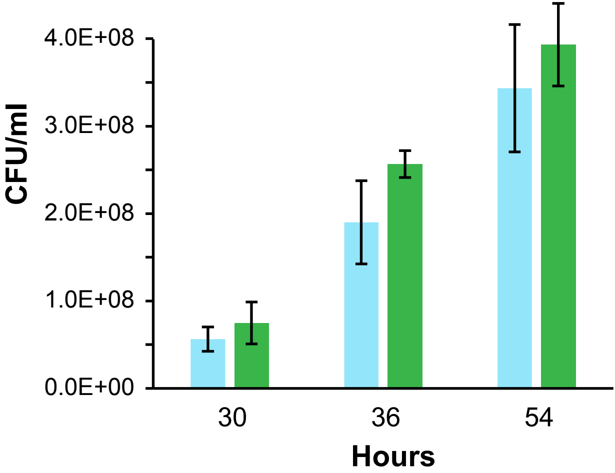

FIG S1

Enterobactin does not affect growth of *B. subtilis*. The total CFU/ml calculated for *B. subtilis* cells treated with 10 µM enterobactin (green) or solvent (blue) at 30, 36, and 54 hours. Samples were taken from microcolony agar assay plates grown in the presence or absence of enterobactin and non-heat treated cells were plated to determine total number of cells. No significant differences were observed between samples treated with enterobactin compared to untreated samples (n=3). Error bars represent standard deviations.

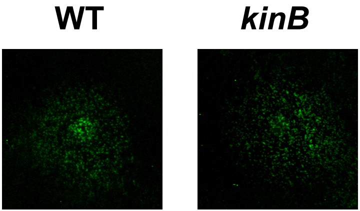

FIG S2

Sporulation gene promotion by enterobactin is independent of KinB. Representative fluorescence images of wild-type and *kinB B. subtilis* P_{sspB}-*yfp* micro-colony lawns on agar plates with wells containing 10 μM enterobactin. Sporulation gene promotion is observed in both wild-type and the *kinB* mutant.

Table S1

Summary of results from the Keio Collection screen. Each mutant within the collection was spotted onto B. subtilis PsspB-yfp microcolony lawns and imaged for fluorescence. Sporulation gene stimulation for each mutant was then noted as either no, low, high, or normal promotion. The table lists all mutants that altered sporulation gene expression compared to wildtype and the corresponding GO terms for each gene where applicable (GO term designations obtained from EcoCyc (Gehring AM, Bradley KA, Walsh CT, *Biochemistry,* 36:8495–503, 1997).

Plate/Well	No induction	Low induction	High induction	Gene	GO terms (biological processes)
P1 A2		x		*bglG*	GO:0045893 - positive regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P1 A9		x		*tyrR*	GO:0008152 - metabolic process GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated GO:0019439 - aromatic compound catabolic process GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system
P1 A10		x		*rcsC*	GO:0023014 - signal transduction by protein phosphorylation GO:0018106 - peptidyl-histidine phosphorylation GO:0016310 - phosphorylation GO:0007165 - signal transduction GO:0006355 - regulation of transcription, DNA-templated GO:0046777 - protein autophosphorylation GO:0044010 - single-species biofilm formation GO:0071470 - cellular response to osmotic stress GO:0000160 - phosphorelay signal transduction system
P1 A11		x		*aceF*	GO:0055114 - oxidation-reduction process GO:0008152 - metabolic process GO:0006090 - pyruvate metabolic process GO:0006086 - acetyl-CoA biosynthetic process from pyruvate GO:0006096 - glycolytic process
P1 B2		x		*btuR*	GO:0006779 - porphyrin-containing compound biosynthetic process GO:0019250 - aerobic cobalamin biosynthetic process GO:0009236 - cobalamin biosynthetic process
P1 B9			x	*uidR*	GO:0045892 - negative regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P1 C6		x		*melR*	GO:0006351 - transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated
P1 C7		x		*nhaR*	GO:0006351 - transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated
P1 C8		x		*soxR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006979 - response to oxidative stress GO:0006351 - transcription, DNA-templated
P1 C9		x		*uxuR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P1 D4	x			*galS*	GO:0006351 - transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated
P1 E1	x			*appY*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0016036 - cellular response to phosphate starvation GO:0045893 - positive regulation of transcription, DNA-templated
P1 E2	x			*chbR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated
P1 E5		x		*leuO*	GO:0006351 - transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated
P1 E6	x			*metR*	GO:0006351 - transcription, DNA-templated GO:0008652 - cellular amino acid biosynthetic process GO:0006355 - regulation of transcription, DNA-templated GO:0009086 - methionine biosynthetic process
P1 E9		x		*zntR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated
P1 E10		x		*rbsR*	GO:0045893 - positive regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated

P1 F1		x		*argR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0006310 - DNA recombination GO:0051259 - protein oligomerization GO:0006525 - arginine metabolic process GO:2000143 - negative regulation of DNA-templated transcription, initiation GO:0042150 - plasmid recombination GO:0008652 - cellular amino acid biosynthetic process GO:0006526 - arginine biosynthetic process
P1 F3		x		*envY*	GO:0009266 - response to temperature stimulus GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P1 F6		x		*mhpR*	GO:0045892 - negative regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0019439 - aromatic compound catabolic process GO:0006351 - transcription, DNA-templated
P1 F10		x		*sdiA*	GO:0051301 - cell division GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0032467 - positive regulation of cytokinesis GO:2000144 - positive regulation of DNA-templated transcription, initiation GO:0007049 - cell cycle
P1 F11	x			*cyoB*	GO:0055114 - oxidation-reduction process GO:0015992 - proton transport GO:0009060 - aerobic respiration GO:0006811 - ion transport GO:0015990 - electron transport coupled proton transport GO:0019646 - aerobic electron transport chain
P1 F12	x			*sucB*	GO:0008152 - metabolic process GO:0033512 - L-lysine catabolic process to acetyl-CoA via saccharopine GO:0006099 - tricarboxylic acid cycle
P1 G1		x		*asnC*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated GO:0043200 - response to amino acid
P1 G2		x		*csgD*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:1900190 - regulation of single-species biofilm formation GO:2000144 - positive regulation of DNA-templated transcription, initiation
P1 G3		x		*fadR*	GO:0045723 - positive regulation of fatty acid biosynthetic process GO:0006631 - fatty acid metabolic process GO:0006629 - lipid metabolic process GO:0019217 - regulation of fatty acid metabolic process GO:0019395 - fatty acid oxidation GO:0045892 - negative regulation of transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P1 G10			x	*srlR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P1 H1	x			*betI*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0019285 - glycine betaine biosynthetic process from choline GO:0045892 - negative regulation of transcription, DNA-templated GO:0006970 - response to osmotic stress
P1 H2		x		*cynR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P1 H3		x		*fis*	GO:0006351 - transcription, DNA-templated GO:0034401 - chromatin organization involved in regulation of transcription GO:0006355 - regulation of transcription, DNA-templated
P1 H4	x			*hupA*	GO:0030261 - chromosome condensation GO:0006974 - cellular response to DNA damage stimulus GO:0006351 - transcription, DNA-templated
P1 H5		x		*malI*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated

P1 H8		x		*trpR*	GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated
P3 A2			x	*adhE*	GO:0008152 - metabolic process GO:0006066 - alcohol metabolic process GO:0015976 - carbon utilization GO:0006115 - ethanol biosynthetic process GO:0055114 - oxidation-reduction process
P3 A6		x		*mdh*	GO:0019752 - carboxylic acid metabolic process GO:0055114 - oxidation-reduction process GO:0005975 - carbohydrate metabolic process GO:0006108 - malate metabolic process GO:0006096 - glycolytic process GO:0006099 - tricarboxylic acid cycle GO:0009061 - anaerobic respiration GO:0006113 - fermentation
P3 B4		x		*nuoK*	GO:0055114 - oxidation-reduction process GO:0042773 - ATP synthesis coupled electron transport GO:0006810 - transport
P3 B5		x		*nuoA*	GO:0055114 - oxidation-reduction process GO:0006810 - transport
P3 B6			x	*yhfW*	GO:0043094 - cellular metabolic compound salvage GO:0009117 - nucleotide metabolic process GO:0008152 - metabolic process
P3 B8	x			*frdC*	GO:0044780 - bacterial-type flagellum assembly GO:0001539 - cilium or flagellum-dependent cell motility GO:0006810 - transport GO:0009061 - anaerobic respiration GO:0006113 - fermentation
P3 B12		x		*atoC*	GO:0010967 - regulation of polyamine biosynthetic process GO:0043086 - negative regulation of catalytic activity GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system
P3 C4		x		*nuoJ*	GO:0055114 - oxidation-reduction process
P3 C9			x	*citB*	GO:0009605 - response to external stimulus GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system GO:0006351 - transcription, DNA-templated
P3 C11			x	*uvrY*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system
P3 D7		x		*aceB*	GO:0006099 - tricarboxylic acid cycle GO:0006097 - glyoxylate cycle
P3 E5	x			*talA*	GO:0005975 - carbohydrate metabolic process GO:0006098 - pentose-phosphate shunt
P3 E6		x		*gpmI*	GO:0006979 - response to oxidative stress GO:0008152 - metabolic process GO:0006007 - glucose catabolic process GO:0006096 - glycolytic process
P3 E7		x		*aceA*	GO:0019752 - carboxylic acid metabolic process GO:0008152 - metabolic process GO:0006099 - tricarboxylic acid cycle GO:0006097 - glyoxylate cycle
P3 E8		x		*deoB*	GO:0009166 - nucleotide catabolic process GO:0009264 - deoxyribonucleotide catabolic process GO:0043094 - cellular metabolic compound salvage GO:0009117 - nucleotide metabolic process GO:0008152 - metabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0006015 - 5-phosphoribose 1-diphosphate biosynthetic process
P3 E12		x		*narQ*	GO:0023014 - signal transduction by protein phosphorylation GO:0018106 - peptidyl-histidine phosphorylation GO:0007165 - signal transduction GO:0042128 - nitrate assimilation GO:0016310 - phosphorylation GO:0071249 - cellular response to nitrate GO:0071250 - cellular response to nitrite GO:0000160 - phosphorelay signal transduction system

