Supplementary Table S1

List of the 50 best ranked negative pairs detected in this study.

P1	**Description**	**P2**	**Description**	**Score**	**Evidence from STRING**	**STRING combined score**	**REMARKS**
thiQ	Thiamin transporter subunit; Part of the ABC transporter complex thiBPQ involved in thiamine import, Responsible for energy coupling to the transport system (Probable) (232 aa)	modC	molybdate transporter subunit; Part of the ABC transporter complex modABC involved in molybdenum import, Responsible for energy coupling to the transport system (By similarity) (352 aa)	366.59	none		Both are part of the ABC transporters
ilvH	acetolactate synthase III, thiamin-dependent, small subunit (163 aa)	leuC	3-isopropylmalate dehydratase large subunit (EC-4,2,1,33); Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate (466 aa)	271.35	Neighborhood in the Genome (homologous genes in other genomes): 0.800 Coexpression: 0.419	0.875	
rpoH	RNA polymerase, sigma 32 (sigma H) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This sigma factor is responsible for the expression of heat shock promoters (284 aa)	oxaA	membrane protein insertase; Inner membrane protein required for the insertion of integral membrane proteins into the membrane, Probably plays an essential role in the integration of proteins of the respiratory chain complexes, Involved in integration of membrane proteins that insert dependently and independently of the Sec translocase complex, Essential for the integration of subunits a and c of the F(1)F(0)ATP synthase, and secE proteins (548 aa)	199.34	none		
glpC	sn-glycerol-3-phosphate dehydrogenase (anaerobic), small subunit; Electron transfer protein; may also function as the membrane anchor for the glpAB dimer (396 aa)	nrfC	formate-dependent nitrite reductase, 4Fe4S subunit; Probably involved in the transfer of electrons from the quinone pool to the type-c cytochromes (223 aa)	128.35	none		Electron transfer proteins

fruA	fused fructose-specific PTS enzymes- IIBcomponent/IIC components; The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane, This system is involved in fructose transport (563 aa)	mtlA	fused mannitol-specific PTS enzymes- IIA components/IIB components/IIC components; The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane, This system is involved in mannitol transport (637 aa)	101.74	none		sugar PTS fructose & mannitol transport
recC	exonuclease V (RecBCD complex), gamma chain; Exhibits a wide variety of catalytic activities including ATP-dependent exonuclease, ATP-stimulated endonuclease, ATP-dependent helicase and DNA-dependent ATPase activities (1122 aa)	secE	preprotein translocase membrane subunit; Essential for protein export (127 aa)	82.86	none		
trpA	tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate (By similarity) (268 aa)	hisH	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit with HisF; IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate, The hisH subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hisF for the synthesis of IGP and AICAR (196 aa)	50.10	Neighborhood in the Genome (homologous genes in other genomes): 0.788 Cooccurence: 0.303 Co-Mentioned in PubMed Abstracts (putative homologs mentioned together in other species): 0.227	0.87	

ihfB	integration host factor (IHF), DNA-binding protein, beta subunit; This protein is one of the two subunits of integration host factor, a specific DNA-binding protein that functions in genetic recombination as well as in transcriptional and translational control (By similarity) (94 aa)	rpoH	RNA polymerase, sigma 32 (sigma H) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This sigma factor is responsible for the expression of heat shock promoters (284 aa)	44.51	none	
trpA	tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate (By similarity) (268 aa)	trpE	component I of anthranilate synthase (520 aa)	32.44	Neighborhood in the Genome: 0.800 Cooccurence Across Genomes: 0.766 Co-Expression: 0.999 Co-Mentioned in PubMed Abstracts: 0.733	0.999
trpA	tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate (By similarity) (268 aa)	hisF	imidazole glycerol phosphate synthase, catalytic subunit with HisH; IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate, The hisF subunit catalyzes the cyclization activity that produces IGP and AICAR from PRFAR using the ammonia provided by the hisH subunit (By similarity) (258 aa)	31.42	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.680 Co-Mentioned in PubMed Abstracts (putative homologs mentioned together in other species): 0.364	0.783

clpP	proteolytic subunit of ClpA-ClpP and ClpX-ClpP ATP-dependent serine proteases; Cleaves peptides in various proteins in a process that requires ATP hydrolysis, Has a chymotrypsin-like activity, Plays a major role in the degradation of misfolded proteins, May play the role of a master protease which is attracted to different substrates by different specificity factors such as clpA or clpX (207 aa)	pnp	polynucleotide phosphorylase/polyadenylase; Involved in mRNA degradation, Hydrolyzes single-stranded polyribonucleotides processively in the 3'- to 5'-direction (711 aa)	15.06	none	
tolB	periplasmic protein; Involved in the tonB-independent uptake of group A colicins (colicins A, E1, E2, E3 and K), Necessary for the colicins to reach their respective targets after initial binding to the bacteria (430 aa)	oxaA	membrane protein insertase; Inner membrane protein required for the insertion of integral membrane proteins into the membrane, Probably plays an essential role in the integration of proteins of the respiratory chain complexes, Involved in integration of membrane proteins that insert dependently and independently of the Sec translocase complex, Essential for the integration of subunits a and c of the F(1)F(0)ATP synthase, and secE proteins (548 aa)	12.28	none	Linked to transmembrane activity

clpX	ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease; ATP-dependent specificity component of the Clp protease, It directs the protease to specific substrates, It may bind to the lambda O substrate protein and present it to the clpP protease in a form that can be recognized and readily hydrolyzed by clpP, Can perform chaperone functions in the absence of clpP (424 aa)	pnp	polynucleotide phosphorylase/polyadenylase; Involved in mRNA degradation, Hydrolyzes single-stranded polyribonucleotides processively in the 3'- to 5'-direction (711 aa)	10.71	none		
recO	gap repair protein; Involved in DNA repair and recF pathway recombination (By similarity) (242 aa)	recC	exonuclease V (RecBCD complex), gamma chain; Exhibits a wide variety of catalytic activities including ATP-dependent exonuclease, ATP-stimulated endonuclease, ATP-dependent helicase and DNA-dependent ATPase activities (1122 aa)	9.32	Co-Mentioned in PubMed Abstracts: 0.741	0.74	
crr	glucose-specific enzyme IIA component of PTS; The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate active -transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane, This system is involved in glucose transport (169 aa)	chbA	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS; The phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system, catalyzes the phosphorylation of incoming sugar substrates concomitant with their translocation across the cell membrane, This system is involved in N,N'-diacetylchitobiose transport (116 aa)	7.73	none		sugar PTS glucose & N,N'-diacetylchitobiose transport

acrB	multidrug efflux system protein; AcrAB is a drug efflux protein with a broad substrate specificity (1049 aa)	cusC	copper/silver efflux system, outer membrane component; Part of a cation efflux system that mediates resistance to copper and silver, In pathogenic strains it allows the bacteria to invade brain microvascular endothelial cells (BMEC) thus allowing it to cross the blood-brain barrier and cause neonatal meningitis (457 aa)	6.94	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.716 Gene Fusions: 0.026 Cooccurence Across Genomes: 0.582 Co-Mentioned in PubMed Abstracts (putative homologs mentioned together in other species): 0.219	0.894
oppD	oligopeptide transporter subunit; Part of the binding-protein-dependent transport system for oligopeptides, Probably responsible for energy coupling to the transport system (337 aa)	dppF	dipeptide transporter; Part of the binding-protein-dependent transport system for dipeptides, Probably responsible for energy coupling to the transport system (334 aa)	6.28	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.310 Cooccurence Across Genomes: 0.766 Co-Expression: 0.575	0.724
dnaK	chaperone HSP70. co-chaperone with DnaJ; 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, possibly through an analogous interaction with the dnaA protein, Also participates actively in the response to hyperosmotic shock (638 aa)	gyrA	DNA gyrase (type II topoisomerase), subunit A; DNA gyrase negatively supercoils closed circular double- stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (875 aa)	5.74	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.139 Cooccurence Across Genomes: 0.316 Experimental/Biochemical Data: 0.853 Co-Mentioned in PubMed Abstracts (putative homologs mentioned together in other species): 0.054	0.901

aceF	pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2; The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2), It contains multiple copies of three enzymatic components-pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3) (630 aa)	recO	gap repair protein; Involved in DNA repair and recF pathway recombination (By similarity) (242 aa)	5.19	none		
chbA	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS; The phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system, catalyzes the phosphorylation of incoming sugar substrates concomitant with their translocation across the cell membrane, This system is involved in N,N'-diacetylchitobiose transport (116 aa)	mtlA	fused mannitol-specific PTS enzymes- IIA components/IIB components/IIC components; The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate active -transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane, This system is involved in mannitol transport (637 aa)	4.56	none		sugar PTS N,N'-diacetylchitobiose & mannitol transport
trpE	component I of anthranilate synthase (520 aa)	hisF	imidazole glycerol phosphate synthase, catalytic subunit with HisH; IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate, The hisF subunit catalyzes the cyclization activity that produces IGP and AICAR from PRFAR using the ammonia provided by the hisH subunit (By similarity) (258 aa)	3.83	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.465 Gene Fusions: 0.322 Co-Expression (putative homologs are coexpressed in other species): 0.112	0.633	

