1 OS=Escherichia coli O6 GN=folE
P0A7K6	rplS	0.788062358	50S ribosomal protein L19 OS=Escherichia coli O6 GN=rplS
P0A9J6	rbsK	0.78936314	Ribokinase OS=Escherichia coli O6 GN=rbsK
Q46871	yqjH	0.790793522	Putative uncharacterized protein yqjH OS=Escherichia coli O6 GN=yqjH
P0A6W5	greA	0.791893557	Transcription elongation factor greA OS=Escherichia coli O6 GN=greA
Q55BF4	ucpA	0.792487507	Oxidoreductase ucpA OS=Escherichia coli O6 GN=ucpA
P0A8F0	upp	0.794111207	Uracil phosphoribosyltransferase OS=Escherichia coli O6 GN=upp
P0AFG8	aceE	0.795551463	Pyruvate dehydrogenase E1 component OS=Escherichia coli O6 GN=aceE
P0A7V3	rpsC	0.795594541	30S ribosomal protein S3 OS=Escherichia coli O6 GN=rpsC
P21513	rne	0.795666105	Ribonuclease E OS=Escherichia coli O6 GN=rne
P07004	proA	0.796219782	Gamma-glutamyl phosphate reductase OS=Escherichia coli O6 GN=proA
P0C8J8	gatZ	0.796511401	D-tagatose-1,6-bisphosphate aldolase subunit gatZ OS=Escherichia coli O6 GN=gatZ
P0AG30	rho	0.80074555	Transcription termination factor Rho OS=Escherichia coli O6 GN=rho
P0AG67	rpsA	0.801305131	30S ribosomal protein S1 OS=Escherichia coli O6 GN=rpsA
P0AD61	pykF	0.80441438	Pyruvate kinase I OS=Escherichia coli O6 GN=pykF
P46853	yhhX	0.806185211	Putative oxidoreductase yhhX OS=Escherichia coli O6 GN=yhhX
A0A0H2V4R2	c0460	0.806575512	LacI protein OS=Escherichia coli O6 GN=c0460
P77269	yphF	0.806675162	ABC transporter Periplasmic binding protein yphF OS=Escherichia coli O6 GN=yphF
P0A698	uvrA	0.807359898	UvrABC system protein A OS=Escherichia coli O6 GN=uvrA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A6F5	groL	0.807955827	60 kDa chaperonin OS=Escherichia coli O6 GN=groL
P0A6F9	groS	0.8083466	10 kDa chaperonin OS=Escherichia coli O6 GN=groS
P0AFY8	seqA	0.808743547	Protein seqA OS=Escherichia coli O6 GN=seqA
P15977	malQ	0.809482834	4-alpha-glucanotransferase OS=Escherichia coli O6 GN=malQ
P42641	obg	0.811559254	GTPase obg OS=Escherichia coli O6 GN=obg
P29745	pepT	0.811917558	Peptidase T OS=Escherichia coli O6 GN=pepT
P08997	aceB	0.812554028	Malate synthase A OS=Escherichia coli O6 GN=aceB
P0A850	tig	0.818739487	Trigger factor OS=Escherichia coli O6 GN=tig
P0A8M0	asnS	0.820188588	Asparaginyl-tRNA synthetase OS=Escherichia coli O6 GN=asnS
P25665	metE	0.821710075	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Escherichia coli O6 GN=metE
P0ADR8	ygdH	0.821737193	LOG family protein ygdH OS=Escherichia coli O6 GN=ygdH
Q54GJ2	purD	0.821855673	Phosphoribosylamine--glycine ligase OS=Escherichia coli O6 GN=purD
P0AE91	creA	0.822613284	Protein CreA OS=Escherichia coli O6 GN=creA
P60438	rplC	0.824145615	50S ribosomal protein L3 OS=Escherichia coli O6 GN=rplC
P0A794	pdxJ	0.824875598	Pyridoxine 5'-phosphate synthase OS=Escherichia coli O6 GN=pdxJ
P08390	usg	0.826105303	USG-1 protein OS=Escherichia coli O6 GN=usg
P39160	uxuB	0.826454387	D-mannonate oxidoreductase OS=Escherichia coli O6 GN=uxuB
P0AF03	mog	0.829639561	Molybdopterin biosynthesis mog protein OS=Escherichia coli O6 GN=mog
P0A6P7	engB	0.833367385	Probable GTP-binding protein engB OS=Escherichia coli O6 GN=engB
P76108	ydcS	0.833835947	Putative ABC transporter Periplasmic binding protein ydcS OS=Escherichia coli O6 GN=ydcS
P45565	ais	0.836435444	Lipopolysaccharide core heptose(II)-phosphate phosphatase OS=Escherichia coli O6 GN=ais
P23839	yicC	0.836567165	Protein yicC OS=Escherichia coli O6 GN=yicC
P77398	arnA	0.838774461	Bifunctional polymyxin resistance protein ArnA OS=Escherichia coli O6 GN=arnA
P00579	rpoD	0.8400357	RpoD protein OS=Escherichia coli O6 GN=rpoD
P0AGE9	sucD	0.840335313	Succinyl-CoA ligase [ADP-forming] subunit alpha OS=Escherichia coli O6 GN=sucD
P15254	purL	0.841520453	Phosphoribosylformylglycinamidine synthase OS=Escherichia coli O6 GN=purL
P0A991	fbaB	0.845307973	Fructose-bisphosphate aldolase class 1 OS=Escherichia coli O6 GN=fbaB
P0AG90	secD	0.848169739	Protein-export membrane protein secD OS=Escherichia coli O6 GN=secD

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A9P0	lpdA	0.850458589	Dihydrolipoyl dehydrogenase OS=Escherichia coli O6 GN=lpdA
P69776	lpp	0.850666202	Major outer membrane lipoprotein OS=Escherichia coli O6 GN=lpp
P22256	gabT	0.854200489	4-aminobutyrate aminotransferase OS=Escherichia coli O6 GN=gabT
W8ZQY3	yijP	0.855350971	Protein yijP OS=Escherichia coli O6 GN=yijP
P08839	ptsI	0.860492767	Phosphoenolpyruvate-protein phosphotransferase OS=Escherichia coli O6 GN=ptsI
P33136	mdoG	0.860525644	Glucans biosynthesis protein G OS=Escherichia coli O6 GN=mdoG
W8ZVD2	hisS	0.861425217	Histidyl-tRNA synthetase OS=Escherichia coli O6 GN=hisS
P63224	gmhA	0.862072031	Phosphoheptose isomerase OS=Escherichia coli O6 GN=gmhA
P27550	acs	0.863260143	Acetyl-coenzyme A synthetase OS=Escherichia coli O6 GN=acs