P3 F4		x		*nuoG*	GO:0055114 - oxidation-reduction process GO:0042773 - ATP synthesis coupled electron transport GO:0009060 - aerobic respiration
P3 F9		x		*dps*	GO:0006950 - response to stress GO:0030261 - chromosome condensation GO:0042594 - response to starvation GO:0055114 - oxidation-reduction process GO:0006879 - cellular iron ion homeostasis
P3 F12		x		*yfhA*	
P3 G3		x		*nuoN*	GO:0055114 - oxidation-reduction process GO:0015990 - electron transport coupled proton transport GO:0042773 - ATP synthesis coupled electron transport GO:0006810 - transport GO:0009060 - aerobic respiration
P3 H1	x			*icd*	GO:0006979 - response to oxidative stress GO:0055114 - oxidation-reduction process GO:0022900 - electron transport chain GO:0006097 - glyoxylate cycle GO:0006099 - tricarboxylic acid cycle
P3 H4	x			*nuoE*	GO:0022904 - respiratory electron transport chain GO:0055114 - oxidation-reduction process
P5 A1			x	*barA*	GO:0023014 - signal transduction by protein phosphorylation GO:0018106 - peptidyl-histidine phosphorylation GO:0016310 - phosphorylation GO:0007165 - signal transduction GO:0006468 - protein phosphorylation GO:0006355 - regulation of transcription, DNA-templated GO:0071310 - cellular response to organic substance GO:0046777 - protein autophosphorylation GO:0042542 - response to hydrogen peroxide GO:0006351 - transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system
P5 A2			x	*uhpA*	GO:0006351 - transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system
P5 A4			x	*treA*	GO:0008152 - metabolic process GO:0005991 - trehalose metabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0005993 - trehalose catabolic process GO:0071474 - cellular hyperosmotic response
P5 A9		x		*coaE*	GO:0016310 - phosphorylation GO:0015937 - coenzyme A biosynthetic process
P5 B1		x		*qseB*	GO:0010038 - response to metal ion GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system GO:0006351 - transcription, DNA-templated
P5 B3		x		*dcuR*	GO:0045893 - positive regulation of transcription, DNA-templated GO:0009605 - response to external stimulus GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system GO:0006351 - transcription, DNA-templated
P5 B4		x		*cpsB*	GO:0009058 - biosynthetic process GO:0005976 - polysaccharide metabolic process GO:0000271 - polysaccharide biosynthetic process GO:0009298 - GDP-mannose biosynthetic process GO:0006972 - hyperosmotic response GO:0009103 - lipopolysaccharide biosynthetic process GO:0009242 - colanic acid biosynthetic process
P5 B8		x		*tap*	GO:0007165 - signal transduction GO:0006935 - chemotaxis
P5 B9		x		*ykfA*	GO:0000027 - ribosomal large subunit assembly
P5 B12	x			*ypjB*	
P5 C4		x		*rbsB*	GO:0015749 - monosaccharide transport GO:0008643 - carbohydrate transport GO:0006935 - chemotaxis GO:0006810 - transport
P5 C6			x	*yfdF*	
P5 D1		x		*rpoN*	GO:0006352 - DNA-templated transcription, initiation GO:0006525 - arginine metabolic process GO:0006355 - regulation of transcription, DNA-templated

P5 D4		x		*oppA*	GO:0055085 - transmembrane transport GO:0061077 - chaperone-mediated protein folding GO:0009408 - response to heat GO:0015833 - peptide transport GO:0006810 - transport GO:0015031 - protein transport GO:0006857 - oligopeptide transport
P5 D5		x		*lldD*	GO:0055114 - oxidation-reduction process GO:0006089 - lactate metabolic process GO:0019516 - lactate oxidation GO:0009061 - anaerobic respiration GO:0042355 - L-fucose catabolic process GO:0009060 - aerobic respiration
P5 D8		x		*helD*	GO:0032508 - DNA duplex unwinding GO:0023014 - signal transduction by protein phosphorylation GO:0000160 - phosphorelay signal transduction system GO:0006310 - DNA recombination
P5 E1			x	*arcB*	GO:0023014 - signal transduction by protein phosphorylation GO:0018106 - peptidyl-histidine phosphorylation GO:0016310 - phosphorylation GO:0007165 - signal transduction GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0046777 - protein autophosphorylation GO:0000160 - phosphorelay signal transduction system
P5 E2			x	*cpxR*	GO:0007155 - cell adhesion GO:0010810 - regulation of cell-substrate adhesion GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system
P5 E5	x			*pgm*	GO:0071704 - organic substance metabolic process GO:0019388 - galactose catabolic process GO:0005978 - glycogen biosynthetic process GO:0005975 - carbohydrate metabolic process GO:0006006 - glucose metabolic process
P5 E6		x		*cusA*	GO:1902601 - silver ion transmembrane transport GO:0006825 - copper ion transport GO:0006812 - cation transport GO:0006811 - ion transport GO:0006810 - transport GO:0006878 - cellular copper ion homeostasis GO:0010272 - response to silver ion GO:0010273 - detoxification of copper ion GO:0015673 - silver ion transport GO:0015679 - plasma membrane copper ion transport GO:0046688 - response to copper ion GO:0060003 - copper ion export
P5 E8	x			*hrpA*	GO:0009451 - RNA modification GO:0006397 - mRNA processing
P5 E9		x		*yahL*	
P5 E11		x		*yfiN*	GO:0036460 - cellular response to cell envelope stress GO:0008152 - metabolic process GO:1902201 - negative regulation of bacterial-type flagellum-dependent cell motility GO:0007165 - signal transduction
P5 E12	x			*yqaD*	GO:0005975 - carbohydrate metabolic process
P5 F2		x		*zraS*	GO:0007165 - signal transduction GO:0023014 - signal transduction by protein phosphorylation GO:0018106 - peptidyl-histidine phosphorylation GO:0016310 - phosphorylation GO:0071294 - cellular response to zinc ion GO:0071284 - cellular response to lead ion GO:0046777 - protein autophosphorylation GO:0000160 - phosphorelay signal transduction system
P5 F3		x		*arcA*	GO:0006351 - transcription, DNA-templated GO:0045892 - negative regulation of transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system

P5 F4	x			*rnt*	GO:0090503 - RNA phosphodiester bond hydrolysis, exonucleolytic GO:0090501 - RNA phosphodiester bond hydrolysis GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0008033 - tRNA processing GO:0006396 - RNA processing GO:0042780 - tRNA 3'-end processing
P5 F7		x		*gspA*	GO:0006810 - transport
P5 F8		x		*moaA*	GO:0009408 - response to heat GO:0006777 - Mo-molybdopterin cofactor biosynthetic process
P5 F9		x		*aceE*	GO:0008152 - metabolic process GO:0055114 - oxidation-reduction process GO:0006096 - glycolytic process
P5 G5		x		*cydB*	GO:0019646 - aerobic electron transport chain GO:0006119 - oxidative phosphorylation GO:0055114 - oxidation-reduction process
P5 G6		x		*fhuA*	GO:0044718 - siderophore transmembrane transport GO:0015891 - siderophore transport GO:0055072 - iron ion homeostasis GO:0006811 - ion transport GO:0006810 - transport
P5 G8		x		*speE*	GO:0006596 - polyamine biosynthetic process GO:0008295 - spermidine biosynthetic process
P5 G9	x			*lpd*	GO:0006979 - response to oxidative stress GO:0045454 - cell redox homeostasis GO:0006103 - 2-oxoglutarate metabolic process GO:0006090 - pyruvate metabolic process GO:0055114 - oxidation-reduction process GO:0006096 - glycolytic process GO:0019464 - glycine decarboxylation via glycine cleavage system
P5 G10		x		*ypdI*	GO:0009242 - colanic acid biosynthetic process
P5 G12	x			*hha*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0010468 - regulation of gene expression
P5 H1		x		*uhpB*	GO:0006470 - protein dephosphorylation GO:0023014 - signal transduction by protein phosphorylation GO:0018106 - peptidyl-histidine phosphorylation GO:0016310 - phosphorylation GO:0046777 - protein autophosphorylation GO:0000160 - phosphorelay signal transduction system
P5 H6		x		*pstB*	GO:0008152 - metabolic process GO:0006810 - transport GO:0035435 - phosphate ion transmembrane transport GO:0006817 - phosphate ion transport
P5 H9		x		*fbp*	GO:0030388 - fructose 1,6-bisphosphate metabolic process GO:0006002 - fructose 6-phosphate metabolic process GO:0006000 - fructose metabolic process GO:0005986 - sucrose biosynthetic process GO:0006001 - fructose catabolic process GO:0051289 - protein homotetramerization GO:0016311 - dephosphorylation GO:0016051 - carbohydrate biosynthetic process GO:0008152 - metabolic process GO:0005975 - carbohydrate metabolic process GO:0006094 - gluconeogenesis
P7 A3		x		*ybhC*	GO:0008152 - metabolic process GO:0042545 - cell wall modification
P7 A12		x		*pepT*	GO:0043171 - peptide catabolic process GO:0008152 - metabolic process GO:0006518 - peptide metabolic process GO:0006508 - proteolysis
P7 G8		x		*yidZ*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P7 G11		x		*pepN*	GO:0043171 - peptide catabolic process GO:0006508 - proteolysis
P9 E1			x	*ptrB*	GO:0006508 - proteolysis
P9 E2			x	*pepB*	GO:0043171 - peptide catabolic process GO:0019538 - protein metabolic process GO:0006508 - proteolysis
P9 E3			x	*yggG*	
P9 E4			x	*degQ*	GO:0051603 - proteolysis involved in cellular protein catabolic process GO:0006508 - proteolysis

