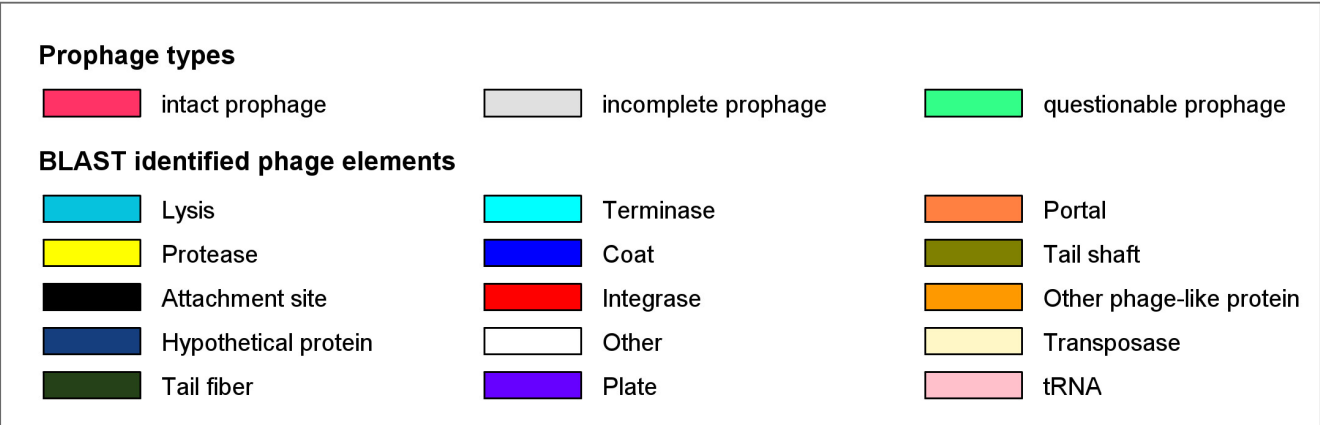
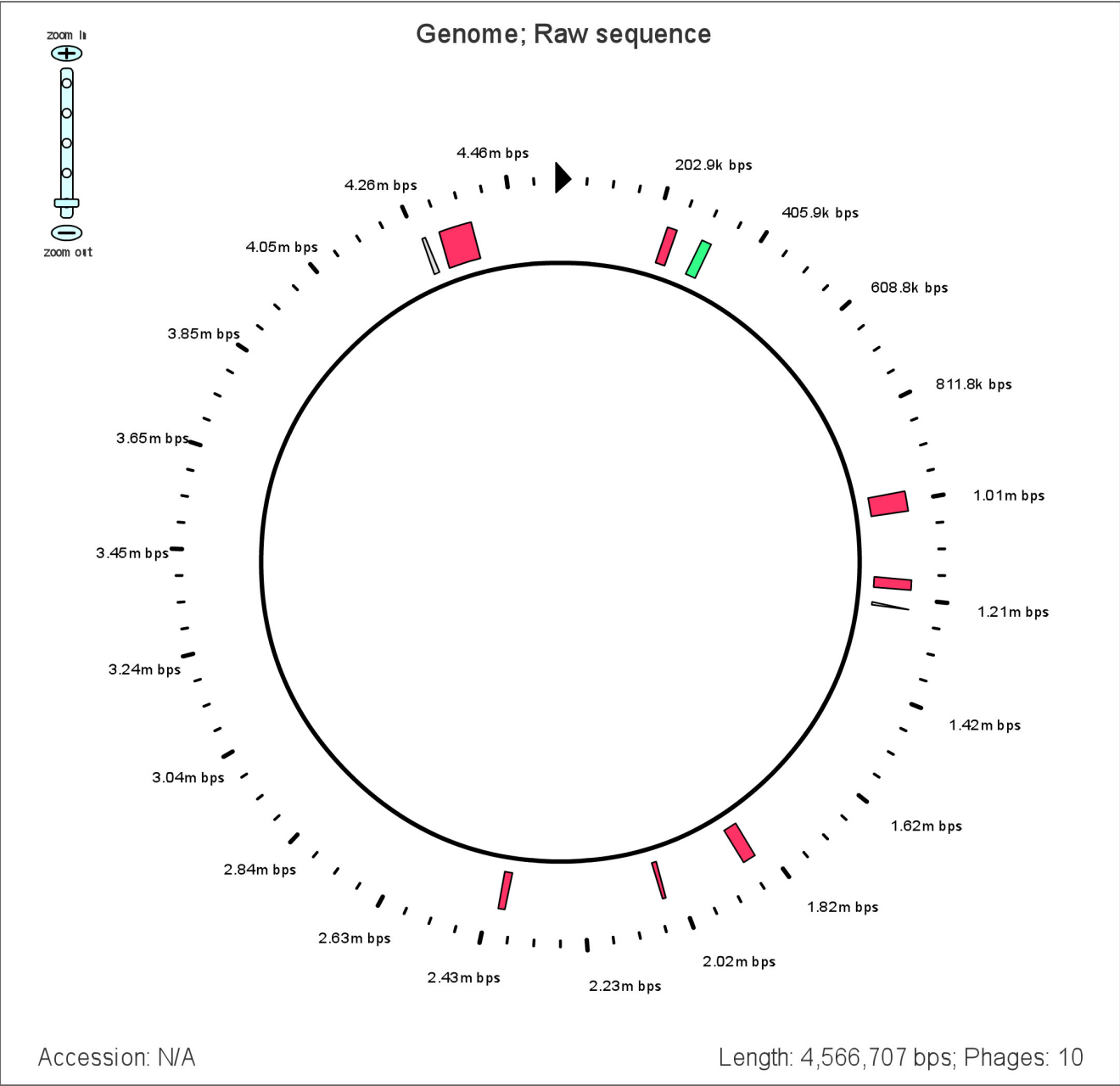


Table S1. Misassembly report based on the alignment of *C. amazonense* strain 56AF, extracted from QUAST.

Misassemblies	0
Relocations	0
Translocations	0
Inversions	0
Misassembled contigs	0
Misassembled contig length	0
Local misassemblies	1
Scaffold gap size misassemblies	0
Indels	1194
Short indels	59
Long indels	59
Indels length	74

Table S2. Phages present in the genome of *C. amazonense* strain 56AF.

Size Kb)	Completness	Possible phage	CDS (n)	Score	Location	Access number
22.3	Intact	Mannhe_VB_MhM	25	140	223399-245719	NC028766
24	Questionable	Burkho_BcepMU	27	70	298005-322006	NC005882
42.9	Intact	Ralsto RSY1	38	100	9932300-1035214	NC025115
24.1	Intact	BurKho KS9	26	140	1175203-1199347	NC013055
6.5	Incomplete	Entero 186	7	60	1233457-1240011	NC001317
31.5	Intact	Ralsto RS 138	33	120	1853482-1885064	NC029107
10.6	Intact	Stx2 converting	11	110	2058319-2068998	NC011357
18.1	Intact	Ralsto RSB2	19	100	2394605-2412770	NC023736
12.9	Incomplete	Escher HK 639	20	20	4266813-4279731	NC016158
75.5	Intact	Shigel sfIV	109	150	4304439-4379944	NC022749



VFDB accession number	Gene product description	Chromobacterium amazonense 564F predicted gene
VFG000031[gb NP_878988]	[bplH] putative glycosyl transferase [LPS [VF0033]] [Bordetella pertussis Tohama I]	c_amazonense.gapfilled_200_mauve.fasta.3615
VFG000034[gb NP_878991]	[bplE] probable glycosyl transferase [LPS [VF0033]] [Bordetella pertussis Tohama I]	c_amazonense.gapfilled_200_mauve.fasta.3613
VFG000048[gb NP_880888]	[bscN] ATP synthase in type III secretion system [TTSS [VF0035]] [Bordetella pertussis Tohama I]	c_amazonense.gapfilled_200_mauve.fasta.547
VFG000077[gb NP_465991]	[clpP] ATP-dependent Clp protease proteolytic subunit [ClpP [VF0074]] [Listeria monocytogenes EGD-e]	c_amazonense.gapfilled_200_mauve.fasta.1612
VFG000079[gb NP_463763]	[clpC] endopeptidase Clp ATP-binding chain C [ClpC [VF0072]] [Listeria monocytogenes EGD-e]	c_amazonense.gapfilled_200_mauve.fasta.3253
VFG000099[gb NP_230484]	[tceP] toxin co-regulated pilus biosynthesis protein E [TCP [VF0126]] [Vibrio cholerae O1 biovar El Tor str. N16961]	c_amazonense.gapfilled_200_mauve.fasta.4213
VFG000104[gb NP_230488]	[acB] accessory colonization factor AcfB [ACF [VF0127]] [Vibrio cholerae O1 biovar El Tor str. N16961]	c_amazonense.gapfilled_200_mauve.fasta.744
VFG000112[gb NP_253216]	[pilB] type 4 fimbrial biogenesis protein PilB [Type IV pili [VF0082]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.3405