P31663	panC	0.863925006	Pantothenate synthetase OS=Escherichia coli O6 GN=panC
P33599	nuoC	0.864562569	NADH-quinone oxidoreductase subunit C/D OS=Escherichia coli O6 GN=nuoC
P27298	prlC	0.866535001	Oligopeptidase A OS=Escherichia coli O6 GN=prlC
P15639	putH	0.869232714	Bifunctional purine biosynthesis protein purH OS=Escherichia coli O6 GN=purH
P35340	ahpF	0.869589115	Alkyl hydroperoxide reductase subunit F OS=Escherichia coli O6 GN=ahpF
P0ADG7	guaB	0.86983954	Inosine-5'-monophosphate dehydrogenase OS=Escherichia coli O6 GN=guaB
P0ACB7	hemY	0.87711997	Protein hemY OS=Escherichia coli O6 GN=hemY
P21499	vacB	0.877362497	Ribonuclease R OS=Escherichia coli O6 GN=vacB
P0A7R1	rplI	0.877478269	50S ribosomal protein L9 OS=Escherichia coli O6 GN=rplI
P0AB77	kbl	0.877927709	2-amino-3-ketobutyrate coenzyme A ligase OS=Escherichia coli O6 GN=kbl
P0AGD7	ffh	0.879227228	Signal recognition particle protein OS=Escherichia coli O6 GN=ffh
P33232	lldD	0.88084775	L-lactate dehydrogenase [cytochrome] OS=Escherichia coli O6 GN=lldD
P0AE88	cpxR	0.884613141	Transcriptional Regulatory protein cpxR OS=Escherichia coli O6 GN=cpxR
P39099	degQ	0.884826584	Protease degQ OS=Escherichia coli O6 GN=degQ
P04425	gshB	0.886001136	Glutathione synthetase OS=Escherichia coli O6 GN=gshB
P28304	qor	0.887158917	Quinone oxidoreductase OS=Escherichia coli O6 GN=qor
P00363	frdA	0.887703171	Fumarate reductase flavoprotein subunit OS=Escherichia coli O6 GN=frdA
P08660	lysC	0.887722498	Lysine-sensitive aspartokinase III OS=Escherichia coli O6 GN=lysC
P0A7L0	rplA	0.887779567	50S ribosomal protein L1 OS=Escherichia coli O6 GN=rplA
P0A6W9	gshA	0.889010407	Glutamate--cysteine ligase OS=Escherichia coli O6 GN=gshA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P08506	dacC	0.892327243	Penicillin-binding protein 6 OS=Escherichia coli O6 GN=dacC
P07118	valS	0.89235814	Valyl-tRNA synthetase OS=Escherichia coli O6 GN=valS
P0AAI5	fabF	0.894683526	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Escherichia coli O6 GN=fabF
P0A9S5	gldA	0.895697626	Glycerol dehydrogenase OS=Escherichia coli O6 GN=gldA
P0ABA6	atpG	0.896572752	ATP synthase gamma chain OS=Escherichia coli O6 GN=atpG
P23882	fmt	0.897478847	Methionyl-tRNA formyltransferase OS=Escherichia coli O6 GN=fmt
P00961	glyS	0.900945515	Glycyl-tRNA synthetase beta subunit OS=Escherichia coli O6 GN=glyS
P0A6Q3	fabA	0.902619409	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Escherichia coli O6 GN=fabA
P0A6L2	dapA	0.902995333	Dihydrodipicolinate synthase OS=Escherichia coli O6 GN=dapA
P0A905	slyB	0.903518669	Outer membrane lipoprotein slyB OS=Escherichia coli O6 GN=slyB
P15034	pepP	0.90737064	Xaa-Pro aminopeptidase OS=Escherichia coli O6 GN=pepP
P0ACA7	yliJ	0.909305467	Uncharacterized GST-like protein yliJ OS=Escherichia coli O6 GN=yliJ
P77581	astC	0.909890378	Succinylornithine transaminase OS=Escherichia coli O6 GN=astC
P33602	nuoG	0.912911733	NADH-quinone oxidoreductase subunit G OS=Escherichia coli O6 GN=nuoG
P0ABB0	atpA	0.912998743	ATP synthase subunit alpha OS=Escherichia coli O6 GN=atpA
P31142	sseA	0.914032308	3-mercaptopyruvate sulfurtransferase OS=Escherichia coli O6 GN=sseA
W8ZP47	tdcE	0.915973351	Keto-acid formate acetyltransferase OS=Escherichia coli O6 GN=tdcE
P0A796	pfkA	0.916474708	6-phosphofructokinase OS=Escherichia coli O6 GN=pfkA
P04036	dapB	0.916931303	Dihydrodipicolinate reductase OS=Escherichia coli O6 GN=dapB
P0ACC7	glmU	0.919559384	Bifunctional protein glmU OS=Escherichia coli O6 GN=glmU
P04693	tyrB	0.920135759	Aromatic-amino-acid aminotransferase OS=Escherichia coli O6 GN=tyrB
P09831	gltB	0.920455414	Glutamate synthase [NADPH] large chain OS=Escherichia coli O6 GN=gltB
P0AG63	rpsQ	0.9224248	30S ribosomal protein S17 OS=Escherichia coli O6 GN=rpsQ
P0A8Y8	ybdB	0.922982921	Esterase YbdB OS=Escherichia coli O6 GN=ybdB
P0A9M2	hpt	0.923137682	Hypoxanthine phosphoribosyltransferase OS=Escherichia coli O6 GN=hpt
P10121	ftsY	0.924331817	Cell division protein ftsY OS=Escherichia coli O6 GN=ftsY
P31057	panB	0.925718182	3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Escherichia coli O6 GN=panB
P69797	manX	0.925803798	PTS system mannose-specific EIIAB component OS=Escherichia coli O6 GN=manX

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P05055	pnp	0.926533686	Polyribonucleotide nucleotidyltransferase OS=Escherichia coli O6 GN=pnp
P09546	putA	0.927023588	PutA protein OS=Escherichia coli O6 GN=putA
P61714	ribE	0.927606024	Riboflavin synthase alpha chain OS=Escherichia coli O6 GN=ribE
P37095	pepB	0.928106268	Peptidase B OS=Escherichia coli O6 GN=pepB
P21888	cysS	0.928643149	Cysteinyl-tRNA synthetase OS=Escherichia coli O6 GN=cysS
P0A6A3	ackA	0.930446025	Acetate kinase OS=Escherichia coli O6 GN=ackA
P0A7C6	pepE	0.931268242	Peptidase E OS=Escherichia coli O6 GN=pepE