P9 G6		x		*pepE*	GO:0006508 - proteolysis
P9 G10		x		*yfcR*	GO:0007155 - cell adhesion
P13 G7		x		*yciC*	
P13 G8		x		*mpaA*	GO:0006508 - proteolysis GO:0009253 - peptidoglycan catabolic process GO:0009050 - glycopeptide catabolic process
P15 C9	x			*ybfQ*	
P15 D4			x	*yaiV*	GO:0006351 - transcription, DNA-templated
P15 E9		x		*ybgE*	
P15 F7			x	*ybdD*	
P15 G5	x			*ybaP*	
P15 G6		x		*ybcO*	
P15 G7		x		*ybdM*	
P15 H6		x		*ybcQ*	GO:0044010 - single-species biofilm formation GO:0060567 - negative regulation of DNA-templated transcription, termination GO:0006355 - regulation of transcription, DNA-templated GO:0031564 - transcription antitermination GO:0006351 - transcription, DNA-templated
P15 H10	x			*ybjN*	GO:1902209 - negative regulation of bacterial-type flagellum assembly GO:0010212 - response to ionizing radiation GO:1902208 - regulation of bacterial-type flagellum assembly GO:1900232 - negative regulation of single-species biofilm formation on inanimate substrate GO:0030308 - negative regulation of cell growth GO:0009297 - pilus assembly GO:1902201 - negative regulation of bacterial-type flagellum-dependent cell motility
P17 A2			x	*ycjX*	
P17 B3		x		*yniA*	GO:0016310 - phosphorylation
P17 B4		x		*yejL*	
P17 E5		x		*yfhJ*	GO:0043086 - negative regulation of catalytic activity GO:0016226 - iron-sulfur cluster assembly
P17 E6		x		*yaaX*	
P17 F11		x		*ybeA*	GO:0032259 - methylation GO:0006364 - rRNA processing GO:0031167 - rRNA methylation GO:0070475 - rRNA base methylation
P17 G3		x		*yeeX*	
P17 G4		x		*yfcN*	
P17 H7	x			*yaeQ*	
P17 H9		x		*yeeS*	
P17 H11	x			*ybeT*	
P17 H12	x			*yedK*	GO:0006508 - proteolysis
P19 A9		x		*mraW*	GO:0032259 - methylation GO:0006364 - rRNA processing GO:0070475 - rRNA base methylation
P19 B1	x			*yegU*	GO:0008152 - metabolic process
P19 B2		x		*yaaH*	GO:0015992 - proton transport GO:0006811 - ion transport GO:0006810 - transport GO:0035433 - acetate transmembrane transport GO:0071422 - succinate transmembrane transport
P19 B3		x		*ybgH*	GO:0015992 - proton transport GO:0015833 - peptide transport GO:0006857 - oligopeptide transport GO:0006810 - transport GO:0015031 - protein transport GO:0042938 - dipeptide transport
P19 B4		x		*ydiU*	
P19 D8		x		*ycdO*	GO:0009411 - response to UV GO:0009636 - response to toxic substance GO:0006979 - response to oxidative stress GO:0046677 - response to antibiotic
P19 D11		x		*iscA*	GO:0097428 - protein maturation by iron-sulfur cluster transfer GO:0006790 - sulfur compound metabolic process GO:0016226 - iron-sulfur cluster assembly
P19 E7		x		*ycaP*	
P19 E8	x			*yebC*	GO:0010212 - response to ionizing radiation GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated

P19 E11		x		*ygbL*	GO:0019323 - pentose catabolic process
P19 E12	x			*ybhK*	GO:0008360 - regulation of cell shape
P19 G2		x		*ybbY*	GO:0055085 - transmembrane transport GO:0006810 - transport
P19 H3		x		*ydgR*	
P19 H5		x		*ybbB*	
P19 H6		x		*ybhH*	GO:0008152 - metabolic process
P19 H8		x		*yfaE*	GO:0055114 - oxidation-reduction process GO:0006124 - ferredoxin metabolic process
P19 H9		x		*ydjI*	GO:0005975 - carbohydrate metabolic process
P19 H10		x		*yciV*	GO:0090503 - RNA phosphodiester bond hydrolysis, exonucleolytic GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0016311 - dephosphorylation GO:0006260 - DNA replication GO:0071897 - DNA biosynthetic process
P19 H11		x		*uspE*	GO:0071973 - bacterial-type flagellum-dependent cell motility GO:0034644 - cellular response to UV GO:0044010 - single-species biofilm formation GO:0070301 - cellular response to hydrogen peroxide GO:0006950 - response to stress
P19 H12		x		*abgR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P21 A7			x	*wbbL*	GO:0045226 - extracellular polysaccharide biosynthetic process GO:0009103 - lipopolysaccharide biosynthetic process
P21 D5		x		*ykfG*	
P21 D8		x		*yeiI*	GO:0016310 - phosphorylation
P21 D9		x		*yfbF*	GO:0006629 - lipid metabolic process GO:0036108 - 4-amino-4-deoxy-alpha-L-arabinopyranosyl undecaprenyl phosphate biosynthetic process GO:0046677 - response to antibiotic GO:0009245 - lipid A biosynthetic process GO:0009103 - lipopolysaccharide biosynthetic process
P21 D12	x			*yfhD*	GO:0009253 - peptidoglycan catabolic process GO:0071555 - cell wall organization GO:0000270 - peptidoglycan metabolic process GO:0016998 - cell wall macromolecule catabolic process
P21 E12		x		*yfhH*	GO:0005975 - carbohydrate metabolic process GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P21 F4		x		*ydiF*	GO:0046952 - ketone body catabolic process GO:0008152 - metabolic process GO:0051289 - protein homotetramerization GO:0046459 - short-chain fatty acid metabolic process
P21 F9			x	*yfbB*	GO:0009234 - menaquinone biosynthetic process
P21 F12	x			*yfiC*	GO:0032259 - methylation GO:0008033 - tRNA processing GO:0030488 - tRNA methylation
P21 G10			x	*ypdB*	GO:0046677 - response to antibiotic GO:0048870 - cell motility GO:1900192 - positive regulation of single-species biofilm formation GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system GO:0006351 - transcription, DNA-templated
P23 B8		x		*gmr*	
P23 C1			x	*ygaV*	GO:0045892 - negative regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P23 C3			x	*ycbL*	GO:0019243 - methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione
P23 C10			x	*yddW*	GO:0005975 - carbohydrate metabolic process
P23 F9	x			*ynbA*	GO:0008654 - phospholipid biosynthetic process
P23 G1		x		*yqaB*	GO:0016311 - dephosphorylation GO:0008152 - metabolic process
P23 G8			x	*ynaI*	GO:0006810 - transport GO:0055085 - transmembrane transport GO:0071470 - cellular response to osmotic stress GO:0006811 - ion transport
P25 D7			x	*ybaZ*	
P25 E8		x		*ybeD*	

P25 F12	x			*yccC*	GO:0000271 - polysaccharide biosynthetic process GO:0045226 - extracellular polysaccharide biosynthetic process GO:0016310 - phosphorylation GO:0009103 - lipopolysaccharide biosynthetic process GO:0038083 - peptidyl-tyrosine autophosphorylation
P25 G4		x		*thiP*	GO:0015888 - thiamine transport GO:0006810 - transport
P25 H5	x			*yahA*	GO:0045893 - positive regulation of transcription, DNA-templated GO:0008152 - metabolic process GO:0006355 - regulation of transcription, DNA-templated
P25 H9	x			*ybhS*	GO:0006855 - drug transmembrane transport GO:0055085 - transmembrane transport GO:0006810 - transport
P25 H10	x			*yliG*	GO:0035600 - tRNA methylthiolation GO:0043412 - macromolecule modification GO:0009451 - RNA modification GO:0018339 - peptidyl-L-beta-methylthioaspartic acid biosynthetic process from peptidyl-aspartic acid
P25 H12		x		*wcaJ*	GO:0000271 - polysaccharide biosynthetic process GO:0009242 - colanic acid biosynthetic process GO:0009103 - lipopolysaccharide biosynthetic process
P27 C4			x	*yfhL*	
P27 E1			x	*asmA*	GO:0090313 - regulation of protein targeting to membrane
P29 D6		x		*ydiT*	GO:0055114 - oxidation-reduction process
P29 G12			x	*yiaK*	GO:0008152 - metabolic process GO:0055114 - oxidation-reduction process
P29 H11			x	*tar*	GO:0007165 - signal transduction GO:0006935 - chemotaxis
P29 H12			x	*allD*	GO:0008152 - metabolic process GO:0000256 - allantoin catabolic process GO:0055114 - oxidation-reduction process GO:0006144 - purine nucleobase metabolic process GO:0009442 - allantoin assimilation pathway
P31 A1			x	*aceK*	GO:0006470 - protein dephosphorylation GO:0016311 - dephosphorylation GO:0016310 - phosphorylation GO:0006006 - glucose metabolic process GO:0018105 - peptidyl-serine phosphorylation GO:0050790 - regulation of catalytic activity GO:0006099 - tricarboxylic acid cycle GO:0006097 - glyoxylate cycle
P31 B9			x	*ymgB*	GO:0071229 - cellular response to acid chemical GO:0042710 - biofilm formation GO:0042542 - response to hydrogen peroxide
P31 B11			x	*yddK*	
P31 D2		x		*ahpF*	GO:0045454 - cell redox homeostasis GO:0000302 - response to reactive oxygen species GO:0055114 - oxidation-reduction process
P31 E12		x		*yobG*	GO:0070298 - negative regulation of phosphorelay signal transduction system GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0044092 - negative regulation of molecular function GO:0010447 - response to acidic pH GO:0071286 - cellular response to magnesium ion
P31 G8	x			*elbA*	GO:0045893 - positive regulation of transcription, DNA-templated GO:0009267 - cellular response to starvation GO:0006950 - response to stress GO:0071468 - cellular response to acidic pH GO:0042177 - negative regulation of protein catabolic process GO:0010350 - cellular response to magnesium starvation
P33 A3			x	*yqeB*	
P33 B1			x	*yedX*	GO:0006144 - purine nucleobase metabolic process
P33 B2			x	*ydjL*	GO:0055114 - oxidation-reduction process
P33 D10		x		*sstT*	GO:0055085 - transmembrane transport GO:0003333 - amino acid transmembrane transport GO:0006865 - amino acid transport GO:0006810 - transport GO:0015826 - threonine transport GO:0006835 - dicarboxylic acid transport GO:0032329 - serine transport

P33 E1			x	*yfbN*	
P33 E5		x		*yggH*	GO:0030488 - tRNA methylation GO:0006400 - tRNA modification GO:0036265 - RNA (guanine-N7)-methylation GO:0032259 - methylation GO:0008033 - tRNA processing
P33 E6		x		*yghZ*	
P33 E10		x		*ygjV*	
P33 H12	x			*nlpI*	GO:0051301 - cell division GO:0007049 - cell cycle
P35 D9		x		*mdtF*	GO:0006810 - transport GO:0006855 - drug transmembrane transport GO:0046677 - response to antibiotic
P35 F10			x	*yiaC*	GO:0006474 - N-terminal protein amino acid acetylatior
P37 A4			x	*rmuC*	GO:0006310 - DNA recombination
P37 A6		x		*yiiR*	
P37 B8		x		*yjbI*	
P37 C1			x	*ade*	
P37 C5	x			*yihT*	GO:0061720 - 6-sulfoquinovose(1-) catabolic process to glycerone phosphate and 3-sulfolactaldehyde GO:1902777 - 6-sulfoquinovose(1-) catabolic process
P37 D1	x			*yidG*	
P37 D2	x			*yieF*	GO:0055114 - oxidation-reduction process GO:0006805 - xenobiotic metabolic process
P37 D3	x			*rffC*	GO:0009246 - enterobacterial common antigen biosynthetic process
P37 D4	x			*yihI*	GO:0042254 - ribosome biogenesis GO:0043547 - positive regulation of GTPase activity GO:0090071 - negative regulation of ribosome biogenesis
P37 D6			x	*yiiX*	
P37 D11	x			*yjeN*	
P37 E6		x		*yijF*	
P37 E7		x		*yjbD*	
P37 E8		x		*yjbM*	
P37 E11			x	*yjeO*	
P37 F3	x			*yigA*	
P37 G8		x		*yjbR*	
P37 G12		x		*yjfM*	
P37 H4	x			*ompL*	GO:0055085 - transmembrane transport GO:0046323 - glucose import GO:0015757 - galactose transport GO:0015751 - arabinose transport GO:0008643 - carbohydrate transport GO:0006811 - ion transport GO:0006810 - transport
P39 B6			x	*yjjK*	
P39 B10			x	*mrr*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0051599 - response to hydrostatic pressure GO:0009307 - DNA restriction-modification system
P39 C7		x		*mfd*	GO:0006283 - transcription-coupled nucleotide-excision repair GO:0006974 - cellular response to DNA damage stimulus GO:0000716 - transcription-coupled nucleotide-excision repair, DNA damage recognition GO:0006355 - regulation of transcription, DNA-templated GO:0006281 - DNA repair
P39 D10		x		*holD*	GO:0071897 - DNA biosynthetic process GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006260 - DNA replication
P39 D12		x		*tauB*	GO:0015837 - amine transport GO:0008152 - metabolic process GO:0010438 - cellular response to sulfur starvation GO:0015734 - taurine transport GO:0006810 - transport
P39 F1		x		*ytfG*	GO:0055114 - oxidation-reduction process
P39 G1		x		*ytfJ*	
P43 A1		x		*serB*	GO:0008152 - metabolic process GO:0016311 - dephosphorylation GO:0008652 - cellular amino acid biosynthetic process GO:0006564 - L-serine biosynthetic process

P43 A2		x		*entF*	GO:0009058 - biosynthetic process GO:0008152 - metabolic process GO:0043041 - amino acid activation for nonribosomal peptide biosynthetic process GO:0009239 - enterobactin biosynthetic process
P43 C2	x			*entE*	GO:0019290 - siderophore biosynthetic process GO:0008152 - metabolic process GO:0009239 - enterobactin biosynthetic process
P43 C6			x	*menE*	GO:0051289 - protein homotetramerization GO:0008152 - metabolic process GO:0009234 - menaquinone biosynthetic process
P43 D2		x		*entB*	GO:0002047 - phenazine biosynthetic process GO:0008152 - metabolic process GO:0009239 - enterobactin biosynthetic process
P43 D11		x		*csgA*	GO:1990000 - amyloid fibril formation GO:0044010 - single-species biofilm formation GO:0007155 - cell adhesion
P43 D12	x			*flgG*	GO:0071978 - bacterial-type flagellum-dependent swarming motility GO:0071973 - bacterial-type flagellum-dependent cell motility GO:0044781 - bacterial-type flagellum organization
P43 E5	x			*cobU*	GO:0051188 - cofactor biosynthetic process GO:0006974 - cellular response to DNA damage stimulus GO:0006779 - porphyrin-containing compound biosynthetic process GO:0016310 - phosphorylation GO:0009236 - cobalamin biosynthetic process
P43 E7	x			*idi*	GO:0009240 - isopentenyl diphosphate biosynthetic process GO:0050992 - dimethylallyl diphosphate biosynthetic process GO:0006974 - cellular response to DNA damage stimulus GO:0008299 - isoprenoid biosynthetic process
P43 E8		x		*fre*	GO:0043085 - positive regulation of catalytic activity GO:0030091 - protein repair GO:0006979 - response to oxidative stress GO:0055072 - iron ion homeostasis GO:0055114 - oxidation-reduction process GO:0006811 - ion transport GO:0006810 - transport
P43 E11		x		*flgN*	GO:0044781 - bacterial-type flagellum organization GO:0044780 - bacterial-type flagellum assembly
P43 F3		x		*moaC*	GO:0034214 - protein hexamerization GO:0032324 - molybdopterin cofactor biosynthetic process GO:0006777 - Mo-molybdopterin cofactor biosynthetic process
P43 F4		x		*paaF*	GO:0006635 - fatty acid beta-oxidation GO:0008152 - metabolic process GO:0010124 - phenylacetate catabolic process GO:0006631 - fatty acid metabolic process GO:0006629 - lipid metabolic process
P43 F11		x		*flgA*	GO:0071973 - bacterial-type flagellum-dependent cell motility GO:0044781 - bacterial-type flagellum organization
P43 G3	x			*moaD*	GO:0006777 - Mo-molybdopterin cofactor biosynthetic process
P43 G4	x			*paaG*	GO:0008152 - metabolic process GO:0010124 - phenylacetate catabolic process
P43 G10		x		*ybgP*	GO:0061077 - chaperone-mediated protein folding GO:0071555 - cell wall organization GO:0043711 - pilus organization GO:0006457 - protein folding
P43 G12		x		*flgK*	GO:0071973 - bacterial-type flagellum-dependent cell motility GO:0044780 - bacterial-type flagellum assembly
P43 H7	x			*gshB*	GO:0006750 - glutathione biosynthetic process
P43 H8	x			*menA*	GO:0009234 - menaquinone biosynthetic process
P45 A5			x	*yraI*	GO:0061077 - chaperone-mediated protein folding GO:0071555 - cell wall organization GO:0006457 - protein folding GO:0043711 - pilus organization
P45 A8			x	*fimA*	GO:0007155 - cell adhesion
P45 A11			x	*cheW*	GO:0051649 - establishment of localization in cell GO:0007165 - signal transduction GO:0006935 - chemotaxis

P45 B9			x	*ahpC*	GO:0045454 - cell redox homeostasis GO:0098869 - cellular oxidant detoxification GO:0033214 - iron assimilation by chelation and transport GO:0006979 - response to oxidative stress GO:0009970 - cellular response to sulfate starvation GO:0033194 - response to hydroperoxide GO:0033195 - response to alkyl hydroperoxide GO:0055114 - oxidation-reduction process
P45 B10		x		*trg*	GO:0007165 - signal transduction GO:0006935 - chemotaxis
P45 B11		x		*motB*	GO:0097588 - archaeal or bacterial-type flagellum-dependent cell motility GO:0006935 - chemotaxis
P45 C11			x	*motA*	GO:0071978 - bacterial-type flagellum-dependent swarming motility GO:0071973 - bacterial-type flagellum-dependent cell motility GO:0015031 - protein transport GO:0097588 - archaeal or bacterial-type flagellum-dependent cell motility GO:0015992 - proton transport GO:0006935 - chemotaxis GO:0006811 - ion transport GO:0006810 - transport
P45 D3		x		*fliL*	GO:0071978 - bacterial-type flagellum-dependent swarming motility GO:0071973 - bacterial-type flagellum-dependent cell motility GO:0097588 - archaeal or bacterial-type flagellum-dependent cell motility GO:0006935 - chemotaxis
P45 D7		x		*rffM*	GO:0009058 - biosynthetic process GO:0009246 - enterobacterial common antigen biosynthetic process
P45 D12		x		*secG*	GO:0006886 - intracellular protein transport GO:0032978 - protein insertion into membrane from inner side GO:0006616 - SRP-dependent cotranslational protein targeting to membrane, translocation GO:0015031 - protein transport GO:0006810 - transport GO:0009306 - protein secretion GO:0043952 - protein transport by the Sec complex GO:0065002 - intracellular protein transmembrane transport
P45 F5			x	*rfaY*	GO:0009244 - lipopolysaccharide core region biosynthetic process GO:0016310 - phosphorylation GO:0009103 - lipopolysaccharide biosynthetic process
P45 G11			x	*hscA*	GO:0097428 - protein maturation by iron-sulfur cluster transfer GO:0006457 - protein folding GO:0070417 - cellular response to cold GO:0016226 - iron-sulfur cluster assembly
P45 H8	x			*betB*	GO:0008152 - metabolic process GO:0051289 - protein homotetramerization GO:0055114 - oxidation-reduction process GO:0019285 - glycine betaine biosynthetic process from choline GO:0006970 - response to osmotic stress
P45 H11			x	*proX*	GO:0006972 - hyperosmotic response GO:0031460 - glycine betaine transport GO:0006865 - amino acid transport GO:0006810 - transport
P47 A6	x			*rfbD*	GO:0019305 - dTDP-rhamnose biosynthetic process GO:0055114 - oxidation-reduction process GO:0045226 - extracellular polysaccharide biosynthetic process GO:0009103 - lipopolysaccharide biosynthetic process GO:0009243 - O antigen biosynthetic process
P47 B4			x	*putA*	GO:0045892 - negative regulation of transcription, DNA-templated GO:0008152 - metabolic process GO:0006560 - proline metabolic process GO:0006561 - proline biosynthetic process GO:0006355 - regulation of transcription, DNA-templated GO:0010133 - proline catabolic process to glutamate GO:0055114 - oxidation-reduction process GO:0006351 - transcription, DNA-templated
P47 B7	x			*hcaB*	GO:0008152 - metabolic process GO:0055114 - oxidation-reduction process GO:0019439 - aromatic compound catabolic process GO:0019380 - 3-phenylpropionate catabolic process
P47 B11			x	*pldB*	GO:0006629 - lipid metabolic process