fliM	flagellar motor switching and energizing component; FliM is one of three proteins (fliG, fliN, fliM) that form a switch complex that is proposed to be located at the base of the basal body, This complex interacts with the cheY and cheZ chemotaxis proteins, in addition to contacting components of the motor that determine the direction of flagellar rotation	cheA	fused chemotactic sensory histidine kinase in two-component regulatory system with CheB and CheY: sensory histidine kinase/signal sensing protein; Involved in the transmission of sensory signals from the chemoreceptors to the flagellar motors, CheA is autophosphorylated; it can transfer its phosphate group to either cheB or cheY	3.82	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.792 Cooccurence Across Genomes: 0.277 Co-Mentioned in PubMed Abstracts: 0.727	0.968
trpA	tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate (By similarity)	leuC	3-isopropylmalate dehydratase large subunit (EC:4,2,1,33); Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate	2.95	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.465	0.465
ilvH	acetolactate synthase III, thiamin-dependent, small subunit (163 aa)	trpA	tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate (By similarity) (268 aa)	2.60		
fliA	RNA polymerase, sigma 28 (sigma F) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This alternative sigma factor is specific for class 3 flagellar operons	flgG	flagellar component of cell-distal portion of basal-body rod	2.46	Neighborhood in the Genome (Neighborhood in the Genome): 0.788 Cooccurence Across Genomes: 0.577 Co-Expression: 0.778 Co-Mentioned in PubMed Abstracts: 0.606	0.991

cheW	purine-binding chemotaxis protein; Involved in the transmission of sensory signals from the chemoreceptors to the flagellar motors, It physically bridges cheA to the MCPs (methyl-accepting chemotaxis proteins) to allow regulated phosphotransfer to cheY and cheB (167 aa)	flgB	flagellar component of cell-proximal portion of basal-body rod (138 aa)	2.39	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.588 Co-Expression: 0.521	0.789
cheW	purine-binding chemotaxis protein; Involved in the transmission of sensory signals from the chemoreceptors to the flagellar motors, It physically bridges cheA to the MCPs (methyl-accepting chemotaxis proteins) to allow regulated phosphotransfer to cheY and cheB (167 aa)	flgG	flagellar component of cell-distal portion of basal-body rod (260 aa)	2.35	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.719 Co-Expression: 0.219	0.765
fliM	flagellar motor switching and energizing component; FliM is one of three proteins (fliG, fliN, fliM) that form a switch complex that is proposed to be located at the base of the basal body, This complex interacts with the cheY and cheZ chemotaxis proteins, in addition to contacting components of the motor that determine the direction of flagellar rotation (334 aa)	fliA	RNA polymerase, sigma 28 (sigma F) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This alternative sigma factor is specific for class 3 flagellar operons (239 aa)	2.35	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.796 Cooccurence Across Genomes: 0.705 Co-Expression: 0.158 Co-Mentioned in PubMed Abstracts: 0.697	0.983

secB	protein export chaperone; One of the proteins required for the normal export of preproteins out of the cell cytoplasm, It is a molecular chaperone that binds to a subset of precursor proteins, maintaining them in a translocation-competent state, It also specifically binds to its receptor secA (155 aa)	parC	DNA topoisomerase IV, subunit A; Topoisomerase IV is essential for chromosome segregation, It has relaxation of supercoiled DNA activity, Performs the decatenation events required during the replication of a circular DNA molecule (752 aa)	2.34	
hflK	modulator for HflB protease specific for phage lambda CII repressor; HflC and hflK govern the stability of phage lambda cII protein and have been proposed to encode or regulate a cII- specific protease (419 aa)	ccmE	periplasmic heme chaperone; Heme chaperone required for the biogenesis of c-type cytochromes, Transiently binds heme delivered by ccmC and transfers the heme to apocytochromes in a process facilitated by ccmF and ccmH (159 aa)	1.98	
malE	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS; The phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system, catalyzes the phosphorylation of incoming sugar substrates concomitant with their translocation across the cell membrane, This system is involved in N,N'-diacetylchitobiose transport (116 aa)	chbA	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS; The phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system, catalyzes the phosphorylation of incoming sugar substrates concomitant with their translocation across the cell membrane, This system is involved in N,N'-diacetylchitobiose transport (116 aa)	1.91	sugar PTS N,N'-diacetylchitobiose transport

