Table 1. Protein spots identification of 2-DE gels and MALDI-TOF sequencing results from *E. coli* isolate GV5

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| ***Sample*** | ***Accession Number*** | ***Protein description*** | ***Species*** | ***Protein Name*** | ***Protein MW*** | ***Protein PI*** | ***Protein Score Confidence Interval (%)*** | ***Information*** | ***References*** |
| 1 | P04475 | Chaperone protein | *E. coli* | DnaK | 68941,4375 | 4,83 | 100 | Essential role in the initiation of phage lambda DNA replication and is involved in chromosomal DNA replication. | 26, 27, 39, 40, 41, 43, 44 |
| 2 | P02349 | 30S Ribosomal protein S1 | *E. coli* | Rs1 | 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, 27, 43, 45, 46 |
| 3 | P06139 | 60 kDa Chaperonin protein | *E. coli* | Ch60 | 57161,64063 | 4,85 | 100 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. Essential for bacteria growth and the assembly of several bacteriophages. | 26, 27, 47 |
| 4 | P22257 | Trigger factor | *E. coli* | Tig | 48162,85938 | 4,83 | 100 | Involved in protein export. Acts as a chaperone by maintaining the newly synthesized protein in an open conformation. | 27, 28, 48 |
| 4 | Q8FKA7 | Trigger factor | *E. coli* O6 | Tig (EcoO6) | 48220,87109 | 4,81 | 100 | 26 |
| 5 | P11665 | Phosphoglycerate kinase | *E. coli* | PgK | 40961,58984 | 5,08 | 100 | Participates in the second step of the second phase of glycolysis. | 26, 28, 49 |
| 6 | P02934 | Outer membrane protein A | *E. coli* | 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, 50, 51 |
| 7 | P02997 | Elongation factor Ts | *E. coli* | Efts | 30272,74023 | 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. | 26, 27, 28, 52 |
| 8 | P04790 | Triosephosphate isomerase | *E. coli* | TpiS | 26954,82031 | 5,64 | 100 | Plays an important role in several metabolic pathways | 26, 27, 53, 54 |
| 8 | P78218 | Dihydrofolate reductase type XV | *E. coli* | Dyr15 | 17491,98047 | 5,56 | 96 | 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. | 55 |
| 9 | P02351 | 30S Ribosomal protein S2 | *E. coli* | Rs2 | 26595,75977 | 6,69 | 100 | Part of the 30S ribosomal subunit. Some nascent polypeptide chains are able to cross-link to this protein *in situ*. | 26, 27, 28, 56 |
| 10 | P06977 | Glyceraldehyde-3-phosphate dehydrogenase A | *E. coli* | G3p1 | 35379,19922 | 6,58 | 100 | Participates in the first step of the second phase of glycolysis. | 26, 27, 28, 57 |
| 11 | P15046 | Acetate kinase | *E. coli* | 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, 27, 28, 58 |
| 12 | P08324 | Enolase | *E. coli* | Eno | 45495,37891 | 5,32 | 100 | Also involved in the RNA degradosome, a multi-enzyme complex important in RNA processing and messenger RNA degradation. | 26, 27,28 |
| 14 | P04949 | Flagellin | *E. coli* | FliC | 51133,53125 | 4,5 | 100 | Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella. | 28, 38 |
| 15 | P00824 | ATP synthase β-chain | *E. coli* | AtpB | 50162,78906 | 4,9 | 100 | Produces ATP from ADP in the presence of a proton gradient across the membrane. The β-chain is the catalytic subunit. | 26, 27, 59 |
| 16 | P06981 | Inosine-5'-monophosphate dehydrogenase | *E. coli* | ImdH | 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. | 26, 28, 60 |
| 17 | P11096 | Cysteine synthase A | *E. coli* | CysK | 34337,26172 | 5,83 | 100 | Cysteine biosynthesis | 26, 27, 61, 62 |
| 18 | Q8FJ50 | Curved DNA-binding protein | *E. coli* O6 | CbpA (EcoO6) | 34463,73047 | 6,33 | 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. | 26 |
| 18 | P36659 | Curved DNA-binding protein | *E. coli* | CbpA | 34433,71875 | 6,33 | 100 | 28, 38, 63 |
| 18 | Q7AFV7 | Curved DNA-binding protein | *E. coli* O157:H7 | CbpA (EcoO57) | 34367,69922 | 6,27 | 100 | 27 |
