Gene	Description	Organism	Accession number	*E* value	Clone ID(s)
abc	ATP-binding component of a transporter	Yersinia pestis KIM	NP_670403.1	1.10E-100	P090081,P150003
accC	biotin carboxylase	Yersinia pseudotuberculosis IP 32953	YP_072054.1	5.80E-24	P080032,P080032
accD	acetyl CoA carboxylase, carboxytransferase component, beta subunit	Yersinia pestis KIM	NP_668919.1	1.50E-129	P080045,P020055
ackA	acetate kinase	Yersinia pseudotuberculosis IP 32953	YP_071107.1	1.80E-175	P030037,P130078,P180068,P150078,P070081,P130057,P050080,P100063,P150015,P190008,P030026,P140014,P010035,P200016,P140040,P090008,P040017,P060093,P120058
acrA	acridine efflux pump, membrane fusion (MFP/HlyD) family protein	Yersinia pseudotuberculosis IP 32953	YP_069525.1	1.00E-126	P110033,P120008,P180060,P150058,P080024
acrB	acridine efflux pump	Yersinia pestis KIM	NP_668379.1	1.70E-69	P200025
adk	adenylate kinase	Yersinia enterocolitica	CAA87696.1	2.40E-40	P070028,P040086
aexT	AexT protein	Aeromonas salmonicida	CAE17664.1	1.30E-19	P170021,P060021,P080077,P060085,P070048,P140063
aidA	putative autotransported protein	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	YP_152718.1	1.90E-34	P090026
alaS	alanyl-tRNA synthetase	Yersinia pestis KIM	NP_668216.1	2.80E-15	P140081,P200001
alr	alanine racemase 1	Yersinia pestis KIM	NP_667915.1	8.40E-80	P120077,P040036,P110062
apaH	diadenosine tetraphosphatase	Yersinia pseudotuberculosis IP 32953	YP_069173.1	4.70E-73	P080068,P110025,P080035,P030049,P150054
artP	Arginine transport ATP-binding protein artP	Escherichia coli CFT073	NP_752927.1	4.30E-105	P170042
artQ	ABC arginine transporter, permease subunit artQ	Yersinia pseudotuberculosis IP 32953	YP_069907.1	9.30E-24	P070044
aspC	aspartate aminotransferase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG75442.1	6.40E-148	P060052,P030036
aspS	aspartyl-tRNA synthetase (aspartate--tRNA ligase) (asprs)	Photorhabdus luminescens subsp. laumondii TTO1	NP_929367.1	3.70E-55	P200065
atpA	ATP synthase alpha chain	Photorhabdus luminescens subsp. laumondii TTO1	NP_927418.1	8.30E-17	P150075
atpC	membrane-bound ATP synthase, F1 sector, epsilon-subunit	Yersinia pestis KIM	NP_671425.1	6.60E-29	P100082,P120082,P110072
atpF	unnamed protein product	Escherichia coli	CAA23592.1	3.70E-15	P150075
barA	putative global response regulation sensor kinase GrrS	Serratia plymuthica	AAL11449.1	1.90E-35	P200055
bioH	putative biotin biosynthesis protein	Yersinia pseudotuberculosis IP 32953	YP_072252.1	7.60E-48	P150038
cafA	ribonuclease G (RNase G) (cytoplasmic axial filament protein)	Photorhabdus luminescens subsp. laumondii TTO1	NP_931259.1	4.10E-109	P140022,P170074,P130005,P060046
carB	carbamoyl-phosphate synthase large subunit	Yersinia pestis KIM	NP_670989.1	2.20E-43	P060070,P180084
clpA	ATP-binding component of serine protease	Yersinia pestis KIM	NP_670109.1	2.80E-96	P060071,P190014,P190017,P190016
clpB	heat shock protein	Yersinia pestis KIM	NP_668245.1	3.50E-105	P010083,P090011,P120091
clpX	ATP-dependent specificity component of clpP serine protease, chaperone	Yersinia pestis KIM	NP_668358.1	1.50E-46	P040054,P120041
cls	cardiolipin synthase	Yersinia pestis KIM	NP_669348.1	1.50E-44	P190042,P190041
coaA	pantothenate kinase	Yersinia pseudotuberculosis IP 32953	YP_068820.1	3.80E-91	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019,P040095,P050050,P010077
COG0286	XmnI methyltransferase	Xanthomonas campestris pv. campestris str. ATCC 33913	NP_639481.1	6.10E-18	P210048,P080033,P110056
COG1525	Micrococcal nuclease (thermonuclease) homologs	Azotobacter vinelandii	ZP_00092271.1	2.80E-37	P130096,P130082
cosB	mannose-1-P guanylyltransferase	Yersinia pseudotuberculosis (type O:1b)	CAB63302.1	2.20E-11	P030035
cpsG	phosphomannomutase	Yersinia pestis KIM	NP_668411.1	2.30E-122	P170026,P200084,P140055,P070015
cpxR	two-component response regulator	Erwinia carotovora subsp. atroseptica SCRI1043	CAG77208.1	4.50E-33	P210063
csrA	RsmA	Pseudomonas fluorescens	AAR21564.1	1.00E-21	P140081,P200001
cyoB	cytochrome o ubiquinol oxidase subunit I	Yersinia pseudotuberculosis IP 32953	YP_069492.1	3.00E-198	P080022,P170080,P190073,P040051
cyoC	cytochrome o ubiquinol oxidase subunit III	Erwinia carotovora subsp. atroseptica SCRI1043	CAG74051.1	4.00E-86	P080022,P170080
cyoE	protoheme IX farnesyltransferase (haeme O biosynthesis)	Yersinia pestis KIM	NP_668348.1	5.30E-82	P040019,P080050,P150026
cysB	CYSB protein	Klebsiella aerogenes	CAA55380.1	4.80E-11	P060049,P130016,P150053,P030082
cysE	serine acetyltransferase	Yersinia pestis KIM	NP_667416.1	2.50E-89	P180071
cytR	transcriptional repressor CytR	Vibrio fischeri ES114	YP_205658.1	5.30E-11	P070078
dapF	diaminopimelate epimerase	Yersinia pseudotuberculosis IP 32953	YP_068736.1	2.10E-24	P140010
dapX	Uncharacterized lipoprotein	Desulfitobacterium hafniense DCB-2	ZP_00100981.1	1.80E-06	P140064
dcm	COG0270: Site-specific DNA methylase	Burkholderia fungorum LB400	ZP_00280731.1	1.60E-06	P130043
deaD	inducible ATP-independent RNA helicase	Yersinia pestis KIM	NP_668033.1	7.60E-177	P090019,P090055,P010037
dedD	putative lipoprotein	Yersinia pestis KIM	NP_668921.1	5.70E-31	P100025,P110036,P020055,P110010,P060036,P040060
dedE	putative colicin V production protein	Yersinia pseudotuberculosis IP 32953	YP_071123.1	4.20E-13	P100025,P110036,P020055,P110010,P060036,P040060
def	polypeptide deformylase (PDF) (formylmethionine deformylase)	Photorhabdus luminescens subsp. laumondii TTO1	NP_931857.1	8.20E-65	P170045,P120044
dgkA	COG0818: Diacylglycerol kinase	Haemophilus somnus 2336	ZP_00133055.2	1.20E-08	P020087,P060011,P020092,P070061,P210070
dgt	deoxyguanosine triphosphate triphosphohydrolase	Yersinia pestis KIM	NP_668142.1	3.00E-06	P120013,P120013
dinJ	COG3077: DNA-damage-inducible protein J	Xylella fastidiosa Ann-1	ZP_00341496.1	4.60E-22	P040061,P200003,P090051

dnaA	DNA biosynthesis protein	Yersinia pestis KIM	NP_671404.1	1.20E-219	P140057
dnaB	replicative DNA helicase	Photorhabdus luminescens subsp. laumondii TTO1	NP_931532.1	1.70E-122	P120077,P040036
dnaE	DNA polymerase III, alpha subunit	Yersinia pestis KIM	NP_670419.1	1.90E-33	P180039
dnaK	chaperone protein DnaK	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76780.1	2.00E-32	P130044,P180046
dnaN	DNA polymerase III, beta subunit protein	Yersinia pseudotuberculosis IP 32953	YP_072417.1	9.50E-73	P130080
dsbA	DsbA precursor	Pectobacterium carotovorum subsp. carotovorum	AAD47613.1	2.00E-61	P180082
efp	elongation factor P (EF-P)	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	AAX68119.1	3.10E-98	P190090,P180027,P080021
era	putative GTP-binding protein	Yersinia pseudotuberculosis IP 32953	YP_071396.1	1.50E-39	P120054
evgA	DNA-binding response regulator, LuxR family	Pseudomonas putida KT2440	AAN66715.1	1.50E-29	P200005,P130096,P200093
evgS	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	Pseudomonas syringae pv. syringae B728a	ZP_00205893.1	1.10E-41	P040041,P100086,P040003,P160094,P030088
fabF	3-oxoacyl-[acyl-carrier-protein] synthase II	Shigella flexneri 2a str. 301	NP_707011.1	1.10E-55	P070089