VFG000119[gb NP_253948]	[algR] alginate biosynthesis regulatory protein AlgR [Alginate [VF0091]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.1262
VFG000121[gb NP_249453]	[algU] alginate biosynthesis protein AlgZ/FimS [Alginate [VF0091]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.2172
VFG000151[gi 15596627]	[lasR] transcriptional regulator LasR [Quorum sensing [VF0093]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.268
VFG000259[gb NP_273145]	[flgA] capsule polysaccharide modification protein LipA [Capsule [VF0079]] [Neisseria meningitidis MC58]	c_amazonense.gapfilled_200_mauve.fasta.429
VFG000313[gb NP_207965]	[glpP] glucose/galactose transporter [LPS [VF0055]] [Helicobacter pylori 26695]	c_amazonense.gapfilled_200_mauve.fasta.478
VFG000322[gb NP_206846]	[wbcJ] GDP fucose synthase [LPS [VF0056]] [Helicobacter pylori 26695]	c_amazonense.gapfilled_200_mauve.fasta.3531
VFG000477[gi 16766230]	[rpoS] sigma S (sigma 38) factor of RNA polymerase, major sigma factor during stationary phase [RpoS [VF0112]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LTZ]	c_amazonense.gapfilled_200_mauve.fasta.3265
VFG000478[gi 16764063]	[fur] transcriptional repressor of iron-responsive genes (Fur family) (ferric uptake regulator) [Fur [VF0113]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LTZ]	c_amazonense.gapfilled_200_mauve.fasta.2732
VFG000607[gb NP_706258]	[gtbB] bactoprenol glycosyl transferase [LPS [VF0124]] [Shigella flexneri 2a str. 301]	c_amazonense.gapfilled_200_mauve.fasta.1081
VFG000607[gb NP_706258]	[gtbB] bactoprenol glycosyl transferase [LPS [VF0124]] [Shigella flexneri 2a str. 301]	c_amazonense.gapfilled_200_mauve.fasta.605
VFG000700[gb AAFA42192]	[bsc1] bifunctional ribulose 5-phosphate reductase CDP-ribitol pyrophosphorylase [Capsule [VF0043]] [Haemophilus influenzae str. 1007]	c_amazonense.gapfilled_200_mauve.fasta.3162
VFG000705[gb AAFA42197]	[hscB] capsular polysaccharide export protein HscB [Capsule [VF0043]] [Haemophilus influenzae str. 1007]	c_amazonense.gapfilled_200_mauve.fasta.428
VFG000751[gb YP_002332159]	[bfpB] BfpB secretin [BFP [VF0174]] [Escherichia coli O127:H6 str. E2348/69]	c_amazonense.gapfilled_200_mauve.fasta.1864
VFG000752[gb YP_002332160]	[bfpC] BfpC, bitopic inner membrane protein [BFP [VF0174]] [Escherichia coli O127:H6 str. E2348/69]	c_amazonense.gapfilled_200_mauve.fasta.1863
VFG000755[gb YP_002332163]	[bfpE] BfpE, polytopic inner membrane protein [BFP [VF0174]] [Escherichia coli O127:H6 str. E2348/69]	c_amazonense.gapfilled_200_mauve.fasta.1860
VFG000756[gb BAAB48485]	[bfpF] retraction ATPase BfpF [BFP [VF0174]] [Escherichia coli B171]	c_amazonense.gapfilled_200_mauve.fasta.1859