ruvA	component of RuvABC resolvasome, regulatory subunit; The ruvA-ruvB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination, RuvAB is an helicase that mediates the Holliday junction migration by localized denaturation and reannealing, RuvA stimulates, in the presence of DNA, the weak ATPase activity of ruvB, Binds both single- and double-stranded DNA (dsDNA), Binds preferentially to supercoiled rather than to relaxed dsDNA	recR	gap repair protein; May play a role in DNA repair, It seems to be involved in an recBC-independent recombinational process of DNA repair, It may act with recF and recO	1.84	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.343 Cooccurence Across Genomes: 0.192 Co-Mentioned in PubMed Abstracts: 0.662	0.873
secE	preprotein translocase membrane subunit; Essential for protein export (127 aa)	tolB	periplasmic protein; Involved in the tonB-independent uptake of group A colicins (colicins A, E1, E2, E3 and K), Necessary for the colicins to reach their respective targets after initial binding to the bacteria (430 aa)	1.45		
secB	protein export chaperone; One of the proteins required for the normal export of preproteins out of the cell cytoplasm, It is a molecular chaperone that binds to a subset of precursor proteins, maintaining them in a translocation-competent state, It also specifically binds to its receptor secA (155 aa)	tolB	periplasmic protein; Involved in the tonB-independent uptake of group A colicins (colicins A, E1, E2, E3 and K), Necessary for the colicins to reach their respective targets after initial binding to the bacteria (430 aa)	1.05		

rpoH	RNA polymerase, sigma 32 (sigma H) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This sigma factor is responsible for the expression of heat shock promoters (284 aa)	flgF	flagellar component of cell-proximal portion of basal-body rod (251 aa)	0.84
recO	gap repair protein; Involved in DNA repair and recF pathway recombination (By similarity) (242 aa)	secG	preprotein translocase membrane subunit; Involved in protein export, Participates in an early event of protein translocation (110 aa)	0.81
recO	gap repair protein; Involved in DNA repair and recF pathway recombination (By similarity) (242 aa)	rne	fused ribonucleaseE-endoribonuclease/RNA-binding protein/RNA degradosome binding protein; Matures 5S rRNA from its precursors from all the rRNA genes, It also cleaves RNA I, a molecule that controls the replication of colE1 plasmid DNA, It is the major endoribonuclease participating in mRNA turnover in E,coli, It initiates the decay of RNAs by cutting them internally near their 5'-end, It is able to remove poly(A) tails by an endonucleolytic process (1061 aa)	0.79

rpoH		rne	fused ribonucleaseE-endoribonuclease/RNA-binding protein/RNA degradosome binding protein; Matures 5S rRNA from its precursors from all the rRNA genes, It also cleaves RNA I, a molecule that controls the replication of colE1 plasmid DNA, It is the major endoribonuclease participating in mRNA turnover in E,coli, It initiates the decay of RNAs by cutting them internally near their 5'-end, It is able to remove poly(A) tails by an endonucleolytic process (1061 aa)	0.65		
fliA	RNA polymerase, sigma 28 (sigma F) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This alternative sigma factor is specific for class 3 flagellar operons (239 aa)	flgC	flagellar component of cell-proximal portion of basal-body rod (134 aa)	0.59	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.777 Co-Expression: 0.864 Experimental/Biochemical Data: 0.496 Co-Mentioned in PubMed Abstracts: 0.723	0.994

ruvB	ATP-dependent DNA helicase, component of RuvABC resolvasome; The ruvA-ruvB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination, RuvAB is an helicase that mediates the Holliday junction migration by localized denaturation and reannealing (336 aa)	recR	gap repair protein; May play a role in DNA repair, It seems to be involved in an recBC-independent recombinational process of DNA repair, It may act with recF and recO (201 aa)	0.55	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.513 Cooccurence Across Genomes: 0.405 Co-Mentioned in PubMed Abstracts: 0.667	0.89	
mtlA	fused mannitol-specific PTS enzymes- IIA components/IIB components/IIC components; The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane, This system is involved in mannitol transport (637 aa)	crr	glucose-specific enzyme IIA component of PTS; The phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS), a major carbohydrate active - transport system, catalyzes the phosphorylation of incoming sugar substrates concomitantly with their translocation across the cell membrane, This system is involved in glucose transport (169 aa)	0.47			PTS sugar Mannitol and glucose transport
dnaQ	DNA polymerase III epsilon subunit; DNA polymerase III is a complex, multichain enzyme responsible for most of the replicative synthesis in bacteria, The epsilon subunit contain the editing function and is a proofreading 3'-5' exonuclease (243 aa)	secB	protein export chaperone; One of the proteins required for the normal export of preproteins out of the cell cytoplasm, It is a molecular chaperone that binds to a subset of precursor proteins, maintaining them in a translocation-competent state, It also specifically binds to its receptor secA (155 aa)	0.44	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.439 Cooccurence Across Genomes: 0.202	0.522	

trpB	tryptophan synthase, beta subunit; The beta subunit is responsible for the synthesis of L-tryptophan from indole and L-serine (By similarity) (397 aa)	leuC	3-isopropylmalate dehydratase large subunit (EC-4,2,1,33); Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate (466 aa)	0.36	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.412	0.412
cysA	sulfate/thiosulfate transporter subunit; Part of the ABC transporter complex cysAWTP involved in sulfate/thiosulfate import, Responsible for energy coupling to the transport system (365 aa)	nuoL	NADH-ubiquinone oxidoreductase, membrane subunit L; NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain, The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone, Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient (613 aa)	0.34		

ihfA	integration host factor (IHF), DNA-binding protein, alpha subunit; This protein is one of the two subunits of integration host factor, a specific DNA-binding protein that functions in genetic recombination as well as in transcriptional and translational control (By similarity) (99 aa)	rne	fused ribonucleaseE-endoribonuclease/RNA-binding protein/RNA degradosome binding protein; Matures 5S rRNA from its precursors from all the rRNA genes, It also cleaves RNA I, a molecule that controls the replication of colE1 plasmid DNA, It is the major endoribonuclease participating in mRNA turnover in E,coli, It initiates the decay of RNAs by cutting them internally near their 5'-end, It is able to remove poly(A) tails by an endonucleolytic process (1061 aa)	0.31		
dnaJ	chaperone HSP40. co-chaperone with DnaK; Interacts with dnaK and grpE to disassemble a protein complex at the origins of replication of phage lambda and several plasmids, Participates actively in the response to hyperosmotic and heat shock by preventing the aggregation of stress-denatured proteins and by disaggregating proteins, also in an autonomous, dnaK-independent fashion, Unfolded proteins bind initially to dnaJ; upon interaction with the dnaJ-bound protein, dnaK hydrolyzes its bound ATP, resulting in the formation of a stable complex, GrpE releases ADP from dnaK; ATP binding to d [,,,] (376 aa)	gyrA	DNA gyrase (type II topoisomerase), subunit A; DNA gyrase negatively supercoils closed circular double- stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (875 aa)	0.28	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.247 Cooccurence Across Genomes: 0.363 Experimental/Biochemical Data: 0.371	0.656

secB	protein export chaperone; One of the proteins required for the normal export of preproteins out of the cell cytoplasm, It is a molecular chaperone that binds to a subset of precursor proteins, maintaining them in a translocation-competent state, It also specifically binds to its receptor secA (155 aa)	ompW	outer membrane protein W; Acts as a receptor for colicin S4 (212 aa)	0.25		
pnp	polynucleotide phosphorylase/polyadenylase; Involved in mRNA degradation, Hydrolyzes single-stranded polyribonucleotides processively in the 3'- to 5'-direction (711 aa)	ruvC	component of RuvABC resolvasome, endonuclease; Nuclease that resolves Holliday junction intermediates in genetic recombination, Cleaves the cruciform structure in supercoiled DNA by nicking to strands with the same polarity at sites symmetrically opposed at the junction in the homologous arms and leaves a 5'-terminal phosphate and a 3'-terminal hydroxyl group (173 aa)	0.22		
atpG	F1 sector of membrane-bound ATP synthase, gamma subunit; Produces ATP from ADP in the presence of a proton gradient across the membrane, The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex (By similarity) (287 aa)	glyQ	glycine tRNA synthetase, alpha subunit (303 aa)	0.22	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.323 Co-Expression (putative homologs coexpressed in other species): 0.265	0.468

rpoD	RNA polymerase, sigma 70 (sigma D) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This is the primary sigma factor of this bacterium	rpoH	RNA polymerase, sigma 32 (sigma H) factor; Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released, This sigma factor is responsible for the expression of heat shock promoters	0.21	Neighborhood in the Genome (homologous genes are neighbors in other genomes): 0.124 Cooccurence Across Genomes: 0.766 Co-Mentioned in PubMed Abstracts: 0.951	0.546