Table 2. Protein spots identification of 2-DE gels and MALDI-TOF sequencing results from *E. coli* isolate C580

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Spot*** | ***Accession Number*** | ***Protein Description*** | ***Species*** | ***Protein Name*** | ***Protein MW*** | ***Protein PI*** | ***Protein Score Confidence Interval (%)*** | ***Information*** | ***References*** |
| 1 | P0A6A4 | Acetate kinase | *E. coli* O6 | ackA | 43263,07813 | 5,85 | 100 | Involved in the activation of acetate to acetyl CoA and the secretion of acetate. During anaerobic growth of the organism, this enzyme is also involved in the synthesis of most of the ATP formed catabolically. | 26 |
| 2 | P0A9B3 | Glyceraldehyde-3-phosphate dehydrogenase A | *E. coli* O6 | gapA | 35510,23828 | 6,61 | 100 | Participates in the first step of the second phase of glycolysis. | 26 |
| 3 | P0ADG7 | Inosine-5'-monophosphate dehydrogenase | *E. coli* (strain K12) | guaA | 51990,01953 | 6,02 | 100 | IMP dehydrogenase subunit of *E. coli* contains a cysteine at the IMP binding site and is inhibited in a simple competitive manner by GMP. | 21, 28, 59 |
| 4 | Q1RFA0 | Trigger factor | *E. coli* (strain UTI89 / UPEC) | tig | 47835,71094 | 4,83 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 93 |
| 4 | Q8FKA7 | Trigger factor | *E. coli* O6 | tig | 48220,87109 | 4,81 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 26 |
| 4 | P0A9P1 | Dihydrolipoyl dehydrogenase | *E. coli* O6 | dldH | 50656,58984 | 5,79 | 100 | Lipoamide dehydrogenase is a component of the glycine cleavage system as well as of the alpha-ketoacid dehydrogenase complexes. | 26 |
| 5 | P0ABB2 | ATP synthase subunit alpha | *E. coli* O157:H7 | atpA | 55187,75 | 5,8 | 100 | Produces ATP from ADP in the presence of a proton gradient across the membrane. The alpha chain is a regulatory subunit. | 27, 91 |
| 6 | Q0TE79 | CTP synthase | *E. coli* O6:K15:H31 (strain 536 / UPEC) | pyrG | 60336,07031 | 5,63 | 100 | Catalyzes the ATP-dependent amination of UTP to CTP with either L-glutamine or ammonia as the source of nitrogen. | 92 |
| 7 | P14178 | Pyruvate kinase I | *E. coli* | Kpyk1 | 50697,26172 | 5,77 | 100 | Glycolysis; final step | 27, 28, 65 |
| 8 | P63286 | Chaperone protein clpB | *E. coli* O6 | clpB | 95525,92969 | 5,37 | 100 | Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with *dnaK*, *dnaJ* and *grpE*. Acts before *dnaK*, in the processing of protein aggregates. Protein binding stimulates the ATPase activity; ATP hydrolysis unfolds the denatured protein aggregates, which probably helps expose new hydrophobic binding sites on the surface of *clpB*-bound aggregates, contributing to the solubilization and refolding of denatured protein aggregates by *dnaK*. | 26, 27, 71 |
| 9 | P0A6Z0 | Chaperone protein | *E. coli* O157:H7 | dnaK | 69072,47656 | 4,83 | 100 | Essential role in the initiation of phage lambda DNA replication and is involved in chromosomal DNA replication. | 27, 91 |
| 10 | P0A860 | Triosephosphate isomerase | *E. coli* O157:H7 | tpiA | 26954,82031 | 5,64 | 100 | Plays an important role in several metabolic pathways. | 27, 91 |
| 10 | P0A9L0 | FKBP-type peptidyl-prolyl cis-trans isomerase | *E. coli* O6 | slyD | 20839,69922 | 4,86 | 100 | Required for lysis of phiX174 infected cells. Binds nickel and zinc with high affinity. Smaller activity than the one found in PPIases with the same substrate. PPIases accelerate the protein folding. | 26 |
| 10 | P78218 | Dihydrofolate reductase type XV | *E. coli* | dhfrXV | 17491,98047 | 5,56 | 93 | Cofactor biosynthesis. The reaction catalyzed by this enzyme represents an essential step for *de novo* glycine and purine synthesis, DNA precursor synthesis, and for the conversion of dUMP to dTMP. | 54 |