VFG000930[gb NP_753504]	[entF] enterobactin synthase multicomplex component, ATP-dependent [Enterobactin [VF0228]] [Escherichia coli CF7073]	c_amazonense.gapfilled_200_mauve.fasta.500
VFG001214[gb NP_253237]	[pilR1] two-component response regulator PilR [Type IV pili [VF0082]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.853
VFG001214[gb NP_253237]	[pilR] two-component response regulator PilR [Type IV pili [VF0082]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.3762
VFG001214[gb NP_253237]	[pilR] two-component response regulator PilR [Type IV pili [VF0082]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.3924
VFG001214[gb NP_253237]	[pilR] two-component response regulator PilR [Type IV pili [VF0082]] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapfilled_200_mauve.fasta.906
VFG001269[gb NP_879579]	[cyaB] cycloysin secretion ATP-binding protein [Cya [VF0028]] [Bordetella pertussis Tohama I]	c_amazonense.gapfilled_200_mauve.fasta.1926
VFG001269[gb NP_879579]	[cyaB] cycloysin secretion ATP-binding protein [Cya [VF0028]] [Bordetella pertussis Tohama I]	c_amazonense.gapfilled_200_mauve.fasta.517
VFG001448[gb AAA21682]	[kpsD] KpsD [K1 capsule [VF0239]] [Escherichia coli O18:K1:H7 str. RS218]	c_amazonense.gapfilled_200_mauve.fasta.436
VFG001449[gb AAA24047]	[kpsT] KpsT [K1 capsule [VF0239]] [Escherichia coli O18:K1:H7 str. RS218]	c_amazonense.gapfilled_200_mauve.fasta.438
VFG001450[gb AAA24046]	[kpsM] KpsM [K1 capsule [VF0239]] [Escherichia coli O18:K1:H7 str. RS218]	c_amazonense.gapfilled_200_mauve.fasta.439
VFG001857[gb YP_094782]	[iraB] di/tripeptide permease [IraAB [VF0293]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	c_amazonense.gapfilled_200_mauve.fasta.3332
VFG001861[gb YP_094248]	[katA] catalase/(hydro)peroxidase [KatAB [VF0168]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	c_amazonense.gapfilled_200_mauve.fasta.2372
VFG001867[gb NP_096960]	[sodB] superoxide dismutase [SodB [VF0169]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	c_amazonense.gapfilled_200_mauve.fasta.1807
VFG001965[gb NP_282578]	[C14317c] aminotransferase [Capsule [VF0329]] [Campylobacter jejuni subsp. jejuni NCTC 11168]	c_amazonense.gapfilled_200_mauve.fasta.500
VFG001990[gb YP_094942]	[flaB] flagellar basal body P-ring biosynthesis protein FlgB [Flagella [VF0157]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	c_amazonense.gapfilled_200_mauve.fasta.1214
VFG002218[gb NP_541012]	[virB11] type IV secretion system protein ATPase VirB11 [VIR type IV secretion system [VF0365]] [Brucella melitensis bv. 1 str. 16M]	c_amazonense.gapfilled_200_mauve.fasta.4204