P23893	hemL	0.931289677	Glutamate-1-semialdehyde 2,1-aminomutase OS=Escherichia coli O6 GN=hemL
Q46832	yghD	0.932903576	Hypothetical oxidoreductase yqhD OS=Escherichia coli O6 GN=yqhD
P0A705	infB	0.935333255	Translation initiation factor IF-2 OS=Escherichia coli O6 GN=infB
P0ABA4	atpH	0.935912013	ATP synthase subunit delta OS=Escherichia coli O6 GN=atpH
P60390	rsmH	0.936294146	Ribosomal RNA small subunit methyltransferase H OS=Escherichia coli O6 GN=rsmH
W8ZMW8	yahK	0.936643232	Hypothetical zinc-type alcohol dehydrogenase-like protein yahK OS=Escherichia coli O6 GN=yahK
P61517	yadF	0.938096588	Protein yadF OS=Escherichia coli O6 GN=yadF
P08312	pheS	0.939150627	Phenylalanyl-tRNA synthetase alpha chain OS=Escherichia coli O6 GN=pheS
W8ZG19	tolB	0.93966195	Protein tolB OS=Escherichia coli O6 GN=tolB
P0AEB2	dacA	0.940455445	D-alanyl-D-alanine carboxypeptidase dacA OS=Escherichia coli O6 GN=dacA
P64429	ypfJ	0.941246386	Uncharacterized protein ypfJ OS=Escherichia coli O6 GN=ypfJ
P11447	argH	0.941382958	Argininosuccinate lyase OS=Escherichia coli O6 GN=argH
P36938	pgm	0.941520311	Phosphoglucomutase OS=Escherichia coli O6 GN=pgm
P06612	topA	0.945504618	DNA topoisomerase I OS=Escherichia coli O6 GN=topA
P39286	rsgA	0.947770826	Putative ribosome biogenesis GTPase RsgA OS=Escherichia coli O6 GN=rsgA
P0A6S7	gpsA	0.949036509	Glycerol-3-phosphate dehydrogenase [NAD(P)+] OS=Escherichia coli O6 GN=gpsA
P21165	pepQ	0.949797485	Xaa-Pro dipeptidase OS=Escherichia coli O6 GN=pepQ
P0A870	talB	0.952714393	Transaldolase B OS=Escherichia coli O6 GN=talB
P25553	aldA	0.952922731	Aldehyde dehydrogenase A OS=Escherichia coli O6 GN=aldA
P37300	glcB	0.9536358	Malate synthase G OS=Escherichia coli O6 GN=glcB
P30177	ybiB	0.954735948	Putative uncharacterized protein ybiB OS=Escherichia coli O6 GN=ybiB

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P00954	trpS	0.956054489	Tryptophanyl-tRNA synthetase OS=Escherichia coli O6 GN=trpS
P0A7J3	rplJ	0.961369923	50S ribosomal protein L10 OS=Escherichia coli O6 GN=rplJ
P0A9W3	yjjK	0.961444369	ABC transporter ATP-binding protein yjjK OS=Escherichia coli O6 GN=yjjK
P0A7S9	rpsM	0.963139285	30S ribosomal protein S13 OS=Escherichia coli O6 GN=rpsM
P07395	pheT	0.965128887	Phenylalanyl-tRNA synthetase beta chain OS=Escherichia coli O6 GN=pheT
P69922	fucI	0.965980887	L-fucose isomerase OS=Escherichia coli O6 GN=fucI
P0ABP8	deoD	0.966982681	Purine nucleoside phosphorylase deoD-type OS=Escherichia coli O6 GN=deoD
P00509	aspC	0.967598105	Aspartate aminotransferase OS=Escherichia coli O6 GN=aspC
P17117	mdaA	0.968077201	Oxygen-insensitive NADPH nitroreductase OS=Escherichia coli O6 GN=mdaA
P76015	ycgT	0.969265941	Putative uncharacterized protein ycgT OS=Escherichia coli O6 GN=ycgT
P23865	prc	0.969719177	Tail-specific protease OS=Escherichia coli O6 GN=prc
P0A7T3	rpsP	0.969823499	30S ribosomal protein S16 OS=Escherichia coli O6 GN=rpsP
P0A9Q5	accD	0.97288678	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta OS=Escherichia coli O6 GN=accD
W8ZMK5	tbpA	0.973981302	Thiamine-binding periplasmic protein OS=Escherichia coli O6 GN=tbpA
W8ZE39	yaiE	0.975849051	UPF0345 protein yaiE OS=Escherichia coli O6 GN=yaiE
P0A6U5	rsmG	0.976420644	Ribosomal RNA small subunit methyltransferase G OS=Escherichia coli O6 GN=rsmG
P0ADW3	yhcB	0.977766582	Putative cytochrome d ubiquinol oxidase subunit 3 OS=Escherichia coli O6 GN=yhcB
P0ADY1	ppiD	0.978234667	Peptidyl-prolyl cis-trans isomerase D OS=Escherichia coli O6 GN=ppiD
P29680	hemE	0.980104973	Uroporphyrinogen decarboxylase OS=Escherichia coli O6 GN=hemE
P04805	gltX	0.980712534	Glutamyl-tRNA synthetase OS=Escherichia coli O6 GN=gltX
P0ABZ6	surA	0.980945947	Chaperone surA OS=Escherichia coli O6 GN=surA
P0A836	sucC	0.982058681	Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O6 GN=sucC
P0AFC7	nuoB	0.98244466	NADH-quinone oxidoreductase subunit B OS=Escherichia coli O6 GN=nuoB
P0AEH5	elaB	0.983452694	Protein elaB OS=Escherichia coli O6 GN=elaB
P62768	yaeH	0.984550969	UPF0325 protein yaeH OS=Escherichia coli O6 GN=yaeH
P08179	purN	0.987225634	Phosphoribosylglycinamide formyltransferase OS=Escherichia coli O6 GN=purN
P0AFF6	nusA	0.987744113	Transcription elongation protein nusA OS=Escherichia coli O6 GN=nusA
P77690	arnB	0.98837784	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase OS=Escherichia coli O6 GN=arnB

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P09029	purK	0.988771664	Phosphoribosylaminoimidazole carboxylase ATPase subunit OS=Escherichia coli O6 GN=purK
P0A729	yceF	0.989500545	Maf-like protein yceF OS=Escherichia coli O6 GN=yceF
P39177	uspG	0.993428204	Universal stress protein G OS=Escherichia coli O6 GN=uspG
P33607	nuoI	0.996187478	NADH-quinone oxidoreductase subunit I OS=Escherichia coli O6 GN=nuoI