| 19 | P12758 | Uridine phosphorylase | *E. coli* | Udp | 27010,80078 | 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. | 28, 38, 61, 64 |
| 20 | P00574 | DNA-directed RNA polymerase α-chain | *E. coli* | RpoA | 36489,14844 | 4,98 | 100 | DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. This subunit plays an important role in subunit assembly since its dimerization is the first step in the sequential assembly of subunits to form the holoenzyme. | 26, 27, 28 |
| 22 | P00391 | Dihydrolipoyl dehydrogenase | *E. coli* | DldH | 50525,55078 | 5,79 | 100 | Lipoamide dehydrogenase is a component of the glycine cleavage system as well as of the α-ketoacid dehydrogenase complexes. | 26, 27, 28 |
| 23 | P00822 | ATP synthase α-chain | *E. coli* | 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. | 26, 27, 65 |
| 24 | P14178 | Pyruvate kinase I | *E. coli* | Kpyk1 | 50697,26172 | 5,77 | 100 | Glycolysis; final step | 27, 28, 66 |
| 25 | P08398 | CTP synthase | *E. coli* | PyrG | 60205,03125 | 5,63 | 100 | Catalyzes the ATP-dependent amination of UTP to CTP with either L-glutamine or ammonia as the source of nitrogen. | 26, 27, 28, 67 |
| 26 | 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. | 28, 38 |
| 27 | P00923 | Fumarate hydratase class I, aerobic | *E. coli* | FumA | 60129,53125 | 6,11 | 100 | 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. | 27, 28 |
| 27 | P14407 | Fumarate hydratase class I, anaerobic | *E. coli* | FumB | 60067,35938 | 5,88 | 100 | It functions in the generation of fumarate for use as an anaerobic electron acceptor. | 28, 38, 68 |
| 28 | P61890 | Malate dehydrogenase | *E. coli* O6 | Mdh (EcoO6) | 32317,21094 | 5,61 | 100 | Catalyzes the reversible oxidation of malate to oxaloacetate. | 27 |
| 29 | P30856 | FKBP-type peptidyl-prolyl cis-trans isomerase | *E. coli* | SlyD | 20839,69922 | 4,86 | 100 | Required for lysis of phiX174 infected cells. Binds nickel and zinc with high affinity and 1:1 stoichiometry, copper and cobalt with lower affinity. No binding detectable for ferrous, ferric, magnesium and calcium ions. | 26, 27, 28, 69 |
| 30 | P39173 | UPF0010 protein | *E. coli* | YeaD | 32645,66016 | 5,89 | 100 |  | 28, 38, 70 |
| 31 | P30849 | Flavoprotein | *E. coli* | WrbA | 20701,38086 | 5,6 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. However, *wrbA* does not specifically influence the affinity or mode of binding of *trpR* to its operator. It seems possible that the association may have a structural, rather than functional, basis. *WrbA* alone does not interact with the operator-bearing DNA; the *trpR/trpO* complex is probably the major target species. The *wrbA* protein may function as an accessory element in blocking *trpR*-specific transcriptional processes. | 27, 28, 71 |
| 31 | Q8X4B4 | Putative Flavoprotein | *E. coli* O157:H7 | WrbA (EcoO57) | 20690,38086 | 5,93 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. | 27 |
| 34 | P33398 | Elongation factor P | *E. coli* | Efp | 20447,38086 | 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. | 26, 27 |
| 34 | P30849 | Flavoprotein | *E. coli* | WrbA | 20701,38086 | 5,6 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. However, *wrbA* does not specifically influence the affinity or mode of binding of *trpR* to its operator. It seems possible that the association may have a structural, rather than functional, basis. *WrbA* alone does not interact with the operator-bearing DNA; the *trpR/trpO* complex is probably the major target species. The *wrbA* protein may function as an accessory element in blocking *trpR*-specific transcriptional processes. | 27, 28, 71 |
| 35 | P63286 | Chaperone *clpB* | *E. coli* O6 | ClpB (EcoO6) | 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, 72 |
| 36 | P09147 | UDP-glucose 4-epimerase | *E. coli* | GalE | 37241,64063 | 5,89 | 100 | Carbohydrate metabolism; galactose metabolism. | 28, 38, 73 |
| 36 | P27297 | BAX protein | *E. coli* | Bax | 30848,03906 | 10,4 | 99 |  | 28, 38, 74 |
| 37 | P25715 | Malonyl CoA-acyl carrier protein transacylase | *E. coli* | FabD | 32265,34961 | 4,95 | 100 | Fatty acid biosynthesis. | 26, 28, 75 |
| 38 | P39377 | Isoaspartyl dipeptidase | *E. coli* | IadA | 41058,23047 | 5,08 | 100 | 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. | 28, 38, 76 |
| 39 | P32665 | Glycerol dehydrogenase | *E. coli* | GldA | 38687,69922 | 4,81 | 100 | Glycerol utilization. | 26, 77 |
| 39 | P62593 | β-lactamase TEM precursor | *E. coli* | BlaT | 31495,18945 | 5,69 | 100 | TEM-type are the most prevalent β-lactamases in enterobacteria; they hydrolyze the β-lactam bond in susceptible β-lactam antibiotics, thus conferring resistance to penicillins and cephalosporins. | 36, 37 |
| 40 | P62593 | β-lactamase TEM precursor | *E. coli* | BlaT | 31495,18945 | 5,69 | 100 | TEM-type are the most prevalent beta-lactamases in enterobacteria; they hydrolyze the β-lactam bond in susceptible β-lactam antibiotics, thus conferring resistance to penicillins and cephalosporins. | 36, 37 |
| 42 | P02990 | Elongation factor Tu | *E. coli* | Eftu | 43155,28125 | 5,3 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 26, 27, 28, 52 |
| 42 | P39173 | UPF0010 protein | *E. coli* | YeaD | 32645,66016 | 5,89 | 98 |  | 28, 38, 70 |
| 42 | Q46856 | Alcohol dehydrogenase | *E. coli* | YqhD | 42070,80078 | 5,72 | 100 | NADP-dependent ADH activity. | 28, 38 |
| 43 | P02990 | Elongation factor Tu | *E. coli* | Eftu | 43155,28125 | 5,3 | 100 | This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. | 26, 27, 28, 52 |
| 45 | P09372 | *GrpE* protein (HSP-70 cofactor) | *E. coli* | 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, 38, 78 |
| 45 | Q8FEY9 | *GrpE* protein (HSP-70 cofactor) | *E. coli* O6 | GrpE (EcoO6) | 21798,17969 | 4,68 | 100 | 26 |
| 46 | P77770 | Citrate lyase β-chain | *E. coli* | CilB | 33089,25 | 5,54 | 100 | Represents a citryl-ACP lyase. | 26, 28 |
| 47 | P13652 | Cytidine deaminase | *E. coli* | Cdd | 31519,91016 | 5,42 | 100 | This enzyme scavenge exogenous and endogenous cytidine and 2'-deoxycytidine for UMP synthesis. | 28, 37, 61 |
| 47 | P39172 | High-affinity zinc uptake system protein | *E. coli* | ZnuA | 33756,19922 | 5,61 | 100 | Involved in the high-affinity zinc uptake transport system.. | 28, 38, 79 |
| 48 | P16659 | Prolyl-tRNA synthetase | *E. coli* | 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). | 28, 38, 80 |
| 49 | P21202 | Chaperone | *E. coli* | 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, 27, 28, 81 |
| 51 | P00477 | Serine hydroxymethyltransferase | *E. coli* | GlyA | 45287,96875 | 6,03 | 100 | Interconversion of serine and glycine. | 26, 28 |
| 51 | Q8XA55 | Serine hydroxymethyltransferase | *E. coli* O157:H7 | GlyA (EcoO57) | 45316 | 6,03 | 100 | Interconversion of serine and glycine. | 27 |
| 53 | P00805 | L-asparaginase II | *E. coli* | AspG2 | 36827,75 | 5,95 | 100 | Important therapeutic enzyme used in the treatmente of leukemia. Catalyzes the conversion of L-asparagine to L-aspartatic acid and ammonia. | 28, 38, 42 |
| 54 | P77770 | Citrate lyase β-chain | *E. coli* | CilB | 33089,25 | 5,54 | 100 | Represents a citryl-ACP lyase. | 26, 28 |
| 55 | P30867 | Acetyl-coenzyme A carboxylase carboxyl transferase subunit α | *E. coli* | AccA | 35088,26172 | 5,76 | 100 | This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA. | 27, 28, 82 |
| 56 | P24223 | Pyridoxal phosphate biosynthetic protein | *E. coli* | Pdxj | 26236,50977 | 5,61 | 100 | Catalyzes the condensation of 1-deoxy-D-xylulose-5-phosphate (DXP) and 1-amino-3 (phosphohydroxy)propan-2-one to form pyridoxine 5'-phosphate (PNP). | 27, 28, 83 |
| 56 | Q8FF18 | Pyridoxine 5'-phosphate synthase | *E. coli* O6 | Pdxj (EcoO6) | 26213,42969 | 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 |
| 57 | P04790 | Triosephosphate isomerase | *E. coli* | Tpis | 26954,82031 | 5,64 | 100 | Plays an important role in several metabolic pathways. | 26, 27, 54 |
| 58 | P03026 | Aerobic respiration control protein | *E. coli* | 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, 27, 84 |
| 59 | P06998 | 6-phosphofructokinase isozyme I | *E. coli* | K6pf1 | 34819,69922 | 5,47 | 97 | Key control step of glycolysis. | 27, 54 |
| 60 | P17579 | 2-dehydro-3-deoxyphosphooctonate aldolase | *E. coli* | KdsA | 30812,91016 | 6,32 | 100 | Synthesis of KDO 8-P which is required for lipid A maturation and cellular growth. | 28, 85 |
| 60 | Q8XDE7 | 2-dehydro-3-deoxyphosphooctonate aldolase | *E. coli* O157:H7 | KdsA (EcoO57) | 30840,91992 | 6,32 | 100 | Bacterial outer membrane biogenesis; lipopolysaccharide biosynthesis. | 27 |
| 61 | P63021 | Protein *gntY* | *E. coli* O6 | GntY (EcoO6) | 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. | 26 |
| 62 | P04475 | Chaperone protein  (Heat shock protein 70) | *E. coli* | DnaK | 68941,4375 | 4,83 | 100 | Plays an essential role in the initiation of phage lambda DNA replication, where it acts in an ATP-dependent fashion with the *dnaJ* protein to release lambda O and P proteins from the preprimosomal complex. *DnaK* is also involved in chromosomal DNA replication. | 26, 27, 39, 40, 41, 43, 44 |
| 63 | P26646 | Protein *yhdH* | *E. coli* | YhdH | 34701,89063 | 5,63 | 100 |  | 28, 38, 82 |
| 64 | P06138 | Cell division protein *ftsZ* | *E. coli* | 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, 27, 28, 86 |
| 65 | P11604 | Fructose-bisphosphate aldolase class II | *E. coli* | Alf | 38991,57031 | 5,52 | 100 | Glycolysis; sixth step. | 26, 27, 49 |
| 66 | P02990 | Elongation factor Tu | *E. coli* | Eftu | 43155,28125 | 5,3 | 100 | May play an important regulatory role in cell growth and in the bacterial response to nutrient deprivation. | 26, 27, 28, 52 |
| 66 | P15046 | Acetate kinase | *E. coli* | 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, 27, 28, 58 |
| 67 | P40681 | Aldose 1-epimerase | *E. coli* | 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, 87 |
| 68 | P06139 | 60 kDa Chaperonin (Protein Cpn60) | *E. coli* | Ch60 | 57161,64063 | 4,85 | 100 | Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. Essential for the growth of the bacteria and the assembly of several bacteriophages. Also plays a role in coupling between replication of the F plasmid and cell division of the cell. | 26, 27, 47 |
| 69 | 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 |
| 71 | P00822 | ATP synthase α-chain | *E. coli* | AtpA | 55187,75 | 5,8 | 97 | Produces ATP from ADP in the presence of a proton gradient across the membrane. The alpha chain is a regulatory subunit. | 26, 41, 65 |
| 71 | P09156 | Seryl-tRNA synthetase | *E. coli* | Sys | 48383,53125 | 5,34 | 100 |  | 26, 27, 28, 88 |
| 72 | P63943 | Dihydrodipicolinate synthase | *E. coli* O6 | DapA (EcoO6) | 31264,11914 | 5,98 | 100 | Amino-acid biosynthesis | 26 |
| 72 | P83842 | ADP-ribose pyrophosphatase | *E. coli* O6 | AdpP (EcoO6) | 23652,10938 | 4,98 | 99 | Acts on ADP-mannose and ADP-glucose as well as ADP-ribose. Prevents glycogen biosynthesis. The reaction catalyzed by this enzyme is a limiting step of the gluconeogenic process. | 26 |
| 73 | P06996 | Outer membrane protein C | *E. coli* | OmpC | 40343,37109 | 4,58 | 99 | Forms passive diffusion pores which allow small molecular weight hydrophilic materials across the outer membrane. | 28, 38, 60 |
| 79 | P30849 | Flavoprotein *wrbA* | *E. coli* | WrbA | 20701,38086 | 5,6 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. However, *wrbA* does not specifically influence the affinity or mode of binding of *trpR* to its operator. It seems possible that the association may have a structural, rather than functional, basis. *WrbA* alone does not interact with the operator-bearing DNA; the *trpR/trpO* complex is probably the major target species. The *wrbA* protein may function as an accessory element in blocking *trpR*-specific transcriptional processes. | 27, 28, 71 |
| 79 | P62593 | β-lactamase TEM precursor | *E. coli* | BlaT | 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 |
| 80 | P30849 | Flavoprotein *wrbA* | *E. coli* | WrbA | 20701,38086 | 5,6 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. However, *wrbA* does not specifically influence the affinity or mode of binding of *trpR* to its operator. It seems possible that the association may have a structural, rather than functional, basis. *WrbA* alone does not interact with the operator-bearing DNA; the *trpR/trpO* complex is probably the major target species. The *wrbA* protein may function as an accessory element in blocking *trpR*-specific transcriptional processes. | 27, 28, 71 |
| 80 | Q8X4B4 | Putative Flavoprotein *wrbA* | *E. coli* O157:H7 | WrbA (EcoO57) | 20690,38086 | 5,93 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the trp repressor protein and operator-bearing DNA. | 27 |
| 81 | P30849 | Flavoprotein *wrbA* | *E. coli* | WrbA | 20701,38086 | 5,6 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. However, *wrbA* does not specifically influence the affinity or mode of binding of *trpR* to its operator. It seems possible that the association may have a structural, rather than functional, basis. *WrbA* alone does not interact with the operator-bearing DNA; the *trpR/trpO* complex is probably the major target species. The *wrbA* protein may function as an accessory element in blocking *trpR*-specific transcriptional processes. | 27, 28, 71 |
| 81 | P30859 | Arginine-binding periplasmic protein 1 | *E. coli* | ArtI | 26912,73047 | 5,79 | 100 | Binds arginine; part of the arginine periplasmic transport system. | 28, 38, 89 |
| 81 | P39174 | Cystine-binding periplasmic protein | *E. coli* | FliY | 29021,21094 | 6,21 | 100 | Part of a binding-protein-dependent transport system for cystine. | 26, 28, 62 |
| 82 | P30849 | Flavoprotein *wrbA* | *E. coli* | WrbA | 20701,38086 | 5,6 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. However, *wrbA* does not specifically influence the affinity or mode of binding of *trpR* to its operator. It seems possible that the association may have a structural, rather than functional, basis. *WrbA* alone does not interact with the operator-bearing DNA; the *trpR/trpO* complex is probably the major target species. The *wrbA* protein may function as an accessory element in blocking *trpR*-specific transcriptional processes. | 27, 28, 71 |
| 82 | Q8X4B4 | Putative Flavoprotein *wrbA* | *E. coli* O157:H7 | WrbA (EcoO57) | 20690,38086 | 5,93 | 100 | Seems to enhance the formation and/or stability of noncovalent complexes between the *trp* repressor protein and operator-bearing DNA. | 27 |
| 84 | Q8FCA0 | ADP-L-glycero-D-manno-heptose-6-epimerase | *E. coli O6* | HldD (EcoO6) | 34872,12109 | 4,76 | 100 | Catalyzes the interconversion between ADP-D-glycero-beta-D-manno-heptose and ADP-L-glycero-beta-D-manno-heptose via an epimerization at carbon 6 of the heptose. | 26 |
| 86 | P21590 | *Mrp* protein | *E. coli* | Mrp | 39912,53125 | 5,85 | 100 |  | 26, 28, 90 |
| 87 | P30148 | Transaldolase B | *E. coli* | TalB | 35066,28125 | 5,1 | 100 | Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway. | 27, 28, 91 |