VFG002268[gb NP_034271]	[trwE] Trw type IV secretion system VirB10 homolog, trwE protein [Trw type IV secretion system [VF0372]] [Bartonella henselae str. Houston-1]	c_amazonense.gapfilled_200_mauve.fasta.4205
VFG002420[gb NP_644838]	[adsA] Adenosine synthase A [AdsA [VF0422]] [Staphylococcus aureus subsp. aureus MW2]	c_amazonense.gapfilled_200_mauve.fasta.2516
VFG002420[gb NP_644838]	[adsA] Adenosine synthase A [AdsA [VF0422]] [Staphylococcus aureus subsp. aureus MW2]	c_amazonense.gapfilled_200_mauve.fasta.2776
VFG002501[gb NP_106857]	[fliG] flagellar motor switch protein G [Flagella [VF0430]] [Burkholderia pseudomallei K96243]	c_amazonense.gapfilled_200_mauve.fasta.2566
VFG002519[gb NP_109887]	[fliA] flagellar biosynthesis sigma factor [Flagella [VF0430]] [Burkholderia pseudomallei K96243]	c_amazonense.gapfilled_200_mauve.fasta.913
VFG002550[gb YP_109386]	[wcbP] capsular polysaccharide biosynthesis dehydrogenase/reductase [Capsule I [VF0436]] [Burkholderia pseudomallei K96243]	c_amazonense.gapfilled_200_mauve.fasta.582
VFG002679[gi 16122052]	[flgC] flagellar basal body rod protein [Flagella (cluster I) [CVF039]] [Yersinia pestis CO92]	c_amazonense.gapfilled_200_mauve.fasta.2360
VFG002705[gi 16123821]	[ddhD] CDP-6-deoxy-4,3-d-glucose reductase [O-antigen [CVF043]] [Yersinia pestis CO92]	c_amazonense.gapfilled_200_mauve.fasta.3361
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.2422
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.2519
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.2520
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.3148
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.3550
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.712
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.713
VFG002901[gi 108808062]	[YPA_2067] histidine transport system permease protein HisQ [O-antigen [CVF043]] [Yersinia pestis Antiqua]	c_amazonense.gapfilled_200_mauve.fasta.97
VFG003393[gi 1595350]	[ddhB] CDP-glucose 4,6-dehydratase [O-antigen [CVF043]] [Yersinia pseudotuberculosis IP 32953]	c_amazonense.gapfilled_200_mauve.fasta.3451
VFG003394[gi 1595351]	[ddhC] putative CDP-4-keto-6-deoxy-D-glucose-3-dehydratase [O-antigen [CVF043]] [Yersinia pseudotuberculosis IP 32953]	c_amazonense.gapfilled_200_mauve.fasta.3532
VFG003413[gi 1596047]	[fliS] flagellar protein Flis [Flagella (cluster I) [CVF039]] [Yersinia pseudotuberculosis IP 32953]	c_amazonense.gapfilled_200_mauve.fasta.3433
VFG003433[gi 1596013]	[fliG] flagellar basal-body rod protein Flig (distal rod protein) [Flagella (cluster I) [CVF039]] [Yersinia pseudotuberculosis IP 32953]	c_amazonense.gapfilled_200_mauve.fasta.2356