P47 C11			x		*metF*	GO:0006730 - one-carbon metabolic process GO:0051289 - protein homotetramerization GO:0046654 - tetrahydrofolate biosynthetic process GO:0006555 - methionine metabolic process GO:0035999 - tetrahydrofolate interconversion GO:0055114 - oxidation-reduction process GO:0009086 - methionine biosynthetic process GO:0008652 - cellular amino acid biosynthetic process
P47 E7	x				*cysN*	GO:0000103 - sulfate assimilation GO:0070814 - hydrogen sulfide biosynthetic process GO:0006790 - sulfur compound metabolic process
P47 E8	x				*gcvP*	GO:0019464 - glycine decarboxylation via glycine cleavage system GO:0006546 - glycine catabolic process GO:0006544 - glycine metabolic process GO:0055114 - oxidation-reduction process
P47 E12		x			*treC*	GO:0008152 - metabolic process GO:0005975 - carbohydrate metabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0005993 - trehalose catabolic process
P47 H5		x			*rfbA*	GO:0045226 - extracellular polysaccharide biosynthetic process GO:0009058 - biosynthetic process GO:0019305 - dTDP-rhamnose biosynthetic process GO:0009103 - lipopolysaccharide biosynthetic process GO:0009243 - O antigen biosynthetic process
P47 H6	x				*dsdA*	GO:0070179 - D-serine biosynthetic process GO:0006563 - L-serine metabolic process GO:0070178 - D-serine metabolic process GO:0046416 - D-amino acid metabolic process GO:0006520 - cellular amino acid metabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0036088 - D-serine catabolic process GO:0051410 - detoxification of nitrogen compound
P47 H7		x			*cysI*	GO:0019419 - sulfate reduction GO:0000103 - sulfate assimilation GO:0070814 - hydrogen sulfide biosynthetic process GO:0055114 - oxidation-reduction process GO:0019344 - cysteine biosynthetic process GO:0008652 - cellular amino acid biosynthetic process
P47 H8	x				*speA*	GO:0033388 - putrescine biosynthetic process from arginine GO:0006596 - polyamine biosynthetic process GO:0009446 - putrescine biosynthetic process GO:0008295 - spermidine biosynthetic process GO:0006527 - arginine catabolic process
P47 H12		x			*idnD*	GO:0055114 - oxidation-reduction process GO:0019521 - D-gluconate metabolic process GO:0046183 - L-idonate catabolic process
P49 B3			x		*atoB*	GO:0006635 - fatty acid beta-oxidation GO:0051289 - protein homotetramerization GO:0043442 - acetoacetic acid catabolic process GO:0008152 - metabolic process GO:0006631 - fatty acid metabolic process GO:0006629 - lipid metabolic process
P49 D5		x			*gpt*	GO:0009116 - nucleoside metabolic process GO:0006166 - purine ribonucleoside salvage GO:0032263 - GMP salvage GO:0032264 - IMP salvage GO:0032265 - XMP salvage
P49 E6			x		*rnk*	GO:0032784 - regulation of DNA-templated transcription, elongation GO:0065007 - biological regulation
P49 F5		x			*sbcD*	GO:0006281 - DNA repair GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006310 - DNA recombination GO:0006260 - DNA replication GO:0006259 - DNA metabolic process
P49 F11			x		*torA*	GO:0055114 - oxidation-reduction process GO:0009060 - aerobic respiration GO:0009061 - anaerobic respiration
P49 F12			x		*ydcW*	GO:0008152 - metabolic process GO:0055114 - oxidation-reduction process GO:0009447 - putrescine catabolic process

P49 G11			x	*grxB*	GO:0006749 - glutathione metabolic process GO:0055114 - oxidation-reduction process GO:0045454 - cell redox homeostasis
P49 H12	x			*narW*	GO:0051131 - chaperone-mediated protein complex assembly GO:0042128 - nitrate assimilation
P51 B5	x			*napF*	GO:0055114 - oxidation-reduction process GO:0006979 - response to oxidative stress
P51 D10	x			*aroB*	GO:0009073 - aromatic amino acid family biosynthetic process GO:0008652 - cellular amino acid biosynthetic process GO:0009423 - chorismate biosynthetic process
P51 E8		x		*yliK*	GO:0008152 - metabolic process
P51 F9		x		*uxaA*	GO:0019698 - D-galacturonate catabolic process
P51 F12		x		*grxC*	GO:0042965 - glutaredoxin biosynthetic process GO:0055114 - oxidation-reduction process GO:0045454 - cell redox homeostasis GO:0009263 - deoxyribonucleotide biosynthetic process
P51 G10		x		*glpE*	GO:0006071 - glycerol metabolic process
P51 H1	x			*ynfG*	GO:0055114 - oxidation-reduction process
P53 B10			x	*sspB*	GO:0045732 - positive regulation of protein catabolic process
P53 C4		x		*xapB*	GO:1901642 - nucleoside transmembrane transport GO:0015863 - xanthosine transport GO:0015858 - nucleoside transport GO:0055086 - nucleobase-containing small molecule metabolic process GO:0006810 - transport
P53 C7		x		*deoC*	GO:0016052 - carbohydrate catabolic process GO:0046386 - deoxyribose phosphate catabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0009264 - deoxyribonucleotide catabolic process GO:0015949 - nucleobase-containing small molecule interconversion
P53 E9	x			*relA*	GO:0042594 - response to starvation GO:0008152 - metabolic process GO:0015970 - guanosine tetraphosphate biosynthetic process GO:0016310 - phosphorylation GO:0015969 - guanosine tetraphosphate metabolic process GO:0015949 - nucleobase-containing small molecule interconversion
P53 E10		x		*phoU*	GO:0055085 - transmembrane transport GO:0044341 - sodium-dependent phosphate transport GO:0035725 - sodium ion transmembrane transport GO:0035435 - phosphate ion transmembrane transport GO:0071467 - cellular response to pH GO:0009405 - pathogenesis GO:2000186 - negative regulation of phosphate transmembrane transport GO:0071236 - cellular response to antibiotic GO:0034605 - cellular response to heat GO:0032413 - negative regulation of ion transmembrane transporter activity GO:0030643 - cellular phosphate ion homeostasis GO:0016036 - cellular response to phosphate starvation GO:0010629 - negative regulation of gene expression GO:0009267 - cellular response to starvation GO:0001558 - regulation of cell growth GO:0045936 - negative regulation of phosphate metabolic process GO:0006817 - phosphate ion transport GO:0006810 - transport
P53 G1	x			*fadB*	GO:0009062 - fatty acid catabolic process GO:0006635 - fatty acid beta-oxidation GO:0055114 - oxidation-reduction process GO:0016042 - lipid catabolic process GO:0008152 - metabolic process GO:0006631 - fatty acid metabolic process GO:0006629 - lipid metabolic process
P53 G4	x			*xseA*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006308 - DNA catabolic process
P53 G5		x		*recJ*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006310 - DNA recombination GO:0006281 - DNA repair
P53 G7		x		*glnK*	GO:0050790 - regulation of catalytic activity GO:0006808 - regulation of nitrogen utilization GO:0006355 - regulation of transcription, DNA-templated GO:0045848 - positive regulation of nitrogen utilization GO:0006351 - transcription, DNA-templated