P14900	murD	0.999337423	UDP-N-acetylmuramoylalanine--D-glutamate ligase OS=Escherichia coli O6 GN=murD
P61889	mdh	1.006453159	Malate dehydrogenase OS=Escherichia coli O6 GN=mdh
P0A9D2	gst	1.007004095	Glutathione S-transferase OS=Escherichia coli O6 GN=gst
P0ADI7	yecD	1.007801805	Hypothetical isochorismatase family protein yecD OS=Escherichia coli O6 GN=yecD
P18335	argD	1.009648676	Acetylornithine/succinyldiaminopimelate aminotransferase OS=Escherichia coli O6 GN=argD
P0A7R5	rpsJ	1.010256091	30S ribosomal protein S10 OS=Escherichia coli O6 GN=rpsJ
P0A815	trmB	1.011513364	tRNA (guanine-N(7)-)-methyltransferase OS=Escherichia coli O6 GN=trmB
P05459	pdxB	1.012337596	Erythronate-4-phosphate dehydrogenase OS=Escherichia coli O6 GN=pdxB
P0A6E4	argG	1.014461809	Argininosuccinate synthase OS=Escherichia coli O6 GN=argG
P0A7DA	purA	1.016111541	Adenylosuccinate synthetase OS=Escherichia coli O6 GN=purA
W8ZP84	ybeJ	1.01855613	Glutamate/aspartate Periplasmic binding protein OS=Escherichia coli O6 GN=ybeJ
P671714	ribH	1.018820009	6,7-dimethyl-8-ribityllumazine synthase OS=Escherichia coli O6 GN=ribH
P0A722	lpxA	1.020638181	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase OS=Escherichia coli O6 GN=lpxA
P04079	guaA	1.020681657	GMP synthase [glutamine-hydrolyzing] OS=Escherichia coli O6 GN=guaA
P77570	anmK	1.021400487	Anhydro-N-acetylmuramic acid kinase OS=Escherichia coli O6 GN=anmK
W8ZRV6	yjgB	1.022975714	Hypothetical zinc-type alcohol dehydrogenase-like protein yjgB OS=Escherichia coli O6 GN=yjgB
P62399	rplE	1.023300229	50S ribosomal protein L5 OS=Escherichia coli O6 GN=rplE
P27248	gcvT	1.028005907	Aminomethyltransferase OS=Escherichia coli O6 GN=gcvT
W8ZWX3	yhbL	1.031653727	Enhancing lycopene biosynthesis protein 2 OS=Escherichia coli O6 GN=yhbL
P23847	dppA	1.035093807	Periplasmic dipeptide transport protein OS=Escherichia coli O6 GN=dppA
P06715	gor	1.037345857	Glutathione reductase OS=Escherichia coli O6 GN=gor
P0ADE8	ygfZ	1.037370853	tRNA-modifying protein ygfZ OS=Escherichia coli O6 GN=ygfZ
P08014	sdhB	1.038731272	Succinate dehydrogenase iron-sulfur protein OS=Escherichia coli O6 GN=sdhB
P0AF18	nagA	1.043415513	N-acetylglucosamine-6-phosphate deacetylase OS=Escherichia coli O6 GN=nagA

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P37647	kdgK	1.044127534	2-dehydro-3-deoxygluconokinase OS=Escherichia coli O6 GN=kdgK
P0A7B5	proB	1.045233065	Glutamate 5-kinase OS=Escherichia coli O6 GN=proB
P63284	clpP	1.047937215	ATP-dependent Clp protease proteolytic subunit OS=Escherichia coli O6 GN=clpP
P0A6K6	deoB	1.05147249	Phosphopentomutase OS=Escherichia coli O6 GN=deoB
P0A6Y1	ihfB	1.052206468	Integration host factor subunit beta OS=Escherichia coli O6 GN=ihfB
P15047	entA	1.054088783	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase OS=Escherichia coli O6 GN=entA
P77554	yahJ	1.055136455	Putative uncharacterized protein yahJ OS=Escherichia coli O6 GN=yahJ
P0A7Z0	rpiA	1.057994203	Ribose-5-phosphate isomerase A OS=Escherichia coli O6 GN=rpiA
P52643	ldhA	1.058046273	D-lactate dehydrogenase OS=Escherichia coli O6 GN=ldhA
P05020	pyrC	1.058459342	Dihydroorotase OS=Escherichia coli O6 GN=pyrC
P38489	nfnB	1.058917586	Oxygen-insensitive NAD(P)H nitroreductase OS=Escherichia coli O6 GN=nfnB
P77804	ydgA	1.059759662	Putative uncharacterized protein ydgA OS=Escherichia coli O6 GN=ydgA
Q47622	sapA	1.063000875	Peptide transport periplasmic protein sapA OS=Escherichia coli O6 GN=sapA
P0ABT2	dps	1.068866042	DNA protection during starvation protein OS=Escherichia coli O6 GN=dps
P0A6F1	carA	1.073049893	Carbamoyl-phosphate synthase small chain OS=Escherichia coli O6 GN=carA
A0A0H2V4R7	c0503	1.074074697	Putative uncharacterized protein OS=Escherichia coli O6 GN=c0503
P0A955	eda	1.076935205	KHG/KDPG aldolase OS=Escherichia coli O6 GN=eda
P04951	kdsB	1.078539673	3-deoxy-manno-octulosonate cytidylyltransferase OS=Escherichia coli O6 GN=kdsB
P0A6C8	argB	1.07862955	Acetylglutamate kinase OS=Escherichia coli O6 GN=argB
P0A9K3	ybeZ	1.079584655	PhoH-like protein OS=Escherichia coli O6 GN=ybeZ
P0A799	pgk	1.080827185	Phosphoglycerate kinase OS=Escherichia coli O6 GN=pgk
P0A9Q1	arcA	1.081859635	Aerobic respiration control protein ArcA OS=Escherichia coli O6 GN=arcA
P24186	folD	1.083334017	Bifunctional protein folD OS=Escherichia coli O6 GN=folD
W8ZS03	infC	1.08464685	Translation initiation factor IF-3 OS=Escherichia coli O6 GN=infC
P00864	ppc	1.08495912	Phosphoenolpyruvate carboxylase OS=Escherichia coli O6 GN=ppc
P76658	hldE	1.089520719	Bifunctional protein hldE OS=Escherichia coli O6 GN=hldE
P0ACY1	ydjA	1.090186871	Protein ydjA OS=Escherichia coli O6 GN=ydjA
P37903	uspF	1.091911406	Universal stress protein F OS=Escherichia coli O6 GN=uspF