VFG003636[gi 16761645]	[orgC] hypothetical protein found within S. typhi pathogenicity island 1 [TTSS (SPI-1 encode) [CVF031]] [Salmonella enterica subsp. enterica serovar Typhi str. CT18]	c_amazonense.gapfilled_200_mauve.fasta.1717
VFG003668[gi 16414826]	[prnH] pathogenicity I island effector protein [TTSS (SPI-1 encode) [CVF031]] [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]	c_amazonense.gapfilled_200_mauve.fasta.1722
VFG003728[gi 16414833]	[prnG] type III secretion protein [TTSS (SPI-1 encode) [CVF031]] [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]	c_amazonense.gapfilled_200_mauve.fasta.1722
VFG003916[gi 16759521]	[fmfE] probable transcriptional regulator [FimZK regulator [Fim [VF003]] [Salmonella enterica subsp. enterica serovar Typhi str. CT18]	c_amazonense.gapfilled_200_mauve.fasta.2037
VFG004379[gi 16767813]	[stB] putative fimbrial usher protein [StB [AO067]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LTZ]	c_amazonense.gapfilled_200_mauve.fasta.1324
VFG005051[gi 13661373]	[SSP0064] putative glycosyltransferase [Capsule [CVF110]] [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]	c_amazonense.gapfilled_200_mauve.fasta.3536
VFG005341[gi 15674453]	[plr/gapA] glyceraldehyde 3-phosphate dehydrogenase [Streptococcal plasmin receptor/GAPDH [CVF123]] [Streptococcus pyogenes M1 GAS]	c_amazonense.gapfilled_200_mauve.fasta.84
VFG005356[gi 11651642]	[plr/gapA] glyceraldehyde 3-phosphate dehydrogenase, type I [Streptococcal plasmin receptor/GAPDH [CVF123]] [Streptococcus pneumoniae D39]	c_amazonense.gapfilled_200_mauve.fasta.448
VFG005535[gi 17911425]	[tig/ropA] trigger factor [Trigger factor [CVF149]] [Streptococcus pyogenes MGAS5005]	c_amazonense.gapfilled_200_mauve.fasta.1611
VFG005582[gi 125717729]	[eno] Enolase, putative [Streptococcal enolase [CVF153]] [Streptococcus sanguinis SK36]	c_amazonense.gapfilled_200_mauve.fasta.3010
VFG005767[gb NP_687682]	[cylG] 3-ketoacyl-ACP-reductase CylG [Beta-hemolysin/cytolysin [CVF171]] [Streptococcus agalactiae 2603V/R]	c_amazonense.gapfilled_200_mauve.fasta.2964
VFG005997[gi 24379858]	[rmlA] putative glucose-1-phosphate thymidyltransferase [Capsule [CVF186]] [Streptococcus mutans UA159]	c_amazonense.gapfilled_200_mauve.fasta.3521
VFG006021[gi 59800790]	[pilT2] putative twitching motility-like protein [GC pili [AO061]] [Neisseria gonorrhoeae FA 1090]	c_amazonense.gapfilled_200_mauve.fasta.75
VFG006242[gi 121635698]	[porB] porin, major outer membrane protein P.1 [PorB [CVF195]] [Neisseria meningitidis FAM18]	c_amazonense.gapfilled_200_mauve.fasta.1512
