Table 1. Protein spots identification of 2-DE gels and MALDI-TOF sequencing results from *E. coli* isolate C583

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Spot*** | ***Accession Number*** | ***Protein Description*** | ***Species*** | ***Protein name*** | ***Protein MW*** | ***Protein PI*** | ***Protein Score Confidence Interval (%)*** | ***Information*** | ***References*** |
| 1 | P0A9L0 | FKBP-type peptidyl-prolyl cis-trans isomerase | *E. coli* O6 | slyD | 20839,69922 | 4,86 | 96 | 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 |
| 2 | 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 |
| 2 | A7ZVV7 | Chaperone protein | *E. coli* O9:H4 (strain HS) | dnaK | 69088,47656 | 4,83 | 100 | Essential role in the initiation of phage lambda DNA replication and is involved in chromosomal DNA replication. | 23 |
| 3 | P0AG68 | 30S ribosomal protein S1 | *E. coli* O6 | rpsA | 61120,71094 | 4,89 | 100 | Binds mRNA, thus facilitating recognition of the initiation point. It is needed to translate mRNA with a short Shine-Dalgarno (SD) purine-rich sequence. | 26 |
| 4 | 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 |
| 4 | 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 |
| 5 | 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 |
| 5 | 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 |
| 5 | 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 |
| 5 | 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 |
| 5 | 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 |
| 6 | 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 |
| 6 | 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 |
| 7 | P0ABB6 | ATP synthase subunit beta | *E. coli* O157:H7 | atpD | 50293,82813 | 4,9 | 100 | Produces ATP from ADP in the presence of a proton gradient across the membrane. The catalytic sites are hosted primarily by the beta subunits. | 27, 91 |
| 8 | 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 |
| 8 | 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 |
| 9 | 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 |
| 11 | P61891 | Malate dehydrogenase | *E. coli* O157:H7 | mdh | 32317,21094 | 5,61 | 100 | Catalyzes the reversible oxidation of malate to oxaloacetate. | 26, 27, 92 |
| 11 | B1IQP3 | Malate dehydrogenase | *E. coli* (strain ATCC 8739 / DSM 1576 / Crooks) | mdh | 32307,18945 | 5,61 | 100 | Catalyzes the reversible oxidation of malate to oxaloacetate. | 22 |
| 11 | P0A9I1 | Citrate lyase subunit beta | *E. coli* (strain K12) | citE | 33089,25 | 5,54 | 100 | Represents a citryl-ACP lyase. | 21, 28, 95 |
| 12 | P0A6P3 | Elongation factor Ts | *E. coli* O157:H7 | tsf | 30403,7793 | 5,22 | 100 | Associates with the EF-Tu.GDP complex and induces the exchange of GDP to GTP. It remains bound to the aminoacyl-tRNA.EF-Tu.GTP complex up to the GTP hydrolysis stage on the ribosome. | 27, 91 |
| 13 | P0AE09 | Alkyl hydroperoxide reductase subunit C | *E. coli* O6 | ahpC | 20748,41016 | 5,03 | 100 | Directly reduces organic hydroperoxides in its reduced dithiol form. | 26 |
| 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 | 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 |
| 14 | P09372 | *GrpE* Protein | *E. coli* (strain K12) | grpE | 21784,16016 | 4,68 | 95 | 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. | 21, 28, 77 |
| 15 | Q7ABI1 | *GrpE* Protein | *E. coli* O157:H7 | 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. | 27, 91 |
| 15 | 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. | 21, 28, 77 |
| 16 | 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. | 28, 91 |
| 16 | P0AGE6 | Uncharacterized protein | *E. coli* (strain K12) | yieF | 20362,59961 | 5,01 | 97 |  | 21, 28 |
| 17 | P62593 | Beta-lactamase TEM | *E. coli* | bla | 31495,18945 | 5,69 | 100 | TEM-type are the most prevalent beta-lactamases in enterobacteria; they hydrolyze the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillins and cephalosporins. | 36, 37 |
| 18 | P0A860 | Triosephosphate isomerase | *E. coli* O157:H7 | tpiA | 26954,82031 | 5,64 | 100 | Plays an important role in several metabolic pathways. | 27, 91 |
| 18 | A7ZY11 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase | *E. coli* O9:H4 (strain HS) | gmpA | 28538,75 | 5,85 | 98 | Catalyzes the interconversion of 2-phosphoglycerate and 3-phosphoglycerate. | 23 |
| 18 | A7ZJD0 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase | *E. coli* O139:H28 (strain E24377A / ETEC) | gmpA | 28570,73047 | 5,85 | 98 | Catalyzes the interconversion of 2-phosphoglycerate and 3-phosphoglycerate. | 23 |