fabG	3-oxoacyl-[acyl-carrier protein] reductase	Erwinia carotovora subsp. atroseptica SCRI1043	YP_049897.1	3.40E-70	P070089
fabZ	unknown	Yersinia enterocolitica	CAA80952.1	4.50E-61	P190063,P040007
fbp		Photorhabdus luminescens subsp. laumondii TTO1	NP_931714.1	1.00E-31	P180051
fcuA	TonB-dependent siderophore receptor	Erwinia carotovora subsp. atroseptica SCRI1043	CAG77012.1	2.20E-16	P030050,P200083,P110094
feoB	ferrous iron transport protein B	Yersinia pestis KIM	NP_671204.1	1.50E-84	P120033
fldA	flavodoxin 1	Yersinia pseudotuberculosis IP 32953	YP_069663.1	6.80E-77	P030094,P020063,P090090,P100013,P090069
fmt	methionyl-tRNA formyltransferase	Yersinia pseudotuberculosis IP 32953	YP_072147.1	5.60E-57	P010008,P180021
folA	dihydrofolate reductase	Vibrio parahaemolyticus RIMD 2210633	NP_796712.1	3.20E-36	P210031
folC	dihydrofolate:folylpolyglutamate synthetase	Yersinia pestis KIM	NP_668920.1	6.10E-79	P100025,P110036,P020055,P110010,P060036,P040060
folE	GTP cyclohydrolase I	Yersinia pestis KIM	NP_669966.1	5.20E-54	P070070
folK	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokina se, PPPK	Yersinia pseudotuberculosis IP 32953	YP_069272.1	1.20E-53	P110033,P120008,P180060
fpr	ferredoxin--NADP reductase	Yersinia pestis biovar Medievalis str. 91001	NP_991494.1	3.10E-76	P150060,P010033,P150062
frr	ribosome releasing factor	Photorhabdus luminescens subsp. laumondii TTO1	NP_928020.1	3.50E-51	P050053,P060028,P140039,P110052
fruA	PTS system, fructose-specific IIBC transport protein	Yersinia pestis KIM	NP_670185.1	2.80E-74	P190093,P200073
fruB	PTS system, fructose-specific II component / phosphocarrier p...	Yersinia pseudotuberculosis IP 32953	YP_069861.1	2.70E-50	P130029,P170056
fruK	1-phosphofructokinase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG75628.1	3.50E-95	P070063
ftn	Ferritin 1	Escherichia coli CFT073	NP_754213.1	7.20E-54	P100070,P150067,P110074,P080010
ftsW	cell division membrane protein FtsW	Yersinia pseudotuberculosis IP 32953	YP_069228.1	1.30E-93	P120079
ftsZ	tubulin-like GTP-binding protein and GTPase, forms circumferential ring in cell division	Yersinia pseudotuberculosis IP 32953	YP_069234.1	1.40E-54	P020051,P020051,P180062
fumC	fumarate hydratase, class II	Yersinia pestis biovar Medievalis str. 91001	NP_993397.1	8.50E-78	P030066,P020057,P060017,P080039,P030005
fur	ferric uptake regulation protein	Pectobacterium chrysanthemi	AAD01582.1	5.00E-63	P030094,P020063,P090090,P100013,P090069
gapA	glyceraldehyde-3-phosphate dehydrogenase A	Yersinia pestis KIM	NP_669476.1	2.60E-70	P170059,P130060
glmS	glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	Erwinia carotovora subsp. atroseptica SCRI1043	CAG77403.1	8.50E-65	P060034,P090021,P030030,P110083,P060007,P060041,P100092
glmU	COG1207: N-acetylglucosamine-1-phosphate uridyltransferase (contains nucleotidyltransferase and I-patch acetyltransferase domains)	Actinobacillus pleuropneumoniae serovar 1 str. 4074	ZP_00134560.2	2.10E-21	P130002
glnQ	glutamine transport ATP-binding protein GlnQ	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	YP_151147.1	1.90E-34	P140093,P090002,P200031
glnS	glutamine tRNA synthetase	Yersinia pestis KIM	NP_668531.1	2.10E-83	P080081
gloB	probable hydroxyacylglutathione hydrolase	Yersinia pestis KIM	NP_670396.1	8.60E-54	P080066
gltA	citrate synthase GltA	Yersinia pseudotuberculosis IP 32953	YP_069677.1	5.30E-88	P170086
gltX	glutamate tRNA synthetase, catalytic subunit	Yersinia pestis KIM	NP_668818.1	1.60E-60	P020034,P010078,P140004,P180007,P040092
glyA	serine hydroxymethyltransferase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76148.1	6.40E-29	P090007,P050013,P080063
glyS	glycyl-tRNA synthetase beta subunit	Yersinia pseudotuberculosis IP 32953	YP_072392.1	1.90E-165	P210029,P200057,P010063,P030012
gmk	guanylate kinase	Yersinia pseudotuberculosis IP 32953	YP_068586.1	1.40E-75	P140062
gpmA	phosphoglyceromutase 1	Yersinia pestis KIM	NP_670347.1	3.60E-51	P010066,P010058
gspJ	GspJ, hypothetical type II secretion protein	Escherichia coli	CAE85228.1	9.40E-24	P080003
gspK	GspK, hypothetical type II secretion protein	Escherichia coli	CAE85227.1	2.70E-31	P080031
guaA	COG0519: GMP synthase, PP-ATPase domain/subunit	Haemophilus influenzae R2846	ZP_00155220.2	2.20E-32	P090084,P170087
gyrA	DNA gyrase subunit A	Photorhabdus luminescens subsp. laumondii TTO1	NP_930282.1	3.80E-92	P070084,P030032
gyrB	DNA gyrase subunit B, type II topoisomerase	Yersinia pestis KIM	NP_671401.1	9.60E-49	P030066,P020057,P060017,P080039,P030005,P110018,P100033

ham1	putative ribosomal protein	Yersinia pestis KIM	NP_670630.1	3.80E-67	P130027,P190094
hemA	glutamyl-tRNA reductase	Shigella flexneri 2a str. 301	NP_707119.2	5.60E-64	P100039,P020093
hemC	porphobilinogen deaminase; hydroxymethylbilane synthase	Yersinia pestis KIM	NP_667719.1	8.00E-52	P160027
hemF	coproporphyrinogen III oxidase, aerobic HemF	Yersinia pseudotuberculosis IP 32953	YP_071261.1	1.60E-14	P060051
hemH	ferrochelatase	Yersinia pseudotuberculosis IP 32953	YP_069538.1	1.20E-115	P120023,P150042
hemK	putative protoporphyrinogen oxidase	Yersinia pseudotuberculosis IP 32953	YP_070523.1	1.60E-92	P150085,P150034,P070052,P030096
hemL	glutamate-1-semialdehyde aminotransferase	Yersinia pestis KIM	NP_668135.1	5.50E-57	P210072,P090041,P120073,P210072,P090041,P120073
hemX	uroporphyrinogen III methylase	Yersinia pestis KIM	NP_667717.1	1.60E-72	P040030
himA	integration host factor alpha subunit	Erwinia chrysanthemi	CAA52768.1	6.20E-25	P130028
hmuR	tonB dependent outer membrane hemin receptor, hmuR	Yersinia pseudotuberculosis IP 32953	YP_068886.1	8.30E-112	P010064,P080065,P110061
hofB	putative integral membrane protein	Yersinia pestis KIM	NP_668096.1	3.40E-97	P080083,P020010
hrpA	helicase, ATP-dependent	Yersinia pestis KIM	NP_669326.1	1.70E-139	P110017
hupA	DNA-binding protein HU (DNA-binding protein II)	Geobacillus kaustophilus HTA426	YP_148068.1	1.60E-17	P170094,P150001
hupB	DNA-binding protein HU-beta	Erwinia carotovora subsp. atroseptica SCRI1043	CAG74061.1	7.30E-15	P170034,P100005
hypothetical	hypothetical protein plu3604	Photorhabdus luminescens subsp. laumondii TTO1	NP_930816.1	3.20E-06	P120075
hypothetical	COG1611: Predicted Rossmann fold nucleotide-binding protein	Actinobacillus pleuropneumoniae serovar 1 str. 4074	ZP_00134702.2	1.50E-09	P110003,P200028
hypothetical	FUSOBACTERIUM OUTER MEMBRANE PROTEIN FAMILY	Fusobacterium nucleatum subsp. vincentii ATCC 49256	ZP_00143593.1	0.00084	P130086
hypothetical	hypothetical protein y0523	Yersinia pestis KIM	NP_667860.1	1.20E-44	P190092,P120012,P050026
hypothetical	hypothetical protein YPTB3225	Yersinia pseudotuberculosis IP 32953	YP_071726.1	1.30E-36	P080055,P090029,P100029
hypothetical	hypothetical protein plu0922	Photorhabdus luminescens subsp. laumondii TTO1	NP_928258.1	1.90E-08	P010089,P010018
hypothetical	hypothetical protein plu1748	Photorhabdus luminescens subsp. laumondii TTO1	NP_929027.1	1.70E-29	P070054,P130056
hypothetical	hypothetical protein XfasO02000019	Xylella fastidiosa Ann-1	ZP_00341653.1	5.20E-31	P010006
hypothetical	hypothetical protein y2778	Yersinia pestis KIM	NP_670079.1	2.30E-61	P130038