VFG006242[gi 121635698]	[porB] porin, major outer membrane protein P.1 [PorB [CVF195]] [Neisseria meningitidis FAM18]	c_amazonense.gapfilled_200_mauve.fasta.2535
VFG006255[gi 59800669]	[rpoB] ABC transporter, ATP-binding protein, iron related [ABC transporter [CVF197]] [Neisseria gonorrhoeae FA 1090]	c_amazonense.gapfilled_200_mauve.fasta.2581
VFG006259[gi 59800668]	[rpoB] ABC transporter, ATP-binding protein, iron related [ABC transporter [CVF197]] [Neisseria gonorrhoeae FA 1090]	c_amazonense.gapfilled_200_mauve.fasta.2421
VFG006259[gi 59800668]	[rpoB] ABC transporter, ATP-binding protein, iron related [ABC transporter [CVF197]] [Neisseria gonorrhoeae FA 1090]	c_amazonense.gapfilled_200_mauve.fasta.336
VFG006259[gi 59800668]	[rpoB] ABC transporter, ATP-binding protein, iron related [ABC transporter [CVF197]] [Neisseria gonorrhoeae FA 1090]	c_amazonense.gapfilled_200_mauve.fasta.98
VFG006288[gi 15794866]	[exdB] biopolymer transport protein [Ton system [CVF202]] [Neisseria meningitidis Z2491]	c_amazonense.gapfilled_200_mauve.fasta.290
VFG006295[gi 59801725]	[exd] Exd [Ton system [CVF202]] [Neisseria gonorrhoeae FA 1090]	c_amazonense.gapfilled_200_mauve.fasta.3893
VFG006392[gi 15611540]	[cagS] cag island protein, DNA transfer protein [Cag PAI type IV secretion system [CVF217]] [Helicobacter pylori J99]	c_amazonense.gapfilled_200_mauve.fasta.4202
VFG006719[gi 16800743]	[lap] hypothetical protein [Listeria adhesion protein [CVF228]] [Listeria innocua Clip11262]	c_amazonense.gapfilled_200_mauve.fasta.1063
VFG006813[gi 116873279]	[lspA] lipoprotein signal peptidase [Lipoprotein-specific signal peptidase II [CVF249]] [Listeria welshimeri serovar 6b str. SLCCS334]	c_amazonense.gapfilled_200_mauve.fasta.3093
VFG006892[gi 147673778]	[acB] accessory colonization factor AcfB [Accessory colonization factor [CVF257]] [Vibrio cholerae O395]	c_amazonense.gapfilled_200_mauve.fasta.1009
VFG006948[gi 37681131]	[mshJ] MSHA biogenesis protein MshJ [Mannose-sensitive hemagglutinin (MSHA type IV pilus) [CVF259]] [Vibrio vulnificus YJ016]	c_amazonense.gapfilled_200_mauve.fasta.4274
VFG006967[gi 59710969]	[mshE] type 4 fimbrial assembly protein PilB [Mannose-sensitive hemagglutinin (MSHA type IV pilus) [CVF259]] [Vibrio fisheri ES114]	c_amazonense.gapfilled_200_mauve.fasta.4277
VFG007025[gi 17366166]	[rtxB] ABC-type bacteriocin/fimbriolysin [RTX toxin [CVF263]] [Vibrio vulnificus CMCP6]	c_amazonense.gapfilled_200_mauve.fasta.3567
VFG007026[gi 37676694]	[rtxB] RTX toxin transporter [RTX toxin [CVF263]] [Vibrio vulnificus YJ016]	c_amazonense.gapfilled_200_mauve.fasta.516