| 18 | 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 |
| 19 | Q8FHD2 | NADP-dependent L-serine/L-allo-threonine dehydrogenase | *E. coli* O6 | ydfG | 27229,81055 | 5,65 | 100 | Catalyzes the NADP-dependent oxidation of L-allo-threonine and L-serine | 26 |
| 20 | P0ABK5 | Cysteine synthase A | *E. coli* (strain k12) | cysK | 34468,30078 | 5,83 | 100 | Cysteine biosynthesis | 21, 28, 60 |
| 21 | 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 |
| 23 | P14407 | Fumarate hydratase class I, anaerobic | *E. coli* (strain k12) | fumB | 60067,35938 | 5,88 | 100 | It functions in the generation of fumarate for use as na anaerobic electron acceptor. | 21, 28 |
| 23 | P0AC34 | Fumarate hydratase class I, aerobic | *E. coli* O6 | fumA | 60260,57031 | 6,11 | 92 | It functions as an aerobic enzyme in the citric acid cycle. It accounts for about 80% of the fumarase activity when the bacteria grows aerobically. | 26 |
| 24 | P0AEE5 | D-galactose-binding periplasmic protein | *E. coli* (strain k12) | mglB | 35690,37109 | 5,68 | 100 | This protein is involved in the active transport of galactose and glucose. It plays a role in the chemotaxis towards the two sugars by interacting with the trg chemoreceptor. | 21, 28 |
| 25 | P0ABZ7 | Chaperone surA | *E. coli* O6 | surA | 47254,26172 | 6,48 | 99 | 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 |
| 26 | Q8XA55 | Serine hydroxymethyltransferase | *E. coli* O157:H7 | glyA | 45316 | 6,03 | 90 | Interconversion of serine and glycine. | 27, 91 |
| 27 | P63286 | Chaperone protein | *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 |
| 27 | P09373 | Formate acetyltransferase 1 | *E. coli* (strain k12) | pflB | 85302,72656 | 5,69 | 95 | Involved in the fermentation of pyruvate. | 21, 28, 67 |
| 27 | P17909 | Protein traJ | *E. coli* | traJ | 13455,15039 | 7,82 | 93 | Involved in the transference of plasmid RP4 during bacterial conjugation requires the plasmid-encoded traJ protein, which binds to a 19-base pair invert sequence repetition within the transfer origin. TraJ protein is bound to only one side of the DNA helix. This nucleoprotein structure is the initial complex in the pathway to assemble a functional relaxosome. | 95 |
| 28 | A7ZWE2 | Prolyl-tRNA synthetase | *E. coli* O9:H4 (strain HS) | Syp | 63582,66016 | 5,08 | 100 | Catalyzes the attachment of proline to tRNA(Pro) in a two-step reaction: proline is first activated by ATP to form Pro-AMP and then transferred to the acceptor end of tRNA(Pro). | 23 |
| 28 | Q8X8W2 | Prolyl-tRNA synthetase | *E. coli* O157:H7 | Syp | 63611,73047 | 5,16 | 100 | Catalyzes the attachment of proline to tRNA(Pro) in a two-step reaction: proline is first activated by ATP to form Pro-AMP and then transferred to the acceptor end of tRNA(Pro). | 27, 91 |
| 28 | Q0TLD7 | Prolyl-tRNA synthetase | *E. coli* O6:K15:H31 (strain 536 / UPEC) | Syp | 63562,69922 | 5,08 | 100 | Catalyzes the attachment of proline to tRNA(Pro) in a two-step reaction: proline is first activated by ATP to form Pro-AMP and then transferred to the acceptor end of tRNA(Pro). | 93 |
| 28 | P16659 | Prolyl-tRNA synthetase | *E. coli* (strain k12) | Syp | 63652,69141 | 5,12 | 100 | Catalyzes the attachment of proline to tRNA(Pro) in a two-step reaction: proline is first activated by ATP to form Pro-AMP and then transferred to the acceptor end of tRNA(Pro). | 21, 28, 79 |
| 31 | P62593 | Beta-lactamase TEM | *E. coli* | bla | 31495,18945 | 5,69 | 100 | TEM-type are the most prevalent beta-lactamases in enterobacteria; they hydrolyze the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillins and cephalosporins. | 36, 37 |
| 31 | Q8FHD2 | NADP-dependent L-serine/L-allo-threonine dehydrogenase | *E. coli* O6 | ydfG | 27229,81055 | 5,65 | 100 | Catalyzes the NADP-dependent oxidation of L-allo-threonine and L-serine | 26 |
| 32 | P0ADG7 | Inosine-5'-monophosphate dehydrogenase | *E. coli* (strain k12) | guaB | 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 |
| 33 | 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 |
| 35 | Q8X926 | 6-phosphogluconolactonase | *E. coli* O157:H7 | pgl | 36367,94922 | 5,13 | 100 | Catalyzes the hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate. | 27, 91 |
| 35 | Q8FJR2 | 6-phosphogluconolactonase | *E. coli* O6 | pgl | 36285,85156 | 5,01 | 100 | Catalyzes the hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate. | 26 |