hypothetical	hypothetical protein NE1307	Nitrosomonas europaea ATCC 19718	NP_841356.1	3.00E-12	P160063,P030022
hypothetical	COG4453: Uncharacterized protein conserved in bacteria	Xylella fastidiosa Dixon	ZP_00039846.1	2.50E-27	P020026
hypothetical	hypothetical protein plu3217	Photorhabdus luminescens subsp. laumondii TTO1	NP_930444.1	1.80E-05	P080059
hypothetical	Protein yciI	Escherichia coli CFT073	NP_753621.1	4.40E-71	P150068,P150061
hypothetical	ORF1	Vibrio harveyi bacteriophage VHML	AAN12318.1	6.40E-27	P040089,P180035
hypothetical	hypothetical protein plu0018	Photorhabdus luminescens subsp. laumondii TTO1	NP_927394.1	8.70E-08	P200076
hypothetical	hypothetical protein YPTB0769	Yersinia pseudotuberculosis IP 32953	YP_069310.1	6.00E-30	P210060,P150082
hypothetical	hypothetical protein y0450	Yersinia pestis KIM	NP_667788.1	5.50E-39	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019
hypothetical	hypothetical protein y3333	Yersinia pestis KIM	NP_670632.1	4.50E-17	P150032,P050071,P140001,P050073,P150013,P090088
hypothetical	hypothetical protein	Plasmodium yoelii yoelii	EAA20445.1	1.10E-06	P200008,P200096
hypothetical	hypothetical protein YPTB3211	Yersinia pseudotuberculosis IP 32953	YP_071712.1	1.50E-146	P040058,P030017,P130015,P050040,P030040,P210021,P130003,P080090,P040077,P050079
hypothetical	hypothetical protein y3486	Yersinia pestis KIM	NP_670783.1	5.20E-95	P140070,P100055
hypothetical	hypothetical protein plu1064	Photorhabdus luminescens subsp. laumondii TTO1	NP_928393.1	3.90E-16	P210003
hypothetical	Orf80	Photorhabdus luminescens	AAO17234.1	4.40E-15	P130091,P080074
hypothetical	hypothetical protein XOO4337	Xanthomonas oryzae pv. oryzae KACC10331	YP_202976.1	1.30E-67	P100095,P210092,P180022,P100095,P210092,P180022
hypothetical	hypothetical protein y1934	Yersinia pestis KIM	NP_669249.1	3.40E-23	P040071,P170050
hypothetical	hypothetical protein	Edwardsiella ictaluri	AAT47204.1	7.00E-12	P170021,P060021,P080077,P060085,P070048,P140063
hypothetical	hypothetical protein YPTB3708	Yersinia pseudotuberculosis IP 32953	YP_072189.1	1.40E-40	P170044,P170069
hypothetical	conserved putative exported protein	Yersinia pestis KIM	NP_667466.1	4.30E-40	P120094,P200036,P190065,P040053
hypothetical	hypothetical protein y1424	Yersinia pestis KIM	NP_668745.1	4.20E-61	P020034,P010078,P140004,P180007,P040092
hypothetical	hypothetical protein y1272	Yersinia pestis KIM	NP_668595.1	1.50E-41	P160054,P180066
hypothetical	hypothetical protein Bucepa03006415	Burkholderia cepacia R1808	ZP_00219004.1	1.80E-07	P100019
hypothetical	hypothetical protein plu0210	Photorhabdus luminescens subsp. laumondii TTO1	NP_927574.1	1.60E-180	P210072,P090041,P120073
hypothetical	hypothetical protein	Pseudomonas syringae pv. pisi	CAB96965.1	1.10E-34	P180080,P130017
hypothetical	hypothetical protein plu0198	Photorhabdus luminescens subsp. laumondii TTO1	NP_927563.1	1.90E-54	P130022,P070093
hypothetical	hypothetical protein MS1777	Mannheimia succiniciproducens MBEL55E	AAU38384.1	2.90E-11	P140070,P100055
hypothetical	CPA-1 family Na+/H+ antiporter	Yersinia pseudotuberculosis IP 32953	YP_071009.1	3.50E-102	P140081,P200001,P110092,P070002
hypothetical	glyoxylase domain hypothetical protein	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	YP_094472.1	9.40E-12	P130004
hypothetical	conserved hypothetical protein	Parachlamydia sp. UWE25	CAF23939.1	6.40E-09	P210003

hypothetical	hypothetical protein PSPTOA0031	Pseudomonas syringae pv. tomato str. DC3000	NP_808689.1	3.00E-121	P070069,P030019,P100080
hypothetical	unknown	Pasteurella multocida subsp. multocida str. Pm70	AAK03257.1	1.20E-51	P210020,P090053
hypothetical	hypothetical protein y3489	Yersinia pestis KIM	NP_670786.1	3.50E-40	P170043
hypothetical	hypothetical protein plu1489	Photorhabdus luminescens subsp. laumondii TTO1	NP_928784.1	8.40E-39	P110046,P100057,P110012,P100027
hypothetical	hypothetical protein RakaH01001082	Rickettsia akari str. Hartford	ZP_00340573.1	4.10E-46	P100091,P110082
hypothetical	hypothetical protein YPTB3706	Yersinia pseudotuberculosis IP 32953	YP_072187.1	2.50E-16	P170044,P170069
hypothetical	hypothetical protein	Edwardsiella ictaluri	AAT77726.1	1.50E-07	P110050,P150005,P110073,P100083,P100061
hypothetical	hypothetical protein YPTB3707	Yersinia pseudotuberculosis IP 32953	YP_072188.1	1.30E-41	P170044,P170069
hypothetical	hypothetical protein plu4598	Photorhabdus luminescens subsp. laumondii TTO1	NP_931762.1	2.70E-08	P090013
hypothetical	unknown protein	Plasmid pSC101	AAB59156.1	2.10E-11	P190059,P100046
hypothetical	hypothetical protein y0659	Yersinia pestis KIM	NP_667996.1	1.80E-81	P080068,P110025,P080035,P030049,P150054,P080068,P110025,P080035,P030049,P150054
hypothetical	hypothetical protein SC1947	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	AAX65853.1	3.20E-07	P120087
hypothetical	hypothetical protein YPTB3529	Yersinia pseudotuberculosis IP 32953	YP_072012.1	9.90E-62	P100043
hypothetical	hypothetical protein plu1344	Photorhabdus luminescens subsp. laumondii TTO1	NP_928648.1	0.0007	P010076,P010057
hypothetical	Hypothetical protein yggJ	Escherichia coli CFT073	NP_755407.1	2.60E-75	P080083,P020010
hypothetical	hypothetical protein y3424	Yersinia pestis KIM	NP_670722.1	5.90E-16	P020078,P130077,P110055,P100065,P120088
hypothetical	hypothetical protein PSPTO5022	Pseudomonas syringae pv. tomato str. DC3000	NP_794755.1	2.10E-18	P060018,P070051,P050022
hypothetical	conserved hypothetical protein	Erwinia carotovora subsp. atroseptica SCRI1043	CAG77065.1	1.70E-12	P020046
hypothetical	hypothetical protein SO1608	Shewanella oneidensis MR-1	NP_717220.1	1.20E-70	P030081,P150040
hypothetical	hypothetical protein t4162	Salmonella enterica subsp. enterica serovar Typhi Ty2	NP_807766.1	3.40E-13	P180076,P130024,P060072,P080001,P180087,P190024,P160070,P070076,P070056
hypothetical	hypothetical protein SPA2928	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	YP_152081.1	1.70E-29	P120045,P010045
hypothetical	hypothetical protein YPTB3401	Yersinia pseudotuberculosis IP 32953	YP_071890.1	6.40E-75	P150085,P150034,P070052,P030096
hypothetical	hypothetical protein YPTB3402	Yersinia pseudotuberculosis IP 32953	YP_071891.1	6.20E-179	P150085,P150034,P070052,P030096
hypothetical	hypothetical protein y3635	Yersinia pestis KIM	NP_670932.1	2.00E-14	P140041
hypothetical	hypothetical protein YPTB2227	Yersinia pseudotuberculosis IP 32953	YP_070742.1	1.20E-82	P060076
hypothetical	Uncharacterized low-complexity proteins	Methanosarcina barkeri str. fusaro	ZP_00297221.1	4.40E-15	P040004
hypothetical	hypothetical protein y1785	Yersinia pestis KIM	NP_669102.1	1.60E-131	P060060,P210096,P100069,P210047
hypothetical	unnamed protein product	Rhizobium leguminosarum	CAA58901.1	4.40E-20	P070094,P090070
hypothetical	hypothetical protein YPTB1998	Yersinia pseudotuberculosis IP 32953	YP_070515.1	2.10E-39	P160025,P210095
hypothetical	conserved hypothetical protein	Erwinia carotovora subsp. atroseptica SCRI1043	CAG74762.1	8.30E-12	P040071,P170050