P12758	udp	1.092448608	Uridine phosphorylase OS=Escherichia coli O6 GN=udp

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A7J7	rplK	1.096459357	50S ribosomal protein L11 OS=Escherichia coli O6 GN=rplK
P05825	fepA	1.096608268	Ferrienterobactin receptor OS=Escherichia coli O6 GN=fepA
P0ABB4	atpD	1.096795997	ATP synthase subunit beta OS=Escherichia coli O6 GN=atpD
P0A7Z4	rpoA	1.098273771	DNA-directed RNA polymerase subunit alpha OS=Escherichia coli O6 GN=rpoA
P0A9Q9	asd	1.101047067	Aspartate-semialdehyde dehydrogenase OS=Escherichia coli O6 GN=asd
P0ABC3	hflC	1.101204735	Protein HflC OS=Escherichia coli O6 GN=hflC
P0AAX8	ybiS	1.102443569	Probable L,D-transpeptidase YbiS OS=Escherichia coli O6 GN=ybiS
P0A8L1	serS	1.103783234	Seryl-tRNA synthetase OS=Escherichia coli O6 GN=serS
P45766	yhdW	1.104801107	Putative amino-acid ABC transporter binding protein yhdW OS=Escherichia coli O6 GN=yhdW
P23869	ppiB	1.105059669	Peptidyl-prolyl cis-trans isomerase B OS=Escherichia coli O6 GN=ppiB
P0A9C5	glnA	1.10645413	Glutamine synthetase OS=Escherichia coli O6 GN=glnA
P0AGJ9	tyrS	1.10703438	Tyrosyl-tRNA synthetase OS=Escherichia coli O6 GN=tyrS
P0A6P1	tsf	1.110916942	Elongation factor Ts OS=Escherichia coli O6 GN=tsf
A0A0H2VEA0	c4748	1.11202637	Putative uncharacterized protein OS=Escherichia coli O6 GN=c4748
P39173	yeaD	1.112404595	Putative uncharacterized protein yeaD OS=Escherichia coli O6 GN=yeaD
P0ABQ2	garR	1.116545823	2-hydroxy-3-oxopropionate reductase OS=Escherichia coli O6 GN=garR
P22255	cysQ	1.116830736	3'(2'),5'-bisphosphate nucleotidase CysQ OS=Escherichia coli O6 GN=cysQ
P02358	rpsF	1.123762801	30S ribosomal protein S6 OS=Escherichia coli O6 GN=rpsF
P0ACF8	hns	1.124572546	DNA-binding protein H-NS OS=Escherichia coli O6 GN=hns
P0AG18	purE	1.125593608	Phosphoribosylaminoimidazole carboxylase catalytic subunit OS=Escherichia coli O6 GN=purE
W8ZX03	yhdH	1.12832771	Protein yhdH OS=Escherichia coli O6 GN=yhdH
P10371	hisA	1.13013415	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Escherichia coli O6 GN=hisA
P33363	bglX	1.130624263	Periplasmic beta-glucosidase OS=Escherichia coli O6 GN=bglX
P06988	hisD	1.133114096	Histidinol dehydrogenase OS=Escherichia coli O6 GN=hisD
P0AE01	trmJ	1.133970847	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ OS=Escherichia coli O6 GN=trmJ
P0AAZ4	rarA	1.141221009	Replication-associated recombination protein A OS=Escherichia coli O6 GN=rarA
P0A904	trxB	1.143306904	Thioredoxin reductase OS=Escherichia coli O6 GN=trxB
P0A9M8	pta	1.144532966	Phosphate acetyltransferase OS=Escherichia coli O6 GN=pta

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0A879	trpB	1.147323859	Tryptophan synthase beta chain OS=Escherichia coli O6 GN=trpB
P12281	moeA	1.148606698	Molybdopterin biosynthesis protein moeA OS=Escherichia coli O6 GN=moeA
P21151	fadA	1.152002029	3-ketoacyl-CoA thiolase OS=Escherichia coli O6 GN=fadA
P0A887	ubiE	1.152765393	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE OS=Escherichia coli O6 GN=ubiE
P39332	yjgF	1.158961038	RutC family protein yjgF OS=Escherichia coli O6 GN=yjgF
P0AG80	ugpB	1.162518068	sn-glycerol-3-phosphate-binding periplasmic protein ugpB OS=Escherichia coli O6 GN=ugpB
P0A858	tpiA	1.162870128	Triosephosphate isomerase OS=Escherichia coli O6 GN=tpiA
P0AFG0	nusG	1.163385311	Transcription antitermination protein nusG OS=Escherichia coli O6 GN=nusG
P63177	rlmB	1.166363593	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB OS=Escherichia coli O6 GN=rlmB
P0ACB2	hemB	1.167335127	Delta-aminolevulinic acid dehydratase OS=Escherichia coli O6 GN=hemB
P60664	hisF	1.169068547	Imidazole glycerol phosphate synthase subunit hisF OS=Escherichia coli O6 GN=hisF
P0A6Z1	hscA	1.171886514	Chaperone protein hscA OS=Escherichia coli O6 GN=hscA
P0A7E5	pyrG	1.181027205	CTP synthase OS=Escherichia coli O6 GN=pyrG
P0AED0	uspA	1.183775503	Universal stress protein A OS=Escherichia coli O6 GN=uspA
P26616	maeA	1.18409828	NAD-dependent malic enzyme OS=Escherichia coli O6 GN=maeA
W8ZPZ2	ybjU	1.184604857	Low-specificity L-threonine aldolase OS=Escherichia coli O6 GN=ybjU
P0A9Z1	glnB	1.187246161	Nitrogen regulatory protein P-II 1 OS=Escherichia coli O6 GN=glnB
P0A6M8	fusA	1.192931176	Elongation factor G OS=Escherichia coli O6 GN=fusA
P0AGJ5	yfiF	1.19442217	Hypothetical tRNA/rRNA methyltransferase yfiF OS=Escherichia coli O6 GN=yfiF
P0A993	fbp	1.195165332	Fructose-1,6-bisphosphatase class 1 OS=Escherichia coli O6 GN=fbp
P0AEP3	galU	1.1972762	UTP--glucose-1-phosphate uridylyltransferase OS=Escherichia coli O6 GN=galU
P11446	argC	1.203881118	N-acetyl-gamma-glutamyl-phosphate reductase OS=Escherichia coli O6 GN=argC
P0ACJ0	lrp	1.207926893	Leucine-responsive regulatory protein OS=Escherichia coli O6 GN=lrp
P36649	yacK	1.209347625	Blue copper oxidase cueO OS=Escherichia coli O6 GN=yacK
P39831	ydfG	1.210067388	NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG OS=Escherichia coli O6 GN=ydfG
P0AF12	mtnN	1.211174935	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase OS=Escherichia coli O6 GN=mtnN
P0C0L2	osmC	1.211451658	Osmotically inducible protein C OS=Escherichia coli O6 GN=osmC
P08244	pyrF	1.214203753	Orotidine 5'-phosphate decarboxylase OS=Escherichia coli O6 GN=pyrF

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0A7W7	rpsH	1.22154099	30S ribosomal protein S8 OS=Escherichia coli O6 GN=rpsH
P0AGC3	slt	1.224184298	Soluble lytic murein transglycosylase OS=Escherichia coli O6 GN=slt
P16095	sdaA	1.225042706	L-serine dehydratase 1 OS=Escherichia coli O6 GN=sdaA
P0ABU0	menB	1.225570979	1,4-Dihydroxy-2-naphthoyl-CoA synthase OS=Escherichia coli O6 GN=menB
P0A8E7	yajQ	1.225648469	UPF0234 protein yajQ OS=Escherichia coli O6 GN=yajQ
P0A825	glyA	1.225880166	Serine hydroxymethyltransferase OS=Escherichia coli O6 GN=glyA
P0A7V0	rpsB	1.22695247	30S ribosomal protein S2 OS=Escherichia coli O6 GN=rpsB
P0A9V1	lptB	1.227846972	Lipopolysaccharide export system ATP-binding protein LptB OS=Escherichia coli O6 GN=lptB
P0A8G6	wrbA	1.228610545	Flavoprotein wrbA OS=Escherichia coli O6 GN=wrbA
P0AC33	fumA	1.228987866	Fumarate hydratase class I, aerobic OS=Escherichia coli O6 GN=fumA
P22259	pckA	1.231991908	Phosphoenolpyruvate carboxykinase [ATP] OS=Escherichia coli O6 GN=pckA
P0A9D8	dapD	1.232254207	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Escherichia coli O6 GN=dapD
P62707	gpmA	1.232752028	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Escherichia coli O6 GN=gpmA
P0AB91	aroG	1.233656947	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Escherichia coli O6 GN=aroG
P0A6B7	iscS	1.233951516	Cysteine desulfurase OS=Escherichia coli O6 GN=iscS
A0A0H2VCZ2	c4771	1.236148393	Putative carboxymethylenebutenolidase OS=Escherichia coli O6 GN=c4771
P0A9L8	proC	1.240281792	Pyrroline-5-carboxylate reductase OS=Escherichia coli O6 GN=proC
P0A749	murA	1.248930199	UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Escherichia coli O6 GN=murA
P0A910	ompA	1.249058905	Outer membrane protein A OS=Escherichia coli O6 GN=ompA
P0A917	ompX	1.249727018	Outer membrane protein X OS=Escherichia coli O6 GN=ompX
P0A7M6	rpmC	1.257643641	50S ribosomal protein L29 OS=Escherichia coli O6 GN=rpmC
W8ZQQ8	prfA	1.257901772	Peptide chain release factor 1 OS=Escherichia coli O6 GN=prfA
P07639	aroB	1.259202969	3-dehydroquinate synthase OS=Escherichia coli O6 GN=aroB
P0A6V8	glk	1.259384284	Glucokinase OS=Escherichia coli O6 GN=glk
P06983	hemC	1.268140463	Porphobilinogen deaminase OS=Escherichia coli O6 GN=hemC
P08142	ilvB	1.268650864	Acetolactate synthase isozyme I large subunit OS=Escherichia coli O6 GN=ilvB
P06999	pfkB	1.275241236	6-phosphofructokinase isozyme 2 OS=Escherichia coli O6 GN=pfkB
P60757	hisG	1.27552843	ATP phosphoribosyltransferase OS=Escherichia coli O6 GN=hisG

Uniprot ID	**Symbol**	**TMT ratio (high/low)**	**Protein description**
P0A988	dnaN	1.276640056	DNA polymerase III subunit beta OS=Escherichia coli O6 GN=dnaN
P0A9S3	gatD	1.277692722	Galactitol-1-phosphate 5-dehydrogenase OS=Escherichia coli O6 GN=gatD
P0A929	yrdA	1.278250572	Protein yrdA OS=Escherichia coli O6 GN=yrdA
P17952	murC	1.279016014	UDP-N-acetylmuramate--L-alanine ligase OS=Escherichia coli O6 GN=murC
P0AB80	ilvE	1.279683062	Branched-chain-amino-acid aminotransferase OS=Escherichia coli O6 GN=ilvE
P0ABD5	accA	1.282931221	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha OS=Escherichia coli O6 GN=accA
P0A877	trpA	1.283044503	Tryptophan synthase alpha chain OS=Escherichia coli O6 GN=trpA
P0ABF6	cdd	1.284546277	Cytidine deaminase OS=Escherichia coli O6 GN=cdd
P22106	asnB	1.285061968	Asparagine synthetase B (Glutamine-hydrolyzing) OS=Escherichia coli O6 GN=asnB
P15042	ligA	1.28525356	DNA ligase OS=Escherichia coli O6 GN=ligA
P0A8D0	nrdR	1.288073057	Transcriptional repressor NrdR OS=Escherichia coli O6 GN=nrdR
P0ACA3	sspA	1.292797802	Stringent starvation protein A OS=Escherichia coli O6 GN=sspA
P0CE47	tufA	1.295164496	Elongation factor Tu OS=Escherichia coli O6 GN=tufA
P30137	thiE	1.298101601	Thiamine-phosphate pyrophosphorylase OS=Escherichia coli O6 GN=thiE
P32132	typA	1.303591024	GTP-binding protein TypA/BipA OS=Escherichia coli O6 GN=typA
P75913	ghrA	1.306354008	Glyoxylate/hydroxypyruvate reductase A OS=Escherichia coli O6 GN=ghrA
P75915	ycdY	1.318890417	Putative uncharacterized protein ycdY OS=Escherichia coli O6 GN=ycdY
P0A8M6	yeeX	1.320450671	UPF0265 protein yeeX OS=Escherichia coli O6 GN=yeeX
P0AES6	gyrB	1.323048259	DNA gyrase subunit B OS=Escherichia coli O6 GN=gyrB
A0A0H2VDG6	c3746	1.324798525	2,5-diketo-D-gluconic acid reductase A OS=Escherichia coli O6 GN=c3746
P0A817	metK	1.325136362	S-adenosylmethionine synthase OS=Escherichia coli O6 GN=metK
P0AC69	grxD	1.332472152	Glutaredoxin-4 OS=Escherichia coli O6 GN=grxD
W9AM00	rph	1.332593529	Ribonuclease PH OS=Escherichia coli O6 GN=rph
P0AET8	hdhA	1.332697936	7-alpha-hydroxysteroid dehydrogenase OS=Escherichia coli O6 GN=hdhA
P23721	serC	1.34372124	Phosphoserine aminotransferase OS=Escherichia coli O6 GN=serC
P25437	frmA	1.349739632	S-(hydroxymethyl)glutathione dehydrogenase OS=Escherichia coli O6 GN=frmA
P0A6L0	deoC	1.35351322	Deoxyribose-phosphate aldolase OS=Escherichia coli O6 GN=deoC
P45799	yrfE	1.354065155	ADP compounds hydrolase nudE OS=Escherichia coli O6 GN=yrfE
W8ZG87	ybiC	1.363678948	Hypothetical oxidoreductase ybiC OS=Escherichia coli O6 GN=ybiC

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0AC41	sdhA	1.365016979	Succinate dehydrogenase flavoprotein subunit OS=Escherichia coli O6 GN=sdhA
P37666	ghrB	1.366973445	Glyoxylate/hydroxypyruvate reductase B OS=Escherichia coli O6 GN=ghrB
P0A6B4	alr	1.378001301	Alanine racemase, biosynthetic OS=Escherichia coli O6 GN=alr
P0ADP0	yigB	1.384491892	Putative uncharacterized protein yigB OS=Escherichia coli O6 GN=yigB
P0ACF0	hupA	1.38702387	DNA-binding protein HU-alpha OS=Escherichia coli O6 GN=hupA
P08622	dnaJ	1.389330207	Chaperone protein dnaJ OS=Escherichia coli O6 GN=dnaJ
P05852	ygjD	1.389732842	Uncharacterized protein yqjD OS=Escherichia coli O6 GN=yqjD
P25745	mnmA	1.392851194	tRNA-specific 2-thiouridylase mnmA OS=Escherichia coli O6 GN=mnmA
P0AGL7	rsmE	1.393882903	Ribosomal RNA small subunit methyltransferase E OS=Escherichia coli O6 GN=rsmE
P07003	poxB	1.396493734	Pyruvate dehydrogenase (Cytochrome) OS=Escherichia coli O6 GN=poxB
P0A9A6	ftsZ	1.407596714	Cell division protein ftsZ OS=Escherichia coli O6 GN=ftsZ
P0A6H5	hslU	1.409506821	ATP-dependent protease ATPase subunit HslU OS=Escherichia coli O6 GN=hslU
P08200	icdA	1.412559707	Isocitrate dehydrogenase (NADP) OS=Escherichia coli O6 GN=icdA
P07650	deoA	1.418720272	Thymidine phosphorylase OS=Escherichia coli O6 GN=deoA
P16456	selD	1.425749282	Selenide, water dikinase OS=Escherichia coli O6 GN=selD
P67826	cutC	1.427459354	Copper homeostasis protein CutC OS=Escherichia coli O6 GN=cutC
P62617	ispF	1.427640495	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase OS=Escherichia coli O6 GN=ispF
P0A6P9	eno	1.430724867	Enolase OS=Escherichia coli O6 GN=eno
P76138	yneI	1.432992723	Aldehyde-dehydrogenase like protein yneI OS=Escherichia coli O6 GN=yneI
P07012	prfB	1.439528443	Peptide chain release factor 2 OS=Escherichia coli O6 GN=prfB
P23843	oppA	1.440141763	Periplasmic oligopeptide-binding protein OS=Escherichia coli O6 GN=oppA
P17115	gutQ	1.44999015	GutQ protein OS=Escherichia coli O6 GN=gutQ
P0AGK8	iscR	1.453345032	HTH-type transcriptional regulator iscR OS=Escherichia coli O6 GN=iscR
P00547	thrB	1.460733836	Homoserine kinase OS=Escherichia coli O6 GN=thrB
P0AGG8	tldD	1.473809929	Protein tldD OS=Escherichia coli O6 GN=tldD
P0A6RO	fabH	1.477338782	3-oxoacyl-[acyl-carrier-protein] synthase 3 OS=Escherichia coli O6 GN=fabH
W9AHZ8	yfbT	1.483138855	Protein yfbT OS=Escherichia coli O6 GN=yfbT
P0ABK5	cysK	1.49081925	Cysteine synthase A OS=Escherichia coli O6 GN=cysK

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P39406	rsmC	1.49279829	Ribosomal RNA small subunit methyltransferase C OS=Escherichia coli O6 GN=rsmC
P0AG07	rpe	1.49781747	Ribulose-phosphate 3-epimerase OS=Escherichia coli O6 GN=rpe
P0AG84	yghA	1.502199945	Hypothetical oxidoreductase yghA OS=Escherichia coli O6 GN=yghA
P0AE18	map	1.509471563	Methionine aminopeptidase OS=Escherichia coli O6 GN=map
P0A6D3	aroA	1.511848107	3-phosphoshikimate 1-carboxyvinyltransferase OS=Escherichia coli O6 GN=aroA
P0AFK0	pmbA	1.518968394	PmbA protein OS=Escherichia coli O6 GN=pmbA
W8ZXE6	yraL	1.519001159	Putative uncharacterized protein yraL OS=Escherichia coli O6 GN=yraL
P75949	nagZ	1.5233278	Beta-hexosaminidase OS=Escherichia coli O6 GN=nagZ
P00934	thrC	1.528649931	Threonine synthase OS=Escherichia coli O6 GN=thrC
P0AFR4	yciO	1.529271491	Uncharacterized protein yciO OS=Escherichia coli O6 GN=yciO
P04391	argI	1.546772025	Ornithine carbamoyltransferase OS=Escherichia coli O6 GN=argI
P0AAB6	galF	1.551110305	UTP--glucose-1-phosphate uridylyltransferase OS=Escherichia coli O6 GN=galF
P37686	yiaY	1.552589159	Probable alcohol dehydrogenase OS=Escherichia coli O6 GN=yiaY
P0A717	prs	1.557467971	Ribose-phosphate pyrophosphokinase OS=Escherichia coli O6 GN=prs
P0A953	fabB	1.55911121	3-oxoacyl-[acyl-carrier-protein] synthase 1 OS=Escherichia coli O6 GN=fabB
P18196	minC	1.567544888	Septum site-determining protein minC OS=Escherichia coli O6 GN=minC
P0A7A2	gpmB	1.569220902	Probable phosphoglycerate mutase gpmB OS=Escherichia coli O6 GN=gpmB
P0A6H1	clpX	1.570297548	ATP-dependent Clp protease ATP-binding subunit ClpX OS=Escherichia coli O6 GN=clpX
P0A7G6	recA	1.571139306	Protein recA OS=Escherichia coli O6 GN=recA
P75957	lolD	1.583522627	Lipoprotein-releasing system ATP-binding protein LolD OS=Escherichia coli O6 GN=lolD
P06720	melA	1.5881827	Alpha-galactosidase OS=Escherichia coli O6 GN=melA
P0AB71	fba	1.588916628	Fructose-bisphosphate aldolase class II OS=Escherichia coli O6 GN=fba
P0AEK4	fabI	1.609352724	Enoyl-[acyl-carrier-protein] reductase (NADH) OS=Escherichia coli O6 GN=fabI
P05791	ilvD	1.627868645	Dihydroxy-acid dehydratase OS=Escherichia coli O6 GN=ilvD
P0A9T0	serA	1.631145487	D-3-phosphoglycerate dehydrogenase OS=Escherichia coli O6 GN=serA
P0ABU2	ychF	1.653265885	Probable GTP-binding protein ychF OS=Escherichia coli O6 GN=ychF
P0ACB0	dnaB	1.655769338	Replicative DNA helicase OS=Escherichia coli O6 GN=dnaB
P21645	lpxD	1.662288392	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase OS=Escherichia coli O6 GN=lpxD

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
P0AAI9	fabD	1.664100661	Malonyl CoA-acyl carrier protein transacylase OS=Escherichia coli O6 GN=fabD
P0A867	talA	1.665675601	Transaldolase A OS=Escherichia coli O6 GN=talA
P60716	lipA	1.675071934	Lipoyl synthase OS=Escherichia coli O6 GN=lipA
P09832	gltD	1.676358545	Glutamate synthase [NADPH] small chain OS=Escherichia coli O6 GN=gltD
P0A940	yaeT	1.678509009	Outer membrane protein assembly factor yaeT OS=Escherichia coli O6 GN=yaeT
P46837	yhgF	1.682844027	Protein yhgF OS=Escherichia coli O6 GN=yhgF
A0A0H2V801	c1628	1.713548636	Protein ycgM OS=Escherichia coli O6 GN=c1628
P0AC13	folP	1.721363234	Dihydropteroate synthase OS=Escherichia coli O6 GN=folP
P28861	fpr	1.723282389	Ferredoxin--NADP reductase OS=Escherichia coli O6 GN=fpr
P0A7D7	purC	1.724075015	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Escherichia coli O6 GN=purC
P21179	katE	1.734845802	Catalase HPII OS=Escherichia coli O6 GN=katE
P05793	ilvC	1.746917834	Ketol-acid reductoisomerase OS=Escherichia coli O6 GN=ilvC
P0AEZ3	minD	1.7782961	Septum site-determining protein minD OS=Escherichia coli O6 GN=minD
P13482	treA	1.783834023	Periplasmic trehalase OS=Escherichia coli O6 GN=treA
P25516	acnA	1.803864059	Aconitate hydratase 1 OS=Escherichia coli O6 GN=acnA
P76034	yciT	1.810665341	Hypothetical transcriptional regulator yciT OS=Escherichia coli O6 GN=yciT
W8ZF88	thiJ	1.868435423	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis enzyme OS=Escherichia coli O6 GN=thiJ
P0A805	frr	1.874556937	Ribosome-recycling factor OS=Escherichia coli O6 GN=frr
P62620	ispG	1.88190573	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase OS=Escherichia coli O6 GN=ispG
P0A8Y5	yidA	1.898055215	Phosphatase YidA OS=Escherichia coli O6 GN=yidA
P31808	yciK	1.904054081	Hypothetical oxidoreductase yciK OS=Escherichia coli O6 GN=yciK
P18843	nadE	1.913925645	NH(3)-dependent NAD(+) synthetase OS=Escherichia coli O6 GN=nadE
P17993	ubiG	1.920751893	3-demethylubiquinone-9 3-methyltransferase OS=Escherichia coli O6 GN=ubiG
P0A812	ruvB	1.925044994	Holliday junction ATP-dependent DNA helicase ruvB OS=Escherichia coli O6 GN=ruvB
P77318	ydeN	1.926846936	Putative sulfatase ydeN OS=Escherichia coli O6 GN=ydeN
P0ACR9	mprA	1.946235523	Transcriptional repressor mprA OS=Escherichia coli O6 GN=mprA
P30138	thiF	1.975714638	Adenylyltransferase thiF OS=Escherichia coli O6 GN=thiF
W8ZIH4	ycjG	1.97572368	Putative uncharacterized protein ycjG OS=Escherichia coli O6 GN=ycjG

Uniprot ID	Symbol	TMT ratio (high/low)	Protein description
A0A0H2V8T6	c2543	2.002115785	Protein yeeZ OS=Escherichia coli O6 GN=c2543
P0AC59	grxB	2.092678674	Glutaredoxin-2 OS=Escherichia coli O6 GN=grxB
A0A0H2V747	c1657	2.112322267	Protein ycgS OS=Escherichia coli O6 GN=c1657
P60560	guaC	2.167848194	GMP reductase OS=Escherichia coli O6 GN=guaC
P0A715	kdsA	2.277294673	2-dehydro-3-deoxyphosphooctonate aldolase OS=Escherichia coli O6 GN=kdsA
P64483	yeaK	2.339571121	Putative uncharacterized protein yeaK OS=Escherichia coli O6 GN=yeaK
P0C8J6	gatY	2.348729289	D-tagatose-1,6-bisphosphate aldolase subunit GatY OS=Escherichia coli O6 GN=gatY
P22333	add	2.380391678	Adenosine deaminase OS=Escherichia coli O6 GN=add
P0ACG1	stpA	2.427237387	DNA-binding protein stpA OS=Escherichia coli O6 GN=stpA
P17444	betA	2.436059284	Choline dehydrogenase OS=Escherichia coli O6 GN=betA
P31678	otsB	2.554313161	Trehalose-phosphatase OS=Escherichia coli O6 GN=otsB
P36683	acnB	2.557021875	Aconitate hydratase 2 OS=Escherichia coli O6 GN=acnB
P0A9X4	mreB	2.681184522	Rod shape-determining protein mreB OS=Escherichia coli O6 GN=mreB
P0AA16	ompR	3.953794376	Transcriptional regulatory protein ompR OS=Escherichia coli O6 GN=ompR