P53 G8	x			*feaR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0045893 - positive regulation of transcription, DNA-templated
P53 G10			x	*yijO*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P53 H5		x		*endA*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006308 - DNA catabolic process
P53 H12		x		*pnuC*	GO:0006810 - transport GO:0034258 - nicotinamide riboside transport
P55 A1		x		*modE*	GO:0055085 - transmembrane transport GO:0015689 - molybdate ion transport GO:0006355 - regulation of transcription, DNA-templated GO:0006810 - transport GO:0006351 - transcription, DNA-templated
P55 A2		x		*yliC*	GO:0006810 - transport GO:0034775 - glutathione transmembrane transport
P55 A4		x		*potC*	GO:1902047 - polyamine transmembrane transport GO:0006810 - transport GO:0015846 - polyamine transport
P55 B2		x		*cmr*	GO:0071805 - potassium ion transmembrane transport GO:0035725 - sodium ion transmembrane transport GO:0030641 - regulation of cellular pH GO:0006855 - drug transmembrane transport GO:0055085 - transmembrane transport GO:0046677 - response to antibiotic GO:0006810 - transport
P55 B10		x		*mglC*	GO:0015765 - methylgalactoside transport GO:0015757 - galactose transport GO:0015749 - monosaccharide transport GO:0006974 - cellular response to DNA damage stimulus GO:0008643 - carbohydrate transport GO:0006810 - transport
P55 C8		x		*ydjE*	GO:0055085 - transmembrane transport GO:0006810 - transport
P55 D1		x		*ybhL*	
P55 D8		x		*manX*	GO:0034219 - carbohydrate transmembrane transport GO:0061490 - glucose import into cell GO:0015761 - mannose transport GO:0032445 - fructose import GO:0015764 - N-acetylglucosamine transport GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0016310 - phosphorylation GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P55 E7			x	*btuE*	GO:0098869 - cellular oxidant detoxification GO:0006979 - response to oxidative stress GO:0033194 - response to hydroperoxide GO:0055114 - oxidation-reduction process
P55 F2		x		*artQ*	GO:1902765 - L-arginine import into cell GO:0006865 - amino acid transport GO:0006810 - transport
P55 G10		x		*glvB*	GO:0034219 - carbohydrate transmembrane transport GO:0016310 - phosphorylation GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P55 H1			x	*ybiT*	GO:0008152 - metabolic process GO:0009409 - response to cold GO:0006810 - transport
P55 H3			x	*potD*	GO:1902047 - polyamine transmembrane transport GO:0006810 - transport GO:0015846 - polyamine transport
P55 H4	x			*sapD*	GO:0008152 - metabolic process GO:0071805 - potassium ion transmembrane transport GO:0015833 - peptide transport GO:0015031 - protein transport GO:0006810 - transport

P57 C1		x		*malK*	GO:0055085 - transmembrane transport GO:0008152 - metabolic process GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0015768 - maltose transport GO:0042956 - maltodextrin transport
P57 C5			x	*rpmF*	GO:0006412 - translation
P57 D6	x			*hyfB*	GO:0042773 - ATP synthesis coupled electron transport GO:0055114 - oxidation-reduction process
P57 D7		x		*fruB*	GO:0032445 - fructose import GO:0016310 - phosphorylation GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P57 D10	x			*proW*	GO:0006972 - hyperosmotic response GO:0031460 - glycine betaine transport GO:0015871 - choline transport GO:0006865 - amino acid transport GO:0006810 - transport
P57 D11	x			*yqeG*	GO:0003333 - amino acid transmembrane transport GO:0006810 - transport
P57 E9		x		*focB*	GO:0015724 - formate transport GO:0006810 - transport
P57 F5	x			*rpmI*	GO:0006412 - translation
P57 F9	x			*yfgO*	GO:0055085 - transmembrane transport GO:0006810 - transport
P57 F11	x			*cmtA*	GO:0034219 - carbohydrate transmembrane transport GO:0015797 - mannitol transport GO:0016310 - phosphorylation GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P57 F12	x			*kbaY*	GO:0051289 - protein homotetramerization GO:0005975 - carbohydrate metabolic process GO:2001059 - D-tagatose 6-phosphate catabolic process
P57 G2		x		*treB*	GO:0043610 - regulation of carbohydrate utilization GO:0034219 - carbohydrate transmembrane transport GO:0015771 - trehalose transport GO:0016310 - phosphorylation GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P57 G3		x		*creD*	
P57 G4	x			*aat*	GO:0030163 - protein catabolic process
P57 G5	x			*selD*	GO:0016260 - selenocysteine biosynthetic process GO:0070329 - tRNA seleno-modification GO:0016310 - phosphorylation
P57 G6		x		*hyfF*	GO:0006974 - cellular response to DNA damage stimulus GO:0055114 - oxidation-reduction process
P57 G8		x		*ptsI*	GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0016310 - phosphorylation GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P57 G9	x			*uraA*	GO:1903791 - uracil transmembrane transport GO:0006810 - transport GO:0055085 - transmembrane transport GO:0015857 - uracil transport
P57 H1	x			*phnC*	GO:0015748 - organophosphate ester transport GO:0008152 - metabolic process GO:0015716 - organic phosphonate transport GO:0006810 - transport GO:0042916 - alkylphosphonate transport
P57 H4		x		*rmf*	GO:0006417 - regulation of translation GO:0032055 - negative regulation of translation in response to stress GO:0033554 - cellular response to stress

P57 H5	x			*rrmA*	GO:0032259 - methylation GO:0006364 - rRNA processing GO:0070475 - rRNA base methylation
P57 H7		x		*hisJ*	GO:1902024 - L-histidine transport GO:0006865 - amino acid transport GO:0006810 - transport
P57 H9	x			*yphD*	GO:0015749 - monosaccharide transport GO:0006810 - transport
P57 H10		x		*gudP*	GO:0006820 - anion transport GO:0055085 - transmembrane transport GO:0006810 - transport
P59 B5			x	*xylF*	GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0015752 - D-ribose transport GO:0015753 - D-xylose transport
P59 B6			x	*tbpA*	GO:0071934 - thiamine transmembrane transport GO:0055085 - transmembrane transport GO:0015888 - thiamine transport GO:0006810 - transport
P59 B7			x	*ybbW*	GO:0055085 - transmembrane transport GO:0015851 - nucleobase transport GO:0015720 - allantoin transport GO:0006810 - transport GO:0006144 - purine nucleobase metabolic process
P59 H5			x	*uhpT*	GO:0006817 - phosphate ion transport GO:0055085 - transmembrane transport GO:0035435 - phosphate ion transmembrane transport GO:0006810 - transport GO:0008643 - carbohydrate transport GO:0015712 - hexose phosphate transport GO:0015760 - glucose-6-phosphate transport
P61 A4			x	*panF*	GO:0071436 - sodium ion export GO:0055085 - transmembrane transport GO:0015887 - pantothenate transmembrane transport GO:0006814 - sodium ion transport GO:0006811 - ion transport GO:0006810 - transport
P61 A8			x	*rusA*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006974 - cellular response to DNA damage stimulus GO:0006310 - DNA recombination GO:0006281 - DNA repair
P61 A10	x			*ampE*	
P61 C2		x		*yggL*	
P61 C5		x		*prmA*	GO:0032259 - methylation GO:0006479 - protein methylation GO:0018023 - peptidyl-lysine trimethylation GO:0018012 - N-terminal peptidyl-alanine trimethylation
P61 C6		x		*dtd*	GO:0006450 - regulation of translational fidelity GO:0009408 - response to heat GO:0019478 - D-amino acid catabolic process GO:0006399 - tRNA metabolic process
P61 C9		x		*rho*	GO:0006355 - regulation of transcription, DNA-templated GO:0006353 - DNA-templated transcription, termination GO:0006351 - transcription, DNA-templated
P61 D8		x		*dgsA*	GO:0005975 - carbohydrate metabolic process GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P61 D12		x		*cspD*	GO:0006950 - response to stress GO:0006355 - regulation of transcription, DNA-templated GO:0042594 - response to starvation GO:0008156 - negative regulation of DNA replication
P61 E1		x		*ygcM*	GO:0008616 - queuosine biosynthetic process
P61 E4		x		*frlA*	GO:1902475 - L-alpha-amino acid transmembrane transport GO:0015807 - L-amino acid transport GO:0003333 - amino acid transmembrane transport GO:0030393 - fructoselysine metabolic process GO:0006865 - amino acid transport GO:0006810 - transport
P61 E8		x		*yegW*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P61 E11		x		*borD*	GO:0071286 - cellular response to magnesium ion

P61 F3	x			*elbB*	GO:0045828 - positive regulation of isoprenoid metabolic process GO:0008299 - isoprenoid biosynthetic process
P61 F6		x		*rplK*	GO:0000027 - ribosomal large subunit assembly GO:0006412 - translation GO:0015968 - stringent response GO:0006415 - translational termination
P61 F10		x		*ampG*	GO:0006810 - transport GO:0055085 - transmembrane transport GO:0015835 - peptidoglycan transport GO:0000270 - peptidoglycan metabolic process
P61 F11		x		*nfrB*	GO:0006810 - transport
P61 G10		x		*ybaA*	
P61 H8		x		*cpdA*	GO:0042545 - cell wall modification GO:0008152 - metabolic process
P63 B1		x		*ymfG*	GO:0006310 - DNA recombination
P63 C7		x		*yiiT*	GO:0006950 - response to stress
P63 D5		x		*emrA*	GO:0055085 - transmembrane transport GO:0006855 - drug transmembrane transport GO:0046677 - response to antibiotic GO:0006810 - transport
P63 E6		x		*acpT*	GO:0019878 - lysine biosynthetic process via aminoadipic acid GO:0018070 - peptidyl-serine phosphopantetheinylation GO:0006633 - fatty acid biosynthetic process
P63 G12			x	*ulaC*	GO:0034219 - carbohydrate transmembrane transport GO:0016310 - phosphorylation GO:0006810 - transport GO:0015882 - L-ascorbic acid transport GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system
P63 H9		x		*hemN*	GO:0006782 - protoporphyrinogen IX biosynthetic process GO:0006779 - porphyrin-containing compound biosynthetic process GO:0019353 - protoporphyrinogen IX biosynthetic process from glutamate GO:0055114 - oxidation-reduction process
P65 E9			x	*yhiL*	
P65 F8		x		*gltB*	GO:0019676 - ammonia assimilation cycle GO:0008652 - cellular amino acid biosynthetic process GO:0008152 - metabolic process GO:0097054 - L-glutamate biosynthetic process GO:0006807 - nitrogen compound metabolic process GO:0055114 - oxidation-reduction process GO:0006541 - glutamine metabolic process GO:0006537 - glutamate biosynthetic process
P65 F11		x		*dsbA*	
P65 F12		x		*ytfA*	
P65 G6			x	*fucK*	GO:0046835 - carbohydrate phosphorylation GO:0019317 - fucose catabolic process GO:0006004 - fucose metabolic process GO:0005975 - carbohydrate metabolic process GO:0016310 - phosphorylation GO:0042355 - L-fucose catabolic process GO:0019571 - D-arabinose catabolic process
P65 G7			x	*tdcC*	GO:0015992 - proton transport GO:0032329 - serine transport GO:0006810 - transport GO:0006865 - amino acid transport GO:0003333 - amino acid transmembrane transport GO:0015825 - L-serine transport GO:0015826 - threonine transport
P67 A1		x		*yjgX*	GO:0009244 - lipopolysaccharide core region biosynthetic process GO:0008152 - metabolic process
P67 A8		x		*mgsA*	GO:0019242 - methylglyoxal biosynthetic process
P67 E9		x		*sieB*	
P69 B3			x	*menD*	GO:0009234 - menaquinone biosynthetic process
P69 B5	x			*amiC*	GO:0051301 - cell division GO:0071555 - cell wall organization GO:0043093 - FtsZ-dependent cytokinesis GO:0009253 - peptidoglycan catabolic process
P69 B8	x			*yghX*	GO:0008152 - metabolic process

P69 B12			x	*kdgT*	GO:0015992 - proton transport GO:0008643 - carbohydrate transport GO:0006810 - transport GO:0046411 - 2-keto-3-deoxygluconate transport GO:0035429 - gluconate transmembrane transport
P69 C3		x		*torI*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:2000143 - negative regulation of DNA-templated transcription, initiation GO:0044349 - DNA excision GO:0006310 - DNA recombination
P69 C6	x			*ygfU*	GO:1903825 - organic acid transmembrane transport GO:0006811 - ion transport GO:0006810 - transport GO:0015992 - proton transport GO:0055085 - transmembrane transport GO:0015747 - urate transport GO:0042906 - xanthine transport
P69 C8		x		*yghY*	GO:0008152 - metabolic process
P69 D1		x		*yoeF*	GO:0006576 - cellular biogenic amine metabolic process
P69 F1		x		*yoeB*	GO:0098795 - mRNA cleavage involved in gene silencing GO:1903507 - negative regulation of nucleic acid-templated transcription GO:0090502 - RNA phosphodiester bond hydrolysis, endonucleolytic GO:0006402 - mRNA catabolic process GO:0044010 - single-species biofilm formation GO:0045947 - negative regulation of translational initiation GO:0006401 - RNA catabolic process GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P69 F2		x		*bcr*	GO:0015833 - peptide transport GO:0015031 - protein transport GO:0015893 - drug transport GO:0035442 - dipeptide transmembrane transport GO:0006855 - drug transmembrane transport GO:0055085 - transmembrane transport GO:0046677 - response to antibiotic GO:0006810 - transport
P69 F5			x	*xdhA*	GO:0009115 - xanthine catabolic process GO:0009114 - hypoxanthine catabolic process GO:0055114 - oxidation-reduction process GO:0006166 - purine ribonucleoside salvage GO:0006144 - purine nucleobase metabolic process
P69 G10	x			*yhdJ*	GO:0032775 - DNA methylation on adenine GO:0032259 - methylation GO:0006306 - DNA methylation
P69 H7		x		*hybF*	GO:0006464 - cellular protein modification process GO:0051604 - protein maturation
P69 H8	x			*yqiH*	GO:0061077 - chaperone-mediated protein folding GO:0071555 - cell wall organization GO:0043711 - pilus organization GO:0006974 - cellular response to DNA damage stimulus
P69 H10		x		*yhdX*	GO:0006865 - amino acid transport GO:0006810 - transport
P69 H11		x		*ptsA*	GO:0016310 - phosphorylation GO:0009401 - phosphoenolpyruvate-dependent sugar phosphotransferase system GO:0008643 - carbohydrate transport GO:0006810 - transport
P71 A4			x	*yicO*	GO:1904823 - purine nucleobase transmembrane transport GO:0006863 - purine nucleobase transport GO:0015853 - adenine transport GO:0055085 - transmembrane transport GO:0006810 - transport
P71 A8			x	*yhhT*	GO:0055085 - transmembrane transport
P71 B9		x		*yhfY*	GO:0006355 - regulation of transcription, DNA-templated
P71 C5			x	*yiaB*	GO:0006974 - cellular response to DNA damage stimulus
P71 F10			x	*ubiC*	GO:0042866 - pyruvate biosynthetic process GO:0006744 - ubiquinone biosynthetic process
P73 A11			x	*yadD*	
P73 B4			x	*fimI*	GO:0007155 - cell adhesion GO:0009297 - pilus assembly
P73 D7	x			*ygiQ*	GO:0008152 - metabolic process

P73 D8	x			*rhtB*	GO:0006865 - amino acid transport GO:0006810 - transport GO:0042968 - homoserine transport
P75 B4		x		*ybgQ*	GO:0055085 - transmembrane transport GO:0009297 - pilus assembly GO:0006810 - transport
P75 B10			x	*yciO*	
P75 C1	x			*yahM*	
P75 C4		x		*ybhT*	GO:0006855 - drug transmembrane transport GO:0046677 - response to antibiotic GO:0006810 - transport GO:0036460 - cellular response to cell envelope stress
P75 C9			x	*ycgH*	
P75 E8		x		*ymfE*	
P75 E9	x			*ycgN*	
P75 E12	x			*ydcO*	GO:0042919 - benzoate transport GO:0055085 - transmembrane transport
P75 G4		x		*ybiO*	GO:0006811 - ion transport GO:0006810 - transport GO:0055085 - transmembrane transport GO:0071470 - cellular response to osmotic stress
P75 G8		x		*ymfT*	
P77 B10			x	*yfbE*	GO:0046493 - lipid A metabolic process GO:0006629 - lipid metabolic process GO:0046677 - response to antibiotic GO:0009103 - lipopolysaccharide biosynthetic process GO:0009245 - lipid A biosynthetic process
P77 E8		x		*yohN*	GO:1901652 - response to peptide GO:0006974 - cellular response to DNA damage stimulus GO:0010045 - response to nickel cation GO:0032025 - response to cobalt ion
P79 B5		x		*nadR*	GO:0045892 - negative regulation of transcription, DNA-templated GO:0009058 - biosynthetic process GO:0006810 - transport GO:0009435 - NAD biosynthetic process GO:0016310 - phosphorylation GO:0008152 - metabolic process GO:0006355 - regulation of transcription, DNA-templated GO:0019363 - pyridine nucleotide biosynthetic process GO:0006351 - transcription, DNA-templated
P79 C9		x		*modA*	GO:0015689 - molybdate ion transport GO:0006810 - transport
P79 D1			x	*yqaC*	GO:0005975 - carbohydrate metabolic process
P79 D6		x		*ybfO*	GO:0097264 - self proteolysis
P79 D9	x			*malT*	GO:0045913 - positive regulation of carbohydrate metabolic process GO:0045893 - positive regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0005975 - carbohydrate metabolic process
P79 E5		x		*ybhR*	GO:0006855 - drug transmembrane transport GO:0055085 - transmembrane transport GO:0006974 - cellular response to DNA damage stimulus GO:0006810 - transport
P79 F9		x		*ydhB*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P79 F12		x		*mutS*	GO:0006281 - DNA repair GO:0006974 - cellular response to DNA damage stimulus GO:0000018 - regulation of DNA recombination GO:0006298 - mismatch repair
P79 G6		x		*rhsD*	GO:0097264 - self proteolysis GO:0010438 - cellular response to sulfur starvation
P79 G9	x			*rtcB*	GO:0006974 - cellular response to DNA damage stimulus GO:0006281 - DNA repair GO:0006266 - DNA ligation GO:0006396 - RNA processing GO:0042245 - RNA repair
P79 G10	x			*rspB*	GO:0055114 - oxidation-reduction process

P79 G12		x		*mutH*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0006974 - cellular response to DNA damage stimulus GO:0006281 - DNA repair GO:0006304 - DNA modification GO:0000018 - regulation of DNA recombination GO:0006298 - mismatch repair
P81 A1			x	*mutY*	GO:0008152 - metabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0006281 - DNA repair GO:0006284 - base-excision repair
P81 A2			x	*gidB*	GO:0070476 - rRNA (guanine-N7)-methylation GO:0032259 - methylation GO:0006364 - rRNA processing GO:0070475 - rRNA base methylation
P81 F5			x	*ycfJ*	GO:1900190 - regulation of single-species biofilm formation
P83 A6			x	*yhgG*	
P83 A7			x	*hemY*	GO:0042168 - heme metabolic process GO:0006779 - porphyrin-containing compound biosynthetic process
P83 A11			x	*gabT*	GO:0042450 - arginine biosynthetic process via ornithine GO:0009448 - gamma-aminobutyric acid metabolic process GO:0009450 - gamma-aminobutyric acid catabolic process
P83 B1			x	*yfeN*	
P83 B6			x	*yzgL*	
P83 H1		x		*ydfE*	
P83 H5	x			*yhfT*	
P83 H6	x			*yibI*	
P83 H9	x			*ppdA*	
P83 H12	x			*glf*	GO:0009103 - lipopolysaccharide biosynthetic process GO:0009243 - O antigen biosynthetic process
P85 A8		x		*alsA*	GO:0015754 - allose transport GO:0015749 - monosaccharide transport GO:0008152 - metabolic process GO:0008643 - carbohydrate transport GO:0006810 - transport
P85 C6			x	*yliD*	GO:0006810 - transport GO:0034775 - glutathione transmembrane transport
P85 C9			x	*ssuE*	GO:0051289 - protein homotetramerization GO:0006974 - cellular response to DNA damage stimulus GO:0055114 - oxidation-reduction process GO:0046306 - alkanesulfonate catabolic process GO:0009970 - cellular response to sulfate starvation
P85 C10			x	*mhpD*	GO:0008152 - metabolic process GO:0019380 - 3-phenylpropionate catabolic process GO:0019439 - aromatic compound catabolic process
P85 D2			x	*fucI*	GO:0019317 - fucose catabolic process GO:0006004 - fucose metabolic process GO:0005996 - monosaccharide metabolic process GO:0005975 - carbohydrate metabolic process GO:0019571 - D-arabinose catabolic process GO:0042355 - L-fucose catabolic process
P85 E2		x		*fucU*	GO:0042354 - L-fucose metabolic process GO:0005996 - monosaccharide metabolic process GO:0006004 - fucose metabolic process GO:0005975 - carbohydrate metabolic process
P85 F6		x		*yecC*	GO:0015830 - diaminopimelate transport GO:1903712 - cysteine transmembrane transport GO:0008152 - metabolic process GO:0003333 - amino acid transmembrane transport GO:0015811 - L-cystine transport GO:0006865 - amino acid transport GO:0006810 - transport
P85 F9		x		*alpA*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:0042710 - biofilm formation GO:0045893 - positive regulation of transcription, DNA-templated
P85 H1		x		*hypE*	GO:0046892 - peptidyl-S-carbamoyl-L-cysteine dehydration GO:0051604 - protein maturation

P85 H5	x			*acrA*	GO:0015721 - bile acid and bile salt transport GO:0055085 - transmembrane transport GO:0006810 - transport GO:0006855 - drug transmembrane transport GO:0046677 - response to antibiotic
P87 B2		x		*yhiM*	GO:0071229 - cellular response to acid chemical
P87 B5		x		*ydbJ*	
P87 B7		x		*pcnB*	GO:0043631 - RNA polyadenylation GO:0006396 - RNA processing GO:0006397 - mRNA processing GO:0006378 - mRNA polyadenylation GO:0006351 - transcription, DNA-templated GO:0006276 - plasmid maintenance GO:0009451 - RNA modification
P87 C5	x			*yncH*	
P87 C9	x			*asr*	GO:0010447 - response to acidic pH GO:0001101 - response to acid chemical GO:0010043 - response to zinc ion
P87 D4	x			*hokE*	GO:0006974 - cellular response to DNA damage stimulus
P87 D11		x		*ygcS*	GO:0015850 - organic hydroxy compound transport GO:0055085 - transmembrane transport GO:0006810 - transport
P87 E2		x		*yjdC*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P87 E3		x		*yjjM*	GO:0006351 - transcription, DNA-templated GO:0019584 - galactonate catabolic process GO:0006355 - regulation of transcription, DNA-templated
P87 E6		x		*ygdI*	
P87 E8		x		*ycfS*	GO:0071555 - cell wall organization GO:0006508 - proteolysis GO:0009252 - peptidoglycan biosynthetic process GO:0008360 - regulation of cell shape GO:0043164 - Gram-negative-bacterium-type cell wall biogenesis GO:0018104 - peptidoglycan-protein cross-linking
P87 E10		x		*yohG*	GO:0006810 - transport GO:0046677 - response to antibiotic
P87 E11		x		*ygeO*	GO:0009405 - pathogenesis
P87 F8		x		*emtA*	GO:0071555 - cell wall organization GO:0000270 - peptidoglycan metabolic process GO:0016998 - cell wall macromolecule catabolic process
P87 G1		x		*yieP*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated
P87 G3	x			*tnaB*	GO:0006865 - amino acid transport GO:0006810 - transport GO:0015801 - aromatic amino acid transport GO:0003333 - amino acid transmembrane transport GO:0006569 - tryptophan catabolic process
P87 G4	x			*ymfP*	
P87 G8	x			*abgT*	GO:1902604 - p-aminobenzoyl-glutamate transmembrane transpor GO:0006865 - amino acid transport GO:0006810 - transport GO:0015814 - p-aminobenzoyl-glutamate transport
P87 H5		x		*nuoC*	GO:0055114 - oxidation-reduction process GO:0008152 - metabolic process GO:0006810 - transport
P87 H9		x		*yedQ*	GO:1902201 - negative regulation of bacterial-type flagellum-dependent cell motility GO:0030244 - cellulose biosynthetic process
P89 B4		x		*ybbN*	GO:0055114 - oxidation-reduction process GO:0061077 - chaperone-mediated protein folding GO:0045454 - cell redox homeostasis GO:0006662 - glycerol ether metabolic process
P89 B8		x		*yibK*	GO:0032259 - methylation GO:0030488 - tRNA methylation GO:0008033 - tRNA processing GO:0006396 - RNA processing GO:0001510 - RNA methylation GO:0002131 - wobble position cytosine ribose methylation GO:0002132 - wobble position uridine ribose methylation
P89 E8		x		*yaaY*	GO:0006974 - cellular response to DNA damage stimulus

P89 E9		x		*ygcW*	GO:0008152 - metabolic process GO:0006974 - cellular response to DNA damage stimulus GO:0055114 - oxidation-reduction process
P89 E12	x			*yfeH*	
P89 G5	x			*rpsT*	GO:0043086 - negative regulation of catalytic activity GO:0006412 - translation
P89 G6	x			*ybiM*	GO:0009242 - colanic acid biosynthetic process
P89 G9		x		*rpsU*	GO:0006412 - translation
P89 G10		x		*yfeS*	
P89 H5		x		*marC*	
P89 H6		x		*dmsD*	GO:0061077 - chaperone-mediated protein folding
P89 H10		x		*baeR*	GO:0006355 - regulation of transcription, DNA-templated GO:0006351 - transcription, DNA-templated GO:2001023 - regulation of response to drug GO:2000144 - positive regulation of DNA-templated transcription, initiation GO:0000160 - phosphorelay signal transduction system
P89 H11		x		*yeeP*	GO:0000027 - ribosomal large subunit assembly
P91 F1		x		*ydfK*	
P91 H2			x	*ydjR*	
P93 D1	x			*ubiX*	GO:0051188 - cofactor biosynthetic process GO:0009108 - coenzyme biosynthetic process GO:0006744 - ubiquinone biosynthetic process
P93 D2		x		*atpB*	GO:0015986 - ATP synthesis coupled proton transport GO:0042777 - plasma membrane ATP synthesis coupled proton transport GO:0015992 - proton transport GO:0006811 - ion transport GO:0006810 - transport GO:0006754 - ATP biosynthetic process
P93 G1	x			*phnN*	GO:0046835 - carbohydrate phosphorylation GO:0019634 - organic phosphonate metabolic process GO:0006015 - 5-phosphoribose 1-diphosphate biosynthetic process GO:0009435 - NAD biosynthetic process
P95 A1		x		*ompR*	GO:0045893 - positive regulation of transcription, DNA-templated GO:0006355 - regulation of transcription, DNA-templated GO:0000160 - phosphorelay signal transduction system GO:0006351 - transcription, DNA-templated
P95 A2		x		*secB*	GO:0051262 - protein tetramerization GO:0043952 - protein transport by the Sec complex GO:0015031 - protein transport GO:0006605 - protein targeting GO:0008104 - protein localization GO:0061077 - chaperone-mediated protein folding GO:0072321 - chaperone-mediated protein transport GO:0006810 - transport GO:0006457 - protein folding
P95 A5			x	*rbfA*	GO:0042254 - ribosome biogenesis GO:0006364 - rRNA processing GO:0006974 - cellular response to DNA damage stimulus GO:0009409 - response to cold GO:0030490 - maturation of SSU-rRNA
P95 A6			x	*ybeY*	GO:0006508 - proteolysis GO:0042254 - ribosome biogenesis GO:0031564 - transcription antitermination GO:0000478 - endonucleolytic cleavage involved in rRNA processing GO:0030490 - maturation of SSU-rRNA GO:0006364 - rRNA processing GO:0009408 - response to heat GO:0042274 - ribosomal small subunit biogenesis GO:0006412 - translation
P95 C3			x	*rpmJ*	GO:0006412 - translation
P95 D2		x		*rnhA*	GO:0090305 - nucleic acid phosphodiester bond hydrolysis GO:0090502 - RNA phosphodiester bond hydrolysis, endonucleolytic GO:0006401 - RNA catabolic process GO:0043137 - DNA replication, removal of RNA primer
P95 D3		x		*nusB*	GO:0006355 - regulation of transcription, DNA-templated GO:0006353 - DNA-templated transcription, termination GO:0006351 - transcription, DNA-templated

P95 D4			x	*envC*	GO:0051345 - positive regulation of hydrolase activity GO:0001896 - autolysis GO:0009273 - peptidoglycan-based cell wall biogenesis GO:0051301 - cell division GO:0007049 - cell cycle GO:0000920 - cell separation after cytokinesis GO:0042493 - response to drug
P95 F1	x			*yfgA*	
P95 F2		x		*fdx*	GO:0055114 - oxidation-reduction process GO:0016226 - iron-sulfur cluster assembly
P95 F4		x		*parC*	GO:0006268 - DNA unwinding involved in DNA replication GO:0006259 - DNA metabolic process GO:0030541 - plasmid partitioning GO:0007062 - sister chromatid cohesion GO:0007059 - chromosome segregation GO:0006265 - DNA topological change
P95 G1		x		*dnaK*	GO:1903506 - regulation of nucleic acid-templated transcription GO:0006461 - protein complex assembly GO:0043241 - protein complex disassembly GO:0051085 - chaperone mediated protein folding requiring cofactor GO:0070389 - chaperone cofactor-dependent protein refolding GO:0034620 - cellular response to unfolded protein GO:0006457 - protein folding GO:0043335 - protein unfolding GO:0009408 - response to heat GO:0006260 - DNA replication
P95 G2		x		*rluD*	GO:0009451 - RNA modification GO:0006364 - rRNA processing GO:0001522 - pseudouridine synthesis GO:0000455 - enzyme-directed rRNA pseudouridine synthesis GO:0000027 - ribosomal large subunit assembly
P95 G3		x		*rfaE*	GO:0046835 - carbohydrate phosphorylation GO:0009058 - biosynthetic process GO:0097171 - ADP-L-glycero-beta-D-manno-heptose biosynthetic process GO:0009244 - lipopolysaccharide core region biosynthetic process GO:0016310 - phosphorylation GO:0008152 - metabolic process GO:0009103 - lipopolysaccharide biosynthetic process GO:0005975 - carbohydrate metabolic process