hypothetical	hypothetical protein y0661	Yersinia pestis KIM	NP_667997.1	1.80E-26	P190047
hypothetical	hypothetical protein y1922	Yersinia pestis KIM	NP_669238.1	8.20E-07	P210077
hypothetical	hypothetical protein plu3864	Photorhabdus luminescens subsp. laumondii TTO1	NP_931069.1	3.00E-14	P140034,P160011,P130062,P070055,P110045
hypothetical	hypothetical protein plu4766	Photorhabdus luminescens subsp. laumondii TTO1	NP_931926.1	2.90E-16	P070019,P150033,P120034,P040016,P030015,P010051
hypothetical	conserved hypothetical protein	Chromobacterium violaceum ATCC 12472	AAQ59864.1	1.00E-18	P150038
hypothetical	Orf78	Photorhabdus luminescens	AAO17232.1	2.20E-16	P040035,P100081
hypothetical	hypothetical protein Pflu02003684	Pseudomonas fluorescens PfO-1	ZP_00264012.1	5.80E-12	P020011
hypothetical	hypothetical protein Cwat03006635	Crocosphaera watsonii WH 8501	ZP_00174638.1	1.30E-09	P190074
hypothetical	hypothetical protein YPTB3173	Yersinia pseudotuberculosis IP 32953	YP_071675.1	1.20E-29	P070019,P150033,P120034,P040016,P030015,P010051
hypothetical	hypothetical protein plu1786	Photorhabdus luminescens subsp. laumondii TTO1	NP_929065.1	5.90E-43	P170092,P030079,P150077
hypothetical	hypothetical protein YPTB1613	Yersinia pseudotuberculosis IP 32953	YP_070140.1	4.10E-40	P030037,P130078,P180068,P150078,P070081,P130057,P050080,P100063,P150015,P190008,P030026,P140014,P010035,P200016,P140040,P090008,P040017,P060093,P120058
hypothetical	putative exported protein	Yersinia pestis CO92	CAC92311.1	8.50E-20	P170062
hypothetical	hypothetical protein y2255	Yersinia pestis KIM	NP_669564.1	3.70E-46	P010091
hypothetical	hypothetical protein	Bacteriophage P27	CAC83533.1	1.30E-36	P170088,P180028,P180034,P120086
hypothetical	conserved hypothetical protein	Chromobacterium violaceum ATCC 12472	AAQ58033.1	8.70E-05	P060006,P200086
hypothetical	conserved hypothetical protein	Yersinia pestis CO92	CAC89783.1	1.00E-09	P060035
ibpB	putative heat shock protein	Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis	YP_054435.1	1.70E-22	P160056
icdA	isocitrate dehydrogenase [NADP]	Photorhabdus luminescens subsp. laumondii TTO1	NP_930035.1	5.50E-189	P030086
infB	translation initiation factor IF2-2	Yersinia pseudotuberculosis IP 32953	YP_069023.1	4.80E-186	P210095,P070045

Integrase	integrase	Salmonella enterica subsp. enterica serovar Typhimurium	AAG03003.1	1.00E-17	P200092,P040081,P200004
invA	invasion protein	Salmonella enterica str. RKS3333	AAC45022.1	2.40E-06	P060066
invC	surface presentation of antigens, secretory proteins	Chromobacterium violaceum ATCC 12472	AAQ60298.1	5.00E-71	P130040,P130070,P110063,P130040,P130070,P110063
iscS/nifS	cysteine desulfurase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76135.1	1.50E-128	P110014,P130022,P040087,P070093
kdtA	3-deoxy-manno-octulosonic acid transferase	Serratia marcescens	AAC44432.1	3.20E-57	P040067,P200082
large repetitive protein	large repetitive protein	Salmonella enterica subsp. enterica serovar Typhi Ty2	NP_807770.1	8.70E-12	P080057,P210017,P100035,P010069,P170066,P160007,P180030,P030013,P080057,P210017,P100035,P010069,P170066,P160007,P180030,P030013,P080057,P210017,P100035,P010069,P170066,P160007,P180030,P030013,P180076,P130024,P060072,P080001,P180087,P190024,P160070,P070076,P070056,P030060,P080030,P020091,P010029,P020068
leuO	probable transcriptional activator for leuABCD operon	Yersinia pestis KIM	NP_670939.1	1.80E-149	P190087,P100060,P110049,P120081
leuS	leucyl-tRNA synthetase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG74219.1	7.40E-27	P050093,P030011,P050085
licD1	Lipooligosaccharide cholinephosphotransferase	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	AAL95442.1	7.90E-13	P100037,P100008
lig	DNA ligase	Yersinia pestis KIM	NP_668812.1	1.70E-79	P120025,P140048,P150010
lipB	lipoate-protein ligase B (lipoate biosynthesis protein B)	Photorhabdus luminescens subsp. laumondii TTO1	NP_928603.1	6.40E-77	P140005,P170054,P140054
lktA	leukotoxin A	Pasteurellaceae bacterium I4	AAW21432.1	1.20E-17	P210040,P110034,P200086,P070041,P160005,P130019
lnt	apolipoprotein N-acyltransferase	Yersinia pestis KIM	NP_668516.1	4.20E-84	P030006
lolD	putative ATP-binding component of a transport system	Yersinia pestis KIM	NP_669103.1	1.70E-88	P060060,P210096,P100069,P210047
lolE	ABC tranporter/lipoprotein releasing system, permease subunit lolE	Yersinia pseudotuberculosis IP 32953	YP_070953.1	2.50E-57	P140052,P090082,P210075,P070032,P060060,P210096,P100069,P210047
lon	ATP-dependent protease la	Erwinia carotovora subsp. atroseptica SCRI1043	CAG74060.1	5.80E-07	P040054,P120041,P200037
lpdA	dihydrolipoamide dehydrogenase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76686.1	1.80E-148	P020054,P010032
lpxA	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG73954.1	1.70E-60	P190063,P040007
lpxH	UDP-2,3-diacylglucosamine hydrolase	Yersinia pseudotuberculosis IP 32953	YP_069573.1	3.10E-55	P060026
lspA	prolipoprotein signal peptidase (SPase II)	Yersinia pseudotuberculosis IP 32953	YP_069160.1	6.00E-15	P020038,P020036,P020037
lysP	lysine-specific permease lysP, APC family	Yersinia pseudotuberculosis IP 32953	YP_069872.1	4.50E-169	P020014,P170040,P110062,P010081
lytB	penicillin tolerance protein	Yersinia pestis KIM	NP_670994.1	1.60E-104	P170021,P060021,P080077,P060085,P070048,P140063
manX	PTS enzyme IIAB, mannose-specific	Escherichia coli O157:H7 EDL933	AAG56806.1	1.20E-24	P090007,P080063
map	methionine aminopeptidase	Yersinia pestis KIM	NP_670437.1	1.10E-49	P050068,P140021
mdfA	multidrug translocase, MFS family	Yersinia pseudotuberculosis IP 32953	YP_072411.1	4.60E-143	P180064,P190045
mdh	malate dehydrogenase	Yersinia pseudotuberculosis IP 32953	YP_069003.1	3.20E-26	P160010
metG	methionine tRNA synthetase	Yersinia pestis KIM	NP_669950.1	3.30E-92	P150095
metJ	transcriptional repressor protein	Yersinia pseudotuberculosis IP 32953	YP_068653.1	7.40E-52	P170068
metK	s-adenosylmethionine synthetase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76817.1	8.50E-68	P210002,P170017,P050066,P210007,P210064
mgtA	Mg2+ transport ATPase	Yersinia pestis KIM	NP_669137.1	3.30E-105	P020048,P050084,P190004,P020042,P170074,P170090,P170091
mobA	relaxase/mobilization nuclease MobA, putative	Pseudomonas syringae pv. tomato str. DC3000	NP_808687.1	4.50E-07	P020025,P030071,P150076,P030076
mrcB	PonB	Pasteurella multocida subsp. multocida str. Pm70	AAK02540.1	1.50E-09	P110006,P040074,P120051,P110006,P040074,P120051
mreB	Rod shape-determining protein mreB	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	AAX67218.1	1.30E-57	P140022,P130005
mreC	rod shape-determining protein MreC	Yersinia pseudotuberculosis IP 32953	YP_072046.1	9.00E-20	P140022,P130005,P140022,P170074,P130005,P060046
mreD	rod shape-determining protein MreD	Yersinia pseudotuberculosis IP 32953	YP_072045.1	3.20E-64	P140022,P170074,P130005,P060046
mrsA	probable phosphoglucomutase/phosphomannomutase	Yersinia pseudotuberculosis IP 32953	YP_069019.1	9.80E-56	P010054,P020007,P020006
mtn	hypothetical protein y0805	Yersinia pestis KIM	NP_668141.1	2.60E-25	P120013
mtr	putative HAAAP family tryptophan-specific transporter mtr	Yersinia pseudotuberculosis IP 32953	YP_069849.1	4.00E-91	P120031,P120004
mukB	cell division protein	Yersinia pseudotuberculosis IP 32953	YP_069961.1	1.00E-177	P010084,P120037,P100022,P100050,P110008
murB	UDP-N-acetylenolpyruvoylglucosamine reductase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG73132.1	5.30E-61	P150028
murE	UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimelate ligase	Yersinia pseudotuberculosis IP 32953	YP_069224.1	2.80E-134	P200049,P130011,P040082,P010088,P120068
murF	D-alanine:D-alanine-adding enzyme	Yersinia pseudotuberculosis IP 32953	YP_069225.1	7.40E-141	P200049,P130011,P040082,P010088,P120068

murG	UDP-N-acetylglucosamine:N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	Yersinia pseudotuberculosis IP 32953	YP_069229.1	4.60E-79	P060083,P120079,P030008
murI	glutamate racemase	Photorhabdus luminescens subsp. laumondii TTO1	NP_931896.1	2.00E-23	P060063,P060050,P060063,P060050
mutL	DNA mismatch repair protein	Yersinia pseudotuberculosis IP 32953	YP_068966.1	8.30E-53	P090034,P210050,P010002,P020088
mutY	adenine glycosylase	Yersinia pestis KIM	NP_670638.1	3.90E-66	P080055,P090029,P100029
nadA	quinolinate synthetase A	Yersinia pseudotuberculosis IP 32953	YP_069697.1	2.50E-49	P060053,P160084
nadB	L-aspartate oxidase	Yersinia pseudotuberculosis IP 32953	YP_071405.1	9.70E-45	P010025
nhaA	Na+/H antiporter, pH dependent	Yersinia pestis KIM	NP_671001.1	3.60E-27	P060089
nleD	non-LEE encoded type III effector D	Citrobacter rodentium	AAS47020.1	9.70E-78	P070087
nlp	putative DNA-binding protein	Yersinia pseudotuberculosis IP 32953	YP_069004.1	2.80E-32	P080071
nth	endonuclease III	Yersinia pseudotuberculosis IP 32953	YP_070677.1	2.80E-85	P060042,P080009
nuoM	NADH dehydrogenase I chain M	Yersinia pestis KIM	NP_668959.1	2.10E-10	P190052
nusA	N utilization substance protein A (nusA protein) (L factor)	Photorhabdus luminescens subsp. laumondii TTO1	NP_931694.1	7.70E-36	P160025,P210095
nusB	transcription termination; L factor	Yersinia pseudotuberculosis IP 32953	YP_069477.1	1.10E-06	P010041
ompA	hypothetical protein plu2481	Photorhabdus luminescens subsp. laumondii TTO1	NP_929717.1	1.10E-32	P060034,P090021,P030030,P110083,P060007,P060041,P100092,P110069,P180079,P100079
ompH	cationic 19 kDa outer membrane protein precursor	Yersinia pestis CO92	CAC89895.1	3.00E-22	P050081
orgA	OrgA	Sodalis glossinidius	AAS66873.1	9.30E-13	P040085
pagO	putative membrane protein	Yersinia pseudotuberculosis	AAL02231.1	4.80E-62	P080002,P060020,P190026
pckA	phosphoenolpyruvate carboxykinase	Escherichia coli O157:H7	NP_312272.1	4.60E-19	P140075,P140013,P030045
pcnB	poly(A) polymerase	Yersinia pestis CO92	CAC92629.1	6.10E-21	P110033,P120008,P180060
pdxB	putative D-isomer specific 2-hydroxyacid dehydrogenase	Yersinia pseudotuberculosis IP 32953	YP_071130.1	1.20E-117	P170065,P010093
pheT	phenylalanyl-tRNA synthetase beta chain	Yersinia pseudotuberculosis IP 32953	YP_070851.1	1.60E-95	P130028
phoU	repressor protein	Edwardsiella tarda	AAN05785.1	2.50E-73	P210041,P110019
pilQ	type IV pilus biogenesis ATPase PilQ	Escherichia coli	NP_065351.1	4.00E-65	P100012,P070030
pilS	PilS2	Pseudomonas aeruginosa	AAP84205.1	3.00E-09	P090092
pilT	PilT	Escherichia coli	AAL05524.1	1.30E-26	P210045,P100032,P080016,P140080
plsB	glycerol-3-phosphate acyltransferase	Yersinia pestis KIM	NP_667907.1	2.10E-66	P010050
plsC	putative acyltransferase (LPAAT)	Yersinia pseudotuberculosis IP 32953	YP_071880.1	6.60E-74	P010068,P020001,P130055
pmbA	putative modulator of DNA gyrase	Yersinia pseudotuberculosis IP 32953	YP_072023.1	7.20E-115	P070019,P150033,P120034,P040016,P030015,P010051,P070019,P150033,P120034,P040016,P030015,P010051
pnp	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) (PNPase) (CAP87K)	Photorhabdus luminescens subsp. laumondii TTO1	NP_931689.1	1.60E-113	P160052
polA	DNA polymerase I	Yersinia pestis KIM	NP_671105.1	4.90E-139	P110006,P040074,P120051,P100006
Possible	possible hemin degradation/transport protein hmuS	Yersinia pseudotuberculosis IP 32953	YP_068885.1	7.70E-53	P010064,P080065,P110061
Possible	possible tetrapyrrole methylase family protein	Yersinia pseudotuberculosis IP 32953	YP_071975.1	9.90E-13	P110030
Possible	possible Yersinia enterocolitica-like Orf1 (AF005744)	Yersinia pseudotuberculosis IP 32953	YP_071857.1	4.80E-05	P150072
Predicted	putative oxidoreductase	Yersinia pestis KIM	NP_670052.1	1.20E-11	P150008
Predicted	hypothetical protein y0135	Yersinia pestis KIM	NP_667478.1	8.50E-75	P120031,P010047,P100015,P180023,P070083,P120004,P100042,P030007
Predicted	hypothetical protein y0415	Yersinia pestis KIM	NP_667753.1	1.10E-56	P020046
Predicted	putative adenine-specific methylase	Yersinia pestis KIM	NP_668902.1	8.90E-36	P130091,P080074
priA	primosomal protein N'	Yersinia pestis KIM	NP_667639.1	5.80E-41	P020016,P020024
prlA	preprotein translocase SecY subunit	Yersinia pseudotuberculosis IP 32953	YP_072159.1	3.30E-187	P140096
prlC	oligopeptidase A	Yersinia pestis KIM	NP_671149.1	8.50E-201	P070016,P150090,P180063
Probable	probable inorganic polyphosphate/ATP-NAD kinase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG73754.1	6.50E-59	P120094,P200036,P190065,P040053
Probable	probable peroxidase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG74027.1	1.90E-43	P210056
prsA	phosphoribosylpyrophosphate synthetase	Yersinia pestis KIM	NP_669603.1	1.00E-163	P090073,P160022
pta	phosphate acetyltransferase	Yersinia pseudotuberculosis IP 32953	YP_071108.1	1.40E-119	P030037,P130078,P180068,P150078,P070081,P130057,P050080,P100063,P150015,P190008,P030026,P140014,P010035,P200016,P140040,P090008,P040017,P060093,P120058,P120046,P170081
ptsH	HPr of PTS system	Serratia marcescens	BAB92987.1	4.70E-24	P090019,P090055,P010037,P090019,P090055,P010037
ptsI	PTS sytem, enzyme I component	Yersinia pseudotuberculosis IP 32953	YP_071226.1	1.90E-108	P090019,P090055,P010037,P090019,P090055,P010037,P210053,P090032
purE	phosphoribosylaminoimidazole carboxylase catalytic subunit	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76054.1	7.10E-53	P170019
purF	amidophosphoribosyltransferase	Yersinia pseudotuberculosis IP 32953	YP_071122.1	1.50E-28	P100025,P110036,P020055,P110010,P060036,P040060

putA	bifunctional PutA protein	includes: proline dehydrogenase and delta-1-pyrroline-5-carboxylate	CAC90668.1	2.90E-80	P030058,P120026,P060058,P050075,P070074,P060079
Putative	putative periplasmic binding transport protein	Yersinia pestis KIM	NP_667956.1	1.70E-76	P070040
Putative	hypothetical protein y1196	Yersinia pestis KIM	NP_668522.1	7.80E-07	P130018,P030021,P060005,P200032
Putative	putative membrane protein	Yersinia pestis biovar Medievalis str. 91001	NP_992261.1	4.50E-45	P160046,P040048,P040043,P090042,P110086,P100094
Putative	putative deaminase	Yersinia pestis KIM	NP_668630.1	4.50E-44	P180014
Putative	putative ABC associated RTX toxin transporter, HlyD/MFP family	Yersinia pseudotuberculosis IP 32953	YP_070687.1	1.50E-64	P040052
Putative	putative ABC-type bacteriocin/lantibiotic exporter	Salmonella typhimurium LT2	AAL23086.1	3.40E-63	P130013,P060075
Putative	putative aminotransferase	Yersinia pestis KIM	NP_668656.1	1.10E-65	P130022,P070093
Putative	putative lipoprotein	Yersinia pseudotuberculosis IP 32953	YP_070641.1	2.40E-26	P040027
Putative	putative dehydrogenase	Yersinia pestis KIM	NP_668678.1	1.90E-47	P050061,P060014,P120071
Putative	putative DMT superfamily metabolite efflux protein	Yersinia pseudotuberculosis IP 32953	YP_071053.1	1.40E-29	P100056,P100059,P110048,P200095,P200007,P170063,P040011,P070020
Putative	putative transformylase	Yersinia pestis KIM	NP_669235.1	1.30E-41	P040026,P040040
Putative	putative membrane protein	Yersinia pseudotuberculosis IP 32953	YP_071346.1	2.20E-17	P050061,P060014,P120071
Putative	putative membrane protein	Yersinia pseudotuberculosis IP 32953	YP_069828.1	5.30E-87	P210058,P080067
Putative	hypothetical protein y2066	Yersinia pestis KIM	NP_669379.1	3.00E-05	P170023
Putative	putative membrane protein	Yersinia pseudotuberculosis IP 32953	YP_071993.1	7.80E-41	P120031,P010047,P100015,P180023,P070083,P120004,P100042,P030007
Putative	Probable extracellular metallopeptidase	Wolbachia endosymbiont strain TRS of Brugia malayi	AAW70972.1	1.70E-13	P180025,P090068,P080007,P210001
Putative	hypothetical protein y2746	Yersinia pestis KIM	NP_670047.1	1.90E-49	P020048,P050084,P190004,P020042,P170074,P170090,P170091
Putative	putative membrane protein	Yersinia pseudotuberculosis IP 32953	YP_071535.1	4.00E-25	P210074,P030053
Putative	hypothetical protein y3018	Yersinia pestis KIM	NP_670318.1	4.20E-15	P080047,P150007
Putative	putative surface antigen	Yersinia pseudotuberculosis IP 32953	YP_071501.1	2.90E-40	P050081
Putative	probable glycosyl transferase	Yersinia pseudotuberculosis IP 32953	YP_070844.1	9.20E-48	P120021
Putative	putative SpoU-family rRNA methylase	Yersinia pseudotuberculosis IP 32953	YP_071368.1	7.40E-75	P030066,P020057,P060017,P080039,P030005
Putative	putative DedA-family membrane protein	Yersinia pseudotuberculosis IP 32953	YP_071965.1	2.80E-44	P080038
Putative	putative autotransporter protein	Yersinia pestis CO92	CAC93445.1	3.90E-08	P080086
Putative	putative HlyD family secretion protein	Yersinia pseudotuberculosis IP 32953	YP_069921.1	4.10E-107	P070010,P010004
Putative	putative glycosyltransferase	Yersinia pseudotuberculosis	AAK69644.1	5.60E-42	P180058
Putative	hypothetical protein y3968	Yersinia pestis KIM	NP_671261.1	1.90E-12	P090065,P170030,P080075
Putative	putative methyl-accepting chemotaxis protein	Salmonella typhimurium LT2	AAL23082.1	9.70E-18	P180076,P130024,P060072,P080001,P180087,P190024,P160070,P070076,P070056,P100038,P070079,P110079,P210008,P040010
Putative	putative carbonic anhydrase	Yersinia pseudotuberculosis IP 32953	YP_069265.1	1.20E-07	P020060,P020052
Putative	hypothetical protein y1938	Yersinia pestis KIM	NP_669253.1	8.40E-93	P040019,P080050,P150026
Putative	putative exonuclease involved in removal of stalled replication fork	Yersinia pseudotuberculosis IP 32953	YP_069454.1	4.10E-18	P170060
Putative	putative O-sialoglycoprotein endopeptidase	Yersinia pestis KIM	NP_670831.1	3.80E-144	P060073,P060016
Putative	putative integral membrane protein	Salmonella enterica subsp. enterica serovar Typhi Ty2	NP_807767.1	5.10E-33	P180076,P130024,P060072,P080001,P180087,P190024,P160070,P070076,P070056
Putative	hypothetical protein y3493	Yersinia pestis KIM	NP_670790.1	9.30E-26	P060004,P170001,P100026
Putative	putative methyltransferase	Yersinia pseudotuberculosis IP 32953	YP_068616.1	2.80E-68	P210063
Putative	putative ABC transporter with fused permease and ATP-binding domains	Yersinia pseudotuberculosis IP 32953	YP_069922.1	5.10E-108	P090050
Putative	Predicted glutamine amidotransferase	Yersinia pestis biovar Medievalis str. 91001	NP_992079.1	2.00E-33	P050078,P070050,P050086
Putative	putative outer membrane protein export (MTB) sytem, hofC subunit	Yersinia pseudotuberculosis IP 32953	YP_069246.1	2.40E-34	P180044,P170052
Putative	PROBABLE TRANSMEMBRANE PROTEIN	Ralstonia solanacearum	CAD13599.1	1.90E-18	P090047
Putative	putative acetyltransferase	Salmonella typhimurium LT2	AAL21379.1	5.10E-13	P020034,P010078,P140004,P180007,P040092
Putative	putative inositol monophosphatase family protein	Yersinia pseudotuberculosis IP 32953	YP_071369.1	3.50E-13	P030066,P020057,P060017,P080039,P030005
Putative	Probable ABC transporter ATP-binding protein yhbG	Photorhabdus luminescens subsp. laumondii TTO1	NP_931237.1	1.00E-97	P140072,P020085,P020058
pykF	pyruvate kinase I	Yersinia pseudotuberculosis IP 32953	YP_070821.1	3.60E-109	P020044,P010061
pyrC	dihydro-orotase	Yersinia pestis KIM	NP_669063.1	1.80E-49	P150070
pyrE	Orotate phosphoribosyltransferase	Escherichia coli CFT073	NP_756328.1	7.10E-69	P210002,P170017,P050066,P210007
pyrG	CTP synthetase (EC 6.3.4.2)	Escherichia coli	AAA24485.1	5.70E-05	P020080
pyrH	uridylate kinase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG73944.1	3.10E-15	P050053,P060028,P140039,P110052,P050053,P060028,P140039,P110052
radC	putative DNA repair protein	Yersinia pseudotuberculosis IP 32953	YP_068595.1	4.50E-64	P040079
recA	DNA-dependent ATPase, DNA- and ATP-dependent coprotease	Yersinia pestis KIM	NP_668214.1	7.70E-66	P170059,P130060

recB	exodeoxyribonuclease V beta chain	Yersinia pseudotuberculosis IP 32953	YP_071531.1	2.10E-21	P120009,P040083
recC	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease	Yersinia pestis KIM	NP_670465.1	3.00E-100	P210074,P030053
recD	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease	Yersinia pestis KIM	NP_670462.1	5.50E-43	P170053,P030067,P110032,P170053,P110032
recG	DNA recombinase	Escherichia coli	AAA62005.1	5.30E-13	P160028,P030065,P030073,P160030
recJ	Single-stranded-DNA-specific exonuclease	Yersinia pseudotuberculosis IP 32953	YP_071667.1	2.70E-190	P030078,P130032,P160055
recR	putative recombination protein, gap repair	Yersinia pseudotuberculosis IP 32953	YP_069535.1	7.30E-27	P020049,P010086
relA	GTP pyrophosphokinase	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	YP_151983.1	1.50E-79	P090065,P170030,P080075,P170082
repA	replication initiator and transcription repressor	Plasmid pSW500	AAB00501.1	2.20E-109	P040022,P090014,P120067
Resolvase	resolvase	Proteus vulgaris	NP_639974.1	1.40E-26	P130074
verseTranscript	putative reverse transcriptase homolog; similar to GII intron	Streptomyces avermitilis MA-4680	BAC67935.1	3.90E-125	P020022,P100064,P020096,P130025,P160078,P040012,P060023,P050092,P150021,P090080,P070026,P160034,P070016,P020022
rfaC	heptosyltransferase I WaaC	Serratia marcescens	AAL23755.1	8.30E-45	P120083,P120083
rfaF	ADP-heptose--LPS heptosyltransferase II	Photorhabdus luminescens subsp. laumondii TTO1	NP_932002.1	9.70E-32	P120083
rfe	putative undecaprenyl-phosphate alpha-GlcNAc transferase	Yersinia pseudotuberculosis IP 32953	YP_068715.1	3.50E-115	P190080
rho	transcription termination factor	Photorhabdus luminescens subsp. laumondii TTO1	NP_931825.1	3.50E-59	P120020,P120056,P170008,P100045,P070025,P160080,P080008,P100030,P120020,P120056,P170008,P100045,P070025,P160080,P080008,P100030
ribA	GTP cyclohydrolase II	Shigella flexneri 2a str. 301	NP_707186.2	4.70E-13	P050011,P120039
ribD	bifunctional pyrimidine deaminase/reductase in pathway of riboflavin synthesis	Yersinia pseudotuberculosis IP 32953	YP_069475.1	1.40E-44	P040039
rnb	RNase II, mRNA degradation	Yersinia pestis KIM	NP_669390.1	4.20E-32	P190044
rnc	ribonuclease III	Salmonella enterica subsp. enterica serovar Typhi	CAD02783.1	1.20E-33	P120054
rnd	RNase D	Yersinia pestis KIM	NP_669544.1	1.00E-124	P060013,P210037
rnhA	RNase HI, degrades RNA of DNA-RNA hybrids	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	AAX64165.1	8.70E-70	P030024,P060029,P030024,P060029
rph	ribonuclease PH	Yersinia pseudotuberculosis IP 32953	YP_068590.1	3.10E-18	P210002,P170017,P050066,P210007
rplI	50S ribosomal protein L9	Yersinia pseudotuberculosis IP 32953	YP_068984.1	1.20E-08	P160087
rplN	50S ribosomal subunit protein L14	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	YP_152424.1	1.90E-56	P060091
rplO	50S ribosomal protein L15	Yersinia pseudotuberculosis IP 32953	YP_072160.1	1.40E-29	P180057
rplQ	50S ribosomal protein L17	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76902.1	1.10E-50	P030038,P140029,P160086
rplR	50S ribosomal protein L18	Yersinia pseudotuberculosis IP 32953	YP_072163.1	2.80E-26	P060091
rplS	50S ribosomal subunit protein L19	Shigella flexneri 2a str. 301	NP_708454.1	2.60E-48	P060018,P070051,P050022
rplU	50S ribosomal subunit protein L21	Yersinia pestis KIM	NP_668009.1	1.40E-30	P100082,P120082,P110072
rplX	50S ribosomal protein L24	Escherichia coli CFT073	NP_755937.1	5.20E-29	P060091
rpmA	50S ribosomal protein L27	Yersinia pseudotuberculosis IP 32953	YP_069008.1	1.20E-38	P100082,P120082,P110072
rpoA	RNA polymerase alpha subunit	Photorhabdus luminescens subsp. laumondii TTO1	NP_931864.1	6.20E-61	P030038,P140029,P160086
rpoB	DNA-directed RNA polymerase beta chain	Yersinia pseudotuberculosis IP 32953	YP_068829.1	3.90E-58	P150091
rpoC	DNA-directed RNA polymerase beta chain	Yersinia pseudotuberculosis IP 32953	YP_068830.1	3.60E-11	P070066
rpoH	RNA polymerase sigma-32 factor	Photorhabdus luminescens subsp. laumondii TTO1	NP_931293.1	1.40E-15	P070049
rpoS	RNA polymerase, sigma S (sigma38) factor	Yersinia pestis KIM	NP_668168.1	1.20E-138	P090083,P150009,P090064,P050055,P050065,P190056,P030048,P000096,P090024,P090071,P070036,P050025,P190086,P090035,P050007,P090056,P090048,P090027,P160042
rpoZ	RNA polymerase, omega subunit	Yersinia pestis KIM	NP_667445.1	3.70E-23	P140062
rpsI	30S ribosomal subunit protein S9	Yersinia pestis KIM	NP_667476.1	4.50E-60	P060051
rsmC	ribosomal RNA small subunit methyltransferase C	Yersinia pseudotuberculosis IP 32953	YP_069114.1	9.20E-82	P110096
rsuA	16S pseudouridylate 516 synthase	Yersinia pestis KIM	NP_670217.1	1.00E-81	P010094
RTX	pore forming RTX toxin family protein	Yersinia pseudotuberculosis IP 32953	YP_071720.1	4.70E-08	P180078,P180078,P120074,P120085,P110075,P100085,P070064,P190061,P120074,P080085,P120085,P130026,P170064,P120014,P130017
RTX1	COG2931: RTX toxins and related Ca2+-binding proteins	Actinobacillus pleuropneumoniae serovar 1 str. 4074	ZP_00134242.1	2.60E-05	P070092
RTX2	putative ABC RTX toxin transporter, fused ATP binding/permease domains	Yersinia pseudotuberculosis IP 32953	YP_070688.1	7.40E-184	P160072
RTX3	RTX (repeat in toxin) cytotoxin	Vibrio vulnificus YJ016	NP_937086.1	0.00044	P200088
rus	endodeoxyribonuclease RUS (Holliday junction resolvase)	Shigella flexneri 2a str. 301	NP_707427.1	6.10E-08	P190056,P120063
ruvA	Holliday junction DNA helicase	Yersinia pseudotuberculosis IP 32953	YP_070557.1	2.80E-14	P040001,P190078,P040001,P190078

ruvB	Holliday junction DNA helicase	Photorhabdus luminescens subsp. laumondii TTO1	NP_929372.1	1.70E-41	P140032,P200048
sapC	Peptide transport system permease protein SapC	Photorhabdus luminescens subsp. laumondii TTO1	NP_929824.1	9.40E-26	P130007,P160006,P040018
sapD	ABC peptide transporter, ATP-binding subunit sapD	Yersinia pseudotuberculosis IP 32953	YP_070790.1	6.50E-111	P130007,P160006,P040018,P130007,P160006,P040018
sbcB	exodeoxyribonuclease I	Yersinia pseudotuberculosis IP 32953	YP_070097.1	2.00E-50	P170092,P030079,P150077
sdaC	HAAAP family serine transporter (serine:H+ symporter), sdaC	Yersinia pseudotuberculosis IP 32953	YP_069884.1	6.50E-115	P080051,P150084
secA	Type II general secretory pathway preprotein translocase ATPase subunit secA	Yersinia pseudotuberculosis IP 32953	YP_069238.1	6.10E-116	P070028,P040086
secF	Protein-export membrane protein SecF	Photorhabdus luminescens subsp. laumondii TTO1	NP_931102.1	5.50E-06	P110004,P180085,P110004,P180085
serC	3-phosphoserine aminotransferase	Photorhabdus luminescens subsp. laumondii TTO1	NP_928908.1	4.40E-106	P180002,P080002,P180002
sfcA	NAD-dependent malic enzyme	Yersinia pseudotuberculosis IP 32953	YP_070054.1	2.80E-59	P120093
sicA	surface presentation of antigens; secretory proteins	Chromobacterium violaceum ATCC 12472	AAQ60290.1	3.70E-52	P180006,P110053
slpA	probable FKBX-type 16KD peptidyl-prolyl cis-trans isomerase	Yersinia pestis KIM	NP_670995.1	4.30E-07	P170021,P060021,P080077,P060085,P070048,P140063
slyB	putative lipoprotein	Yersinia pseudotuberculosis IP 32953	YP_070802.1	2.70E-11	P070027,P020009
sohB	peptidase family U7 protein	Yersinia pseudotuberculosis IP 32953	YP_070655.1	1.50E-116	P110041
spaM	SpaM	Salmonella enterica	AAC44994.1	1.40E-09	P130040,P130070,P110063,P100062,P180049,P120001
spaP	surface presentation of antigens; secretory proteins	Chromobacterium violaceum ATCC 12472	AAQ60294.1	1.50E-31	P210091,P150069,P210091
spaQ	surface presentation of antigens; secretory proteins	Chromobacterium violaceum ATCC 12472	AAQ60293.1	6.50E-26	P210091,P150069
spaR	Type III secretion protein	Shigella flexneri	AAK18474.1	2.90E-22	P060087,P120096,P090010
speA	biosynthetic arginine decarboxylase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76815.1	2.30E-11	P030081,P150040
spiA	putative secretin	Yersinia pestis KIM	NP_667852.1	3.50E-21	P090017
spiB	putative type-III secretion protein	Yersinia pestis biovar Medievalis str. 91001	NP_991805.1	8.80E-38	P010036,P010085,P160085
sppA	protease IV	Yersinia pseudotuberculosis IP 32953	YP_070605.1	1.90E-126	P020050,P010059
ssaG	secretion system apparatus	Chromobacterium violaceum ATCC 12472	AAQ60255.1	4.20E-11	P170007,P160093,P190092,P160069,P120012
ssaH	putative type III secretion apparatus	Yersinia pseudotuberculosis IP 32953	YP_068863.1	9.20E-15	P170007,P160093,P190092,P160069,P120012
ssaN	putative type III secretion system ATPase, EscN/SsaN/YscN	Yersinia pseudotuberculosis IP 32953	YP_068869.1	6.90E-07	P150056,P020082,P150056,P170018,P090082
ssaR	putative type III secretion system component	Yersinia pestis KIM	NP_667867.1	5.00E-31	P210041,P110019
ssaS	putative type III secretion apparatus protein EscS/SsaS/YscS	Yersinia pseudotuberculosis IP 32953	YP_068874.1	1.40E-16	P210041,P110019
ssaT	putative type III secretion apparatus protein EscT/SsaT/YscT	Yersinia pseudotuberculosis IP 32953	YP_068875.1	9.80E-48	P210041,P110019
ssaU	putative type III secretion system component	Yersinia pestis KIM	NP_667870.1	6.30E-93	P020090
ssaV	putative type III secretion system component	Yersinia pestis KIM	NP_667862.1	7.60E-69	P150056
ssb	single-strand DNA-binding protein	Chromobacterium violaceum ATCC 12472	AAQ59563.1	4.80E-15	P170088,P180028,P180034,P120086
sseB	Secretion system effector SseB	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	AAX65325.1	1.20E-08	P100007,P160068,P160082
sspA	stringent starvation protein A, regulator of transcription	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	AAX67186.1	1.10E-16	P050071,P050073,P090088
sspB	stringent starvation protein B	Vibrio fischeri ES114	YP_205598.1	3.30E-27	P050071,P050073,P090088
sucA	2-oxoglutarate dehydrogenase E1 component	Yersinia pseudotuberculosis IP 32953	YP_069682.1	7.50E-228	P150004
sufE	hypothetical protein y1939	Yersinia pestis KIM	NP_669254.1	1.60E-48	P040019,P080050,P150026
sun	tRNA and rRNA cytosine-C5-methylases	Yersinia pestis biovar Medievalis str. 91001	NP_991637.1	4.20E-62	P010008,P180021
tatA	Sec-independent protein translocase protein	Photorhabdus luminescens subsp. laumondii TTO1	NP_931583.1	1.70E-13	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019
tatB	sec-independent protein translocase protein	Salmonella enterica subsp. enterica serovar Typhi Ty2	NP_806991.1	9.90E-09	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019
tatC	Sec-independent protein translocase protein TatC	Yersinia pseudotuberculosis IP 32953	YP_068806.1	4.40E-96	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019
tbpA	thiamin binding protein	Escherichia coli	AAA18833.1	1.00E-07	P180044,P170052,P180044,P170052
terC	TerC	Proteus mirabilis	AAD47287.1	2.30E-60	P050011,P120039
ldisaccharide	tetraacyldisaccharide 4'-kinase	Yersinia pseudotuberculosis IP 32953	YP_069952.1	1.30E-66	P130088
thiQ	putative ATP-binding component of a transport system	Yersinia pestis KIM	NP_670950.1	1.20E-43	P080083,P020010
thrC	threonine synthase	Erwinia carotovora subsp. atroseptica SCRI1043	CAG76787.1	5.90E-100	P050002,P050044
thyA	thymidylate synthetase	Yersinia pestis KIM	NP_670470.1	4.60E-114	P170092,P030079,P150077
tldD	putative modulator of DNA gyrase	Yersinia pseudotuberculosis IP 32953	YP_072040.1	3.20E-125	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019

tnpA	TnpA	Salmonella enterica subsp. enterica serovar Choleraesuis	AAS76350.1	5.20E-94	P170067
tpiA	triosephosphate isomerase (TIM)	Photorhabdus luminescens subsp. laumondii TTO1	NP_931932.1	6.90E-89	P150060,P010033,P150062
traC/sogL	DNA primase TraC4	Aeromonas punctata	YP_067827.1	9.30E-31	P120084,P040009
traL	TraL	Serratia entomophila	NP_938088.1	2.50E-12	P010044,P020040
Transposase	transposase	Nitrosomonas europaea ATCC 19718	NP_841190.1	2.20E-05	P060056
Transposase	putative transposase	Klebsiella pneumoniae	CAA09339.1	3.60E-32	P140028,P040076
Transposase	putative transposase	Vibrio cholerae	AAF71187.1	2.20E-11	P100066,P160059
Transposase	putative transposase	Pseudomonas sp. TW3	AAF23988.1	1.40E-07	P030028,P060027
Transposase	Transposase, ISNCY family	Photorhabdus luminescens subsp. laumondii TTO1	NP_930763.1	1.90E-07	P030016,P040032
Transposase	IS1327 containing a transposase	Pantoea agglomerans	CAA60622.1	7.70E-09	P100018
Transposase	transposase	Photorhabdus luminescens	AAN64216.1	7.50E-18	P130012
Transposase	putative transposase	Nitrosomonas europaea ATCC 19718	NP_841597.1	5.50E-23	P110034,P200086,P070041,P160005,P130019
Transposase	transposase TnpA	Yersinia enterocolitica	AAD16856.1	1.60E-10	P090057
Transposase	putative transposase	uncultured cyanobacterium	CAA42935.1	8.60E-58	P160009,P210024
Transposase	putative transposase	Nitrosomonas europaea ATCC 19718	NP_841596.1	3.90E-05	P110034,P200086,P070041,P160005,P130019,P010019,P020086
Transposase	putative transposase	Xanthomonas oryzae pv. oryzae KACC10331	YP_198703.1	4.60E-30	P050048,P090052
traP	TraP-like protein	Salmonella enterica subsp. enterica serovar Choleraesuis	AAS76352.1	1.50E-17	P140059,P160089
traU	traU protein	Pseudomonas syringae pv. tomato str. DC3000	NP_808718.1	1.90E-47	P160023
traY	traY protein	Pseudomonas syringae pv. tomato str. DC3000	AAO59157.1	2.50E-45	P210051
trbC	conjugal transfer protein, TraG/TraD family	Pseudomonas syringae pv. tomato str. DC3000	NP_808726.1	3.50E-41	P030093
trkA	trk system potassium uptake protein	Yersinia pseudotuberculosis IP 32953	YP_072149.1	1.60E-85	P170004
trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Yersinia pseudotuberculosis IP 32953	YP_070943.1	1.40E-135	P070006,P020043,P130087
truA	tRNA pseudouridine synthase A	Yersinia pseudotuberculosis IP 32953	YP_071128.1	8.10E-39	P180073
tsf	elongation factor EF-Ts	Yersinia pseudotuberculosis IP 32953	YP_071508.1	8.40E-86	P050053,P060028,P140039,P110052
tyrP	HAAAP family tyrosine:H+ symporter, tyrP	Yersinia pseudotuberculosis IP 32953	YP_069783.1	3.50E-86	P020013,P020017,P150019
ubiB	ubiquinone biosynthesis protein	Yersinia pseudotuberculosis IP 32953	YP_068803.1	1.40E-217	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019
ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	Yersinia pseudotuberculosis IP 32953	YP_068801.1	7.20E-110	P140068,P090045,P040037,P070024,P140065,P120015,P090075,P120019,P080019
ubiG	3-demethylubiquinone-9 3-methyltransferase (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB methyltransferase)	Photorhabdus luminescens subsp. laumondii TTO1	NP_930283.1	1.50E-12	P070084,P030032
Unknown	unknown	Yersinia enterocolitica	AAK69266.1	6.60E-33	P040047
Unknown	unknown	Yersinia enterocolitica	AAK69265.1	3.10E-05	P040047
uppS	undecaprenyl pyrophosphate synthetase	Yersinia pseudotuberculosis IP 32953	YP_071504.1	1.20E-96	P040058,P030017,P130015,P050040,P030040,P210021,P130003,P080090,P040077,P050079
uup	putative ATP-binding component of ABC transport system	Yersinia pestis KIM	NP_670051.1	3.00E-155	P140012,P140002,P060031,P060033
uvrA	hypothetical protein Magn03009558	Magnetospirillum magnetotacticum MS-1	ZP_00054903.1	5.10E-48	P120031,P010047,P100015,P180023,P070083,P120004,P100042,P030007,P110080,P170093
vacJ	lipoprotein precursor	Yersinia pestis KIM	NP_668894.1	2.40E-65	P040044,P160048,P130069
visC	hypothetical protein y3295	Yersinia pestis KIM	NP_670594.1	7.90E-83	P130031,P070023
wecE	putative regulator	Yersinia pestis KIM	NP_667707.1	1.30E-26	P100036,P110020
ybiT	Hypothetical ABC transporter ATP-binding protein ybiT	Escherichia coli CFT073	NP_752836.1	9.20E-47	P200080
yjeA	putative Lysyl-tRNA synthetase	Erwinia chrysanthemi	CAC18673.1	8.40E-56	P120091
YPTB0318	putative type III secretion apparatus	Yersinia pseudotuberculosis IP 32953	YP_068864.1	1.70E-05	P170007,P160093,P190092,P160069,P120012
YPTB0324	type III secretion system apparatus protein	Yersinia pseudotuberculosis IP 32953	YP_068870.1	9.40E-10	P170018,P090082
znuA	high-affinity zinc uptake system protein	Erwinia carotovora subsp. atroseptica SCRI1043	CAG75384.1	5.50E-46	P120007
znuC	ABC high-affinity zinc uptake transporter, ATP-binding subunit znuC	Yersinia pseudotuberculosis IP 32953	YP_070560.1	6.00E-40	P030063,P010049