| 11 | P0A9L0 | FKBP-type peptidyl-prolyl cis-trans isomerase | *E. coli* O6 | slyD | 20839,69922 | 4,86 | 100 | Required for lysis of phiX174 infected cells. Binds nickel and zinc with high affinity. Smaller activity than the one found in PPIases with the same substrate. PPIases accelerate the protein folding. | 26 |
| 11 | P0A860 | Triosephosphate isomerase | *E. coli* O157:H7 | tpiA | 26954,82031 | 5,64 | 92 | Plays an important role in several metabolic pathways. | 27, 91 |
| 12 | A7ZYV7 | Flavoprotein | *E. coli* O9:H4 (strain HS) | wrbA | 20832,41992 | 5,59 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. | 23 |
| 12 | Q8X4B4 | Putative flavoprotein | *E. coli* O157:H7 | wrbA | 20821,41992 | 5,91 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. | 27 |
| 13 | A7ZWB5 | 30S ribosomal protein S2 | *E. coli* O9:H4 (strain HS) | rpsB | 26740,82031 | 6,62 | 100 | Part of the 30S ribosomal subunit. Some nascent polypeptide chains are able to cross-link to this protein *in situ*. | 23 |
| 13 | A1A7L3 | 30S ribosomal protein S2 | *E. coli* O1:K1 / APEC | rpsB | 26726,80078 | 6,61 | 100 | Part of the 30S ribosomal subunit. Some nascent polypeptide chains are able to cross-link to this protein *in situ*. | 96 |
| 14 | A7ZQ54 | *GrpE* Protein | *E. coli* O139:H28 (strain E24377A / ETEC) | grpE | 21727,14063 | 4,68 | 100 | Participates actively in the response to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins, in association with *dnaK* and *grpE*. It is the nucleotide exchange factor for *dnaK* and may function as a thermosensor. | 23 |
| 14 | A8A3C0 | *GrpE* Protein | *E. coli* O9:H4 (strain HS) | grpE | 21798,17969 | 4,68 | 100 | Participates actively in the response to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins, in association with *dnaK* and *grpE*. It is the nucleotide exchange factor for *dnaK* and may function as a thermosensor. | 23 |
| 14 | P09372 | *GrpE* Protein | *E. coli* (strain K12) | grpE | 21784,16016 | 4,68 | 100 | Participates actively in the response to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins, in association with *dnaK* and *grpE*. It is the nucleotide exchange factor for *dnaK* and may function as a thermosensor. | 28, 21, 77 |
| 15 | P0A6N6 | Elongation factor P | *E. coli* O157:H7 | efp | 20578,41992 | 4,9 | 100 | Involved in peptide bond synthesis. Stimulates efficient translation and peptide-bond synthesis on native or reconstituted 70S ribosomes in vitro. Probably functions indirectly by altering the affinity of the ribosome for aminoacyl-tRNA, thus increasing their reactivity as acceptors for peptidyl transferase. | 27, 91 |
| 15 | P0AGE6 | Uncharacterized protein yieF | *E. coli* (strain K12) | yieF | 20362,59961 | 5,01 | 100 |  | 21, 28 |
| 16 | Q8FDH9 | 3,4-dihydroxy-2-butanone 4-phosphate synthase | *E. coli* O6 | ribB | 23324,51953 | 4,89 | 100 | Catalyzes the conversion of D-ribulose 5-phosphate to formate and 3,4-dihydroxy-2-butanone 4-phosphate. | 26 |
| 16 | P0A7J1 | 3,4-dihydroxy-2-butanone 4-phosphate synthase | *E. coli* O157:H7 | ribB | 23338,53906 | 4,9 | 100 | Catalyzes the conversion of D-ribulose 5-phosphate to formate and 3,4-dihydroxy-2-butanone 4-phosphate. | 27, 91 |
| 18 | P23843 | Periplasmic oligopeptide-binding protein | *E. coli* | oppA | 60860,92188 | 6,05 | 100 | This protein is a component of the oligopeptide permease, a binding protein-dependent transport system, it binds peptides up to five amino acids long with high affinity. | 21, 28 |
| 18 | P63022 | Fe/S biogenesis protein | *E. coli* O157:H7 | nfuA | 20984,32031 | 4,52 | 100 | Involved in iron-sulfur cluster biogenesis. Binds a 4Fe-4S cluster, can transfer this cluster to apoproteins, and thereby intervenes in the maturation of Fe/S proteins. Could also act as a scaffold/chaperone for damaged Fe/S proteins. | 27, 91 |
| 19 | Q8XA55 | Serine hydroxymethyltransferase | *E. coli* (strain K12) | glyA | 45316 | 6,03 | 100 | Interconversion of serine and glycine. | 21, 28 |
| 19 | A8A359 | Serine hydroxymethyltransferase | *E. coli* O9:H4 (strain HS) | glyA | 45287,96875 | 6,03 | 100 | Interconversion of serine and glycine. | 23 |
| 20 | P0A9I1 | Citrate lyase subunit beta | *E. coli* (strain K12) | citE | 33089,25 | 5,54 | 100 | Represents a citryl-ACP lyase. | 21, 28, 94 |
| 21 | A7ZN88 | Chaperone protein hchA | *E. coli* O139:H28 (strain E24377A / ETEC) | hchA | 31126,58008 | 5,63 | 100 | Uses temperature-induced exposure of structured hydrophobic domains to capture and stabilize early unfolding protein intermediates under severe thermal stress. It rapidly releases them once stress has abated. | 23 |
| 21 | A1ACB2 | Chaperone protein hchA | *E. coli* O1:K1 / APEC | hchA | 31185,57031 | 5,42 | 100 | Uses temperature-induced exposure of structured hydrophobic domains to capture and stabilize early unfolding protein intermediates under severe thermal stress. It rapidly releases them once stress has abated. | 96 |
| 21 | P59331 | Chaperone protein hchA | *E. coli* O6 | hchA | 31216,60938 | 5,62 | 100 | Uses temperature-induced exposure of structured hydrophobic domains to capture and stabilize early unfolding protein intermediates under severe thermal stress. It rapidly releases them once stress has abated. | 26 |
| 22 | P39173 | UPF0010 protein | *E. coli* | YeaD | 32645,66016 | 5,89 | 100 |  | 21, 28, 69 |
| 23 | Q46856 | Alcohol dehydrogenase | *E. coli* (strain K12) | yqhD | 42070,80078 | 5,72 | 100 | NADP-dependent ADH activity. | 21, 28 |
| 24 | P12758 | Uridine phosphorylase | *E. coli* (strain K12) | udp | 27141,83984 | 5,81 | 100 | Catalyzes the reversible phosphorylytic cleavage of uridine and deoxyuridine to uracil and ribose- or deoxyribose-1-phosphate. The produced molecules are then utilized as carbon and energy sources or in the rescue of pyrimidine bases for nucleotide synthesis. | 21, 28, 60, 63 |
| 25 | P0A794 | Pyridoxine 5'-phosphate synthase | *E. coli* (strain K12) | pdxJ | 26367,55078 | 5,61 | 100 | Catalyzes the complicated ring closure reaction between the two acyclic compounds 1-deoxy-D-xylulose-5-phosphate (DXP) and 3-amino-2-oxopropyl phosphate (1-amino-acetone-3-phosphate or AAP) to form pyridoxine 5'-phosphate (PNP) and inorganic phosphate. | 21, 28, 82 |
| 25 | Q8FF18 | Pyridoxine 5'-phosphate synthase | *E. coli* O6 | pdxJ | 26344,4707 | 5,49 | 100 | Catalyzes the complicated ring closure reaction between the two acyclic compounds 1-deoxy-D-xylulose-5-phosphate (DXP) and 3-amino-2-oxopropyl phosphate (1-amino-acetone-3-phosphate or AAP) to form pyridoxine 5'-phosphate (PNP) and inorganic phosphate. | 26 |
| 26 | A8A3C0 | *GrpE* Protein | *E. coli* O9:H4 (strain HS) | grpE | 21798,17969 | 4,68 | 100 | Participates actively in the response to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins, in association with *dnaK* and *grpE*. It is the nucleotide exchange factor for *dnaK* and may function as a thermosensor. | 23 |
| 26 | A7ZQ54 | *GrpE* Protein | *E. coli* O139:H28 (strain E24377A / ETEC) | grpE | 21727,14063 | 4,68 | 100 | Participates actively in the response to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins, in association with *dnaK* and *grpE*. It is the nucleotide exchange factor for *dnaK* and may function as a thermosensor. | 23 |
| 29 | P0A9A7 | Cell division protein | *E. coli* O6 | ftsZ | 40298,57031 | 4,65 | 100 | This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. | 26 |
| 30 | P32665 | Glycerol dehydrogenase | *E. coli* | GldA | 38687,69922 | 4,81 | 100 | Glycerol utilization. | 26, 76 |
| 31 | P23861 | Spermidine/putrescine-binding periplasmic protein | *E. coli* | PotD | 38842,48828 | 5,24 | 100 | Required for the activity of the bacterial periplasmic transport system of putrescine and spermidine. Polyamine binding protein. | 28 |
| 32 | P0A9Q2 | Aerobic respiration control protein | *E. coli* O6 | arcA | 27274,91992 | 5,21 | 100 | Member of the two-component regulatory system *arcB*/*arcA*. Represses a wide variety of aerobic enzymes under anaerobic conditions. Controls the resistance of *E. coli* to dyes; required for expression of the alkaline phosphatase and sex factor F genes; It also may be involved in the osmoregulation of envelope proteins. | 26 |
| 33 | P0A9Q2 | Aerobic respiration control protein | *E. coli* O6 | arcA | 27274,91992 | 5,21 | 100 | Member of the two-component regulatory system *arcB*/*arcA*. Represses a wide variety of aerobic enzymes under anaerobic conditions. Controls the resistance of *E. coli* to dyes; required for expression of the alkaline phosphatase and sex factor F genes; It also may be involved in the osmoregulation of envelope proteins. | 26 |
| 34 | A7ZYV7 | Flavoprotein | *E. coli* O9:H4 (strain HS) | wrbA | 20832,41992 | 5,59 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. | 23 |
| 34 | Q8X4B4 | Putative flavoprotein | *E. coli* O157:H7 | wrbA | 20821,41992 | 5,91 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. | 27 |
| 35 | A7ZYV7 | Flavoprotein | *E. coli* O9:H4 (strain HS) | wrbA | 20832,41992 | 5,59 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. | 23 |
| 35 | Q8X4B4 | Putative flavoprotein | *E. coli* O157:H7 | wrbA | 20821,41992 | 5,91 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. | 27 |
| 35 | Q8XD48 | Adenine phosphoribosyltransferase | *E. coli* O157:H7 | apt | 19859,65039 | 5,26 | 99 | Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than *de novo* synthesis. | 27, 91 |
| 35 | P07110 | Outer membrane usher protein | *E. coli* | papC | 91452,39063 | 6,2 | 84 | Involved in the export and assembly of pili subunits across the outer membrane. Forms a hexameric ring-shaped pore in the outer bacterial membrane. The 2 nanometer-diameter pore allows the passage of the thin tip fibrillum. As for the rod, it probably unwinds into linear fibers which would therefore be narrow enough to pass through the pore. | 98 |
| 36 | P0A860 | Triosephosphate isomerase | *E. coli* O157:H7 | tpiA | 26954,82031 | 5,64 | 100 | Plays an important role in several metabolic pathways. | 27, 91 |
| 36 | A8A3P3 | Phosphoadenosine phosphosulfate reductase | *E. coli* O9:H4 (strain HS) | cysH | 27974,46094 | 5,51 | 100 | Reduction of activated sulfate into sulfite. | 23 |
| 37 | P0A910 | Outer membrane protein A | *E. coli* (strain K12) | ompA | 37177,66016 | 5,99 | 100 | Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. | 27, 28, 49, 50 |
| 38 | A7ZMK7 | NH(3)-dependent NAD(+) synthetase | *E. coli* O139:H28 (strain E24377A / ETEC) | nadE | 30618,76953 | 5,3 | 100 | Involved in cofactor biosynthesis. | 23 |
| 38 | B1IPJ0 | NH(3)-dependent NAD(+) synthetase | *E. coli* (strain ATCC 8739 / DSM 1576 / Crooks) | nadE | 30617,78906 | 5,41 | 100 | Involved in cofactor biosynthesis. | 22 |
| 38 | Q8FH06 | NH(3)-dependent NAD(+) synthetase | *E. coli* O6 | nadE | 30633,75 | 5,3 | 100 | Involved in cofactor biosynthesis. | 26 |
| 38 | Q1RB54 | NH(3)-dependent NAD(+) synthetase | *E. coli* (strain UTI89 / UPEC) | nadE | 30661,7793 | 5,3 | 100 | Involved in cofactor biosynthesis. | 93 |
| 38 | Q8XDZ9 | NH(3)-dependent NAD(+) synthetase | *E. coli* O157:H7 | nadE | 30664,73047 | 5,41 | 100 | Involved in cofactor biosynthesis. | 27, 91 |
| 39 | P0A819 | S-adenosylmethionine synthetase | *E. coli* O157:H7 | metK | 41925,19922 | 5,1 | 100 | Catalyzes the formation of S-adenosylmethionine fom methionine and ATP. The overall synthetic reaction is composed of two sequencial steps, AdoMet formation and the subsequent tripolyphosphate hydrolysis which occurs prior to release of AdoMet from the enzyme. | 27, 91 |
| 40 | P0A6Z0 | Chaperone protein | *E. coli* O157:H7 | dnaK | 69072,47656 | 4,83 | 100 | Essential role in the initiation of phage lambda DNA replication and is involved in chromosomal DNA replication. | 27, 91 |
| 41 | P0ABD6 | Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | *E. coli* O157:H7 | accA | 35219,30078 | 5,76 | 100 | Component of the acetyl coenzyme A carboxylase (ACC) complex. First, biotin carboxylase catalyzes the carboxylaton of biotin on its carrier protein (BCCP) and then the CO(2) group is transferred by the carboxyltransferase to acetyl-coA to form malonyl-coA. | 27, 91 |
| 41 | Q1RG04 | Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | *E. coli* (strain UTI89 / UPEC) | accA | 35249,30859 | 5,76 | 100 | Component of the acetyl coenzyme A carboxylase (ACC) complex. First, biotin carboxylase catalyzes the carboxylaton of biotin on its carrier protein (BCCP) and then the CO(2) group is transferred by the carboxyltransferase to acetyl-coA to form malonyl-coA. | 93 |
| 42 | P26646 | Putative quinone oxidoreductase yhdH | *E. coli* (strain K12) | yhdH | 34701,89063 | 5,63 | 100 |  | 21, 28 |
| 43 | P0ADS6 | Uncharacterized protein yggE | *E. coli* (strain K12) | yggE | 26618,7793 | 6,1 | 100 |  | 21, 28, 48 |
| 44 | P0A9I1 | Citrate lyase subunit beta | *E. coli* (strain K12) | citE | 33089,25 | 5,54 | 100 | Represents a citryl-ACP lyase. | 21, 28, 94 |
| 45 | A1AD04 | Cytidine deaminase | *E. coli* O1:K1 / APEC | cdd | 31546,91992 | 5,42 | 100 | This enzyme scavenge exogenous and endogenous cytidine and 2’-deoxycytidine for UMP synthesis. | 96 |
| 45 | Q8X648 | Cytidine deaminase | *E. coli* O157:H7 | cdd | 31520,90039 | 5,42 | 100 | This enzyme scavenge exogenous and endogenous cytidine and 2’-deoxycytidine for UMP synthesis. | 91 |
| 45 | B1IYC6 | Cytidine deaminase | *E. coli* (strain ATCC 8739 / DSM 1576 / Crooks) | cdd | 31549,91992 | 5,42 | 100 | This enzyme scavenge exogenous and endogenous cytidine and 2’-deoxycytidine for UMP synthesis. | 22 |
| 45 | A7ZNW5 | Cytidine deaminase | *E. coli* O139:H28 (strain E24377A / ETEC) | cdd | 31505,85938 | 5,29 | 100 | This enzyme scavenge exogenous and endogenous cytidine and 2’-deoxycytidine for UMP synthesis. | 23 |
| 45 | P39172 | High-affinity zinc uptake system protein | *E. coli* (strain K12) | znuA | 33756,19922 | 5,61 | 100 | Involved in the high-affinity zinc uptake transport system. | 21, 28 |
| 47 | P09127 | Putative uroporphyrinogen-III C-methyltransferase | *E. coli* (strain K12) | hemX | 42936,91016 | 4,68 | 100 | Involved in th biosynthesis of cofactors and adenosylcobalamin. | 21, 28 |
| 47 | A7ZYV7 | Flavoprotein | *E. coli* O9:H4 (strain HS) | wrbA | 20832,41992 | 5,59 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. | 23 |
| 48 | Q1RFA0 | Trigger factor | *E. coli* (strain UTI89 / UPEC) | tig | 47835,71094 | 4,83 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 93 |
| 49 | A7ZV12 | 60 kDa chaperonin | *E. coli* O139:H28 (strain E24377A / ETEC) | groL | 57292,67969 | 4,85 | 100 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. | 23 |
| 50 | A7ZMN3 | Selenide, water dikinase | *E. coli* O139:H28 (strain E24377A / ETEC) | selD | 36679,69141 | 5,29 | 100 | Synthesizes selenophosphate from selenide and ATP. | 23 |
| 50 | A8A0V7 | Selenide, water dikinase | *E. coli* O9:H4 (strain HS) | selD | 36663,69922 | 5,3 | 100 | Synthesizes selenophosphate from selenide and ATP. | 23 |
| 50 | P06998 | 6-phosphofructokinase isozyme 1 | *E. coli* (strain K12) | pfkA | 34819,69922 | 5,47 | 100 | Key control step of glycolysis. | 27, 53 |
| 50 | Q8FBD0 | 6-phosphofructokinase isozyme 1 | *E. coli* O6 | pfkA | 34833,71094 | 5,48 | 100 | Key control step of glycolysis. | 26 |
| 51 | A8A466 | Phosphoglycerate kinase | *E. coli* O9:H4 (strain HS) | pgk | 41078,62109 | 5,08 | 100 | Participates in the second step of the second phase of glycolysis. | 23 |
| 51 | Q8XD03 | Phosphoglycerate kinase | *E. coli* O157:H7 | pgk | 41104,67188 | 5,08 | 100 | Participates in the second step of the second phase of glycolysis. | 27, 91 |
| 52 | A8A466 | Phosphoglycerate kinase | *E. coli* O9:H4 (strain HS) | pgk | 41078,62109 | 5,08 | 100 | Participates in the second step of the second phase of glycolysis. | 23 |
| 52 | Q8XD03 | Phosphoglycerate kinase | *E. coli* O157:H7 | pgk | 41104,67188 | 5,08 | 100 | Participates in the second step of the second phase of glycolysis. | 27, 91 |
| 53 | P0AF08 | *Mrp* Protein | *E. coli* (strain K12) | mrp | 39912,53125 | 5,85 | 100 |  | 26, 28, 89 |
| 53 | P62622 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | *E. coli* O157:H7 | ispG | 40658,37109 | 5,87 | 100 | Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2, 4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate. | 21, 28 |
| 53 | A8A321 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | *E. coli* O9:H4 (strain HS) | ispG | 40686,41016 | 6,06 | 99 | Converts 2C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2, 4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate. | 23 |
| 55 | A8A5E6 | Elongation factor Tu 1 | *E. coli* O9:H4 (strain HS) | tuf1 | 43256,30859 | 5,3 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 55 | A7ZUJ2 | Elongation factor Tu 2 | *E. coli* O139:H28 (strain E24377A / ETEC) | tuf2 | 43285,33984 | 5,36 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 56 | P0ABK5 | Cysteine synthase A | *E. coli* (strain k12) | cysK | 34468,30078 | 5,83 | 100 | Cysteine biosynthesis | 21, 28, 60 |
| 57 | P0AB71 | Fructose-bisphosphate aldolase class 2 | *E. coli* (strain K12) | fbaA | 39122,60938 | 5,52 | 100 | Catalyzes the aldol condensation of dihydroxyacetone phosphate (DHAP or glycerone-phosphate) with glyceraldehydes 3-phosphate (G3P) to form fructose 1,6-biphosphate (FBP) in gluconeogenesis and the reverse reaction in glycolysis. | 21, 28 |
| 58 | A8A5E6 | Elongation factor Tu 1 | *E. coli* O9:H4 (strain HS) | tuf1 | 43256,30859 | 5,3 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 58 | A7ZUJ2 | Elongation factor Tu 2 | *E. coli* O139:H28 (strain E24377A / ETEC) | tuf2 | 43285,33984 | 5,36 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 59 | P0A991 | Fructose-bisphosphate aldolase class 1 | *E. coli* (strain K12) | fbaB | 38085,17188 | 6,25 | 98 | Involved in the convertion of D-fructose 1,6-biphosphate in glycerone phosphate and D-glyceraldehyde 3-phosphate. | 21, 28 |
| 60 | Q7AFV7 | Curved DNA-binding protein | *E. coli* O157:H7 | cbpA | 34367,69922 | 6,27 | 100 | DNA-binding protein that preferentially recognizes a curved DNA sequence. It is probably a functional analog of *dnaJ*; displays overlapping activities with *dnaJ*, but functions under different conditions, probably acting as a molecular chaperone in an adaptive response to environmental stresses other than heat shock. | 27 |
| 61 | P77395 | Uncharacterized protein ybbN | *E. coli* (strain K12) | ybbN | 31771,33984 | 4,5 | 100 |  | 21, 28 |
| 62 | P25715 | Malonyl CoA-acyl carrier protein transacylase | *E. coli* (strain K12) | fabD | 32396,39063 | 4,95 | 100 | Fatty acid biosynthesis. | 26, 28, 74 |
| 62 | FABD\_ECO57 | Malonyl CoA-acyl carrier protein transacylase | *E. coli* O157:H7 | fabD | 32391,36914 | 5,02 | 100 | Fatty acid biosynthesis. |  |
| 63 | P63286 | Chaperone protein *clpB* | *E. coli* O6 | clpB | 95525,92969 | 5,37 | 100 | Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with *dnaK*, *dnaJ* and *grpE*. Acts before *dnaK*, in the processing of protein aggregates. Protein binding stimulates the ATPase activity; ATP hydrolysis unfolds the denatured protein aggregates, which probably helps expose new hydrophobic binding sites on the surface of *clpB*-bound aggregates, contributing to the solubilization and refolding of denatured protein aggregates by *dnaK*. | 26, 27, 71 |
| 64 | P35340 | Alkyl hydroperoxide reductase subunit F | *E. coli* (strain K12) | ahpF | 56142,08984 | 5,47 | 100 | Serves to protect the cell against DNA damage by alkyl hydroperoxides. It can use either NADH or NADPH as electron donor for direct reduction of redox dyes or of alkyl hydroperoxides when combined with the ahpC protein. | 21, 28, 94 |
| 65 | P35340 | Alkyl hydroperoxide reductase subunit F | *E. coli* (strain K12) | ahpF | 56142,08984 | 5,47 | 100 | Serves to protect the cell against DNA damage by alkyl hydroperoxides. It can use either NADH or NADPH as electron donor for direct reduction of redox dyes or of alkyl hydroperoxides when combined with the ahpC protein. | 21, 28, 94 |
| 66 | A7ZV12 | 60 kDa chaperonin | *E. coli* O139:H28 (strain E24377A / ETEC) | groL | 57292,67969 | 4,85 | 100 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. | 23 |
| 69 | Q8FHG5 | Glutamate decarboxylase beta | *E. coli* O6 | gadB | 52619,16016 | 5,35 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 26 |
| 69 | P69908 | Glutamate decarboxylase alpha | *E. coli* (strain k12) | gadA | 52651,14844 | 5,22 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 21, 28 |
| 69 | P69910 | Glutamate decarboxylase beta | *E. coli* (strain K12) | gadB | 52634,14844 | 5,29 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 21, 28 |
| 69 | P58228 | Glutamate decarboxylase alpha | *E. coli* O157:H7 | gadA | 52665,16016 | 5,23 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 27, 91 |
| 69 | P14081 | Selenocysteine-specific elongation factor | *E. coli* (strain K12) | selB | 68824,64844 | 6,11 | 96 | Translation factornecessary for the incorporation os selenocysteine into proteins. It probably replaces EF-Tu for the insertion of selenocysteine directed by the UGA codon. SelB binds GTP and GDP. | 21, 28 |
| 70 | Q8FHG5 | Glutamate decarboxylase beta | *E. coli* O6 | gadB | 52619,16016 | 5,35 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 26 |
| 70 | P69908 | Glutamate decarboxylase alpha | *E. coli* (strain k12) | gadA | 52651,14844 | 5,22 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 21, 28 |
| 70 | P69910 | Glutamate decarboxylase beta | *E. coli* (strain K12) | gadB | 52634,14844 | 5,29 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 21, 28 |
| 70 | P58228 | Glutamate decarboxylase alpha | *E. coli* O157:H7 | gadA | 52665,16016 | 5,23 | 100 | Converts glutamate to gamma-aminobutyrate (GABA), consuming one intracellular proton in the reaction. The gad system helps to maintain a near-neutral intracellularpH when cells are exposed to extremely acidic conditions. The ability to survive transit through the acidic conditions of the stomach is essential for successful colonization of the mammalian host by commensal and pathogenic bacteria. | 27, 91 |
| 70 | P14081 | Selenocysteine-specific elongation factor | *E. coli* (strain K12) | selB | 68824,64844 | 6,11 | 98 | Translation factornecessary for the incorporation os selenocysteine into proteins. It probably replaces EF-Tu for the insertion of selenocysteine directed by the UGA codon. SelB binds GTP and GDP. | 21, 28 |
| 71 | P0ABZ7 | Chaperone protein *surA* | *E. coli* O6 | surA | 47254,26172 | 6,48 | 100 | Chaperone involved in the folding of extracytoplasmic proteins. Required for the efficient folding of *ompA*, *ompF* and *lamB*. Essential for the survival of *E. coli* in stationary phase. | 26 |
| 72 | A8A5E6 | Elongation factor Tu 1 | *E. coli* O9:H4 (strain HS) | tuf1 | 43256,30859 | 5,3 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 72 | Q1RFA0 | Trigger factor | *E. coli* (strain UTI89 / UPEC) | tig | 47835,71094 | 4,83 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 93 |
| 72 | A7ZX94 | Trigger factor | *E. coli* O9:H4 (strain HS) | tig | 48162,85938 | 4,83 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 23 |
| 72 | A7ZUJ2 | Elongation factor Tu 2 | *E. coli* O139:H28 (strain E24377A / ETEC) | tuf2 | 43285,33984 | 5,36 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 72 | A7ZIJ4 | Trigger factor | *E. coli* O139:H28 (strain E24377A / ETEC) | tig | 48148,85156 | 4,82 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 23 |
| 73 | P09373 | Formate acetyltransferase 1 | *E. coli* (strain K12) | pflB | 85302,72656 | 5,69 | 100 | Involved in the fermentation of pyruvate. | 28, 21, 67 |
| 73 | Q8X9M3 | Polyribonucleotide nucleotidyltransferase | *E. coli* O157:H7 | pnp | 77053,96875 | 5,09 | 100 | Involved in mRNA degradation. Hydrolyzes single-stranded polyribonucleotides processively in the 3’- to 5’-direction. | 27, 91 |
| 74 | P40681 | Aldose 1-epimerase | *E. coli* (strain K12) | galM | 38166,76953 | 4,84 | 100 | Mutarotase converts alpha-aldose to the beta-anomer. It is active on D-glucose, L-arabinose, D-xylose, D-galactose, maltose and lactose. | 28, 86 |
| 75 | P69442 | Adenylate kinase | *E. coli* O157:H7 | adk | 23571,2793 | 5,55 | 100 | Catalyzes the reversible transfer of the terminal phosphate group between ATP and AMP. This small ubiquitous enzyme involved in the energy metabolism and nucleotide synthesis, is essential for maintenance and cell growth. | 27, 91 |
| 76 | A8A5E6 | Elongation factor Tu 1 | *E. coli* O9:H4 (strain HS) | tuf1 | 43256,30859 | 5,3 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 76 | A7ZUJ2 | Elongation factor Tu 2 | *E. coli* O139:H28 (strain E24377A / ETEC) | tuf2 | 43285,33984 | 5,36 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 23 |
| 77 | P0ABU2 | GTP-dependent nucleic acid-binding protein | *E. coli* (strain K12) | engD | 39642,26953 | 4,87 | 100 | GTP-dependent nucleic acid-binding protein which may act as a translation factor. | 21, 28 |
| 80 | P0A6Q1 | Enolase | *E. coli* O157:H7 | eno | 45626,42188 | 5,32 | 100 | Catalyzes the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. It is essential for the degradation of carbohydrates via glycolysis. It is also a component of the RNA degradosome, a multi-enzyme complex involved in RNA processing and messenger RNA degradation. | 27, 91 |
| 81 | A7ZV12 | 60 kDa chaperonin | *E. coli* O139:H28 (strain E24377A / ETEC) | groL | 57292,67969 | 4,85 | 100 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. | 23 |
| 81 | Q0T9P8 | 60 kDa chaperonin | *E. coli* O6:K15:H31 (strain 536 / UPEC) | groL | 57292,67969 | 4,85 | 100 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. | 92 |