| 36 | 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 |
| 37 | P0AAX9 | Uncharacterized protein | *E. coli* O6 | ybiS | 33304,17188 | 5,99 | 98 |  | 26 |
| 38 | 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 |
| 38 | 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 |
| 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 | P06996 | Outer membrane protein C | *E. coli* (strain k12) | ompC | 40343,37109 | 4,58 | 100 | Forms passive diffusion pores which allow small molecular weight hydrophilic materials across the outer membrane. | 21, 28, 59 |
| 42 | P69811 | Multiphosphoryl transfer protein | *E. coli* (strain k12) | fruB | 39623,51953 | 4,77 | 98 | The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate actve-transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane. This system is involved in fructose transport. | 21, 28 |
| 44 | P0A7Z6 | DNA-directed RNA polymerase subunit alpha | *E. coli* O157:H7 | rpoA | 36489,14844 | 4,98 | 100 | DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. | 27, 91 |
| 44 | 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 |
| 44 | 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 |
| 45 | 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 |
| 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 |
| 46 | 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 |
| 46 | 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 |
| 48 | P77395 | Uncharacterized protein | *E. coli* (strain k12) | ybbN | 31771,33984 | 4,5 | 100 |  | 21, 28 |
| 49 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 52 | 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 |
| 53 | P0A9C6 | Glutamine synthetase | *E. coli* O6 | glnA | 51870,73047 | 5,26 | 100 | In involved in the interconversion of L-glutamate and L-glutamine. | 26 |
| 57 | P0A6R2 | 3-oxoacyl-[acyl-carrier-protein] synthase 3 | *E. coli* O157:H7 | fabH | 33493,98047 | 5,08 | 100 | Catalyzes the condensation reaction of fatty acid synthesis by the addition to an acyl acceptor of two carbons from malonyl-ACP. Catalyzes the first condensation reaction which initiates fatty acid synthesis and may therefore play a role in governing the total rate of fatty acid production. | 27, 91 |
| 57 | B1IUH4 | 3-oxoacyl-[acyl-carrier-protein] synthase 3 | *E. coli* (strain ATCC 8739 / DSM 1576 / Crooks) | fabH | 33524,98828 | 5,08 | 100 | Catalyzes the condensation reaction of fatty acid synthesis by the addition to an acyl acceptor of two carbons from malonyl-ACP. Catalyzes the first condensation reaction which initiates fatty acid synthesis and may therefore play a role in governing the total rate of fatty acid production. | 22 |
| 57 | P0A6P3 | Elongation factor Ts | *E. coli* O157:H7 | tsf | 30403,7793 | 5,22 | 100 | Associates with the EF-Tu.GDP complex and induces the exchange of GDP to GTP. It remains bound to the aminoacyl-tRNA.EF-Tu.GTP complex up to the GTP hydrolysis stage on the ribosome. | 27, 91 |
| 58 | 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 |
| 59 | P39377 | Isoaspartyl dipeptidase | *E. coli* (strain k12) | iadA | 41058,23047 | 5,08 | 98 | Catalyzes the hydrolytic cleavage of a subset of L-isoaspartyl (L-beta-aspartyl) dipeptides. Used to degrade proteins damaged by L-isoaspartyl residues formation. The best substrate for the enzyme reported thus far is iso-Asp-Leu. | 21, 28, 75 |
| 60 | P0AEX9 | Maltose-binding periplasmic protein | *E. coli* (strain k12) | malE | 43360,37891 | 5,53 | 100 | Involved in the high-affinity maltose membrane transport system malEFGK. Initial receptor for the active transport of and chemotaxis toward maltooligosaccharides. | 21, 28, 97 |
| 62 | P0AEU1 | Histidine-binding periplasmic protein | *E. coli* O6 | hisJ | 28465,65039 | 5,47 | 98 | Component of the high-affinity histidine permease, a binding-protein-dependent transport system. The other components are proteins hisQ, hisM, and hisP. | 26 |
| 63 | 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 |
| 63 | 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 |
| 64 | P0AF13 | 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase | *E. coli* O6 | mtnN | 24338,57031 | 5,09 | 100 | Catalyzes the irreversible cleavage of the glycosidic bond in both 5’-methylthioadenosine (MTA) and S-adenosylhomocysteine (SAH/AdoHcy) to adenine and the corresponding thioribose, 5’-methylthioribose and S-ribosylhomocysteine, respectively. | 26 |