VFG007033[gi 15600987]	[tth] thermolabile hemolysin [Thermolabile hemolysin [CVF265]] [Vibrio cholerae O1 biovar El Tor str. N16961]	c_amazonense.gapfilled_200_mauve.fasta.242
VFG007274[gi 15642208]	[viuB] vibriobactin utilization protein ViuB [Vibriobactin utilization [CVF275]] [Vibrio cholerae O1 biovar El Tor str. N16961]	c_amazonense.gapfilled_200_mauve.fasta.1765
VFG007406[gi 15642121]	[fliQ] flagellar biosynthesis protein [Flagella [VF0519]] [Vibrio cholerae O1 biovar El Tor str. N16961]	c_amazonense.gapfilled_200_mauve.fasta.2445
VFG007481[gi 27365279]	[fliE] flagellar hook-basal body protein [Flagella [CVF281]] [Vibrio vulnificus CMCP6]	c_amazonense.gapfilled_200_mauve.fasta.2568
VFG007486[gi 28899025]	[fliC] FlaM [Flagella [CVF281]] [Vibrio parahaemolyticus RIMD 2210633]	c_amazonense.gapfilled_200_mauve.fasta.2569
VFG007547[gi 27365304]	[cheW] Chemotaxis signal transduction protein [Flagella [CVF281]] [Vibrio vulnificus CMCP6]	c_amazonense.gapfilled_200_mauve.fasta.897
VFG007662[gi 37678486]	[rmlD] dTDP-4-dehydrohamnose reductase [Capsular polysaccharide [CVF282]] [Vibrio vulnificus YJ016]	c_amazonense.gapfilled_200_mauve.fasta.3520
VFG007663[gi 37678487]	[rmlC] dTDP-6-deoxy-D-xyl-4-hexulose-3-epimerase [Capsular polysaccharide [CVF282]] [Vibrio vulnificus YJ016]	c_amazonense.gapfilled_200_mauve.fasta.3522
VFG007914[gi 120404101]	[ddrA] daunorubicin resistance ABC transporter ATPase subunit [PDIM [phthiocerol dimycoserate] and PGL [phenolic glycolipid] biosynthesis and transport [CVF288]] [Mycobacterium vanbaalenii PPR-1]	c_amazonense.gapfilled_200_mauve.fasta.2009
VFG007914[gi 120404101]	[ddrA] daunorubicin resistance ABC transporter ATPase subunit [PDIM [phthiocerol dimycoserate] and PGL [phenolic glycolipid] biosynthesis and transport [CVF288]] [Mycobacterium vanbaalenii PPR-1]	c_amazonense.gapfilled_200_mauve.fasta.2903
VFG008680[gi 43364447]	[ddrA] daunorubicin resistance ABC transporter ATP-binding subunit [PDIM [phthiocerol dimycoserate] and PGL [phenolic glycolipid] biosynthesis and transport [CVF288]] [Mycobacterium smegmatis J652]	c_amazonense.gapfilled_200_mauve.fasta.1337
VFG008788[gi 43362859]	[msbA] Mycosurfactant acid synthase [PDIM [phthiocerol dimycoserate] and PGL [phenolic glycolipid] biosynthesis and transport [CVF288]] [Mycobacterium canettii CIFT 14006008]	c_amazonense.gapfilled_200_mauve.fasta.384
VFG009135[gi 383308045]	[kasB] 3-oxoacyl-(acyl carrier protein) synthase II [FAS-II [CVF300]] [Mycobacterium tuberculosis H37R327]	c_amazonense.gapfilled_200_mauve.fasta.2971
VFG009305[gi 119870876]	[pntA] pantotate-beta-alanine ligase [Pantothenate synthetase [CVF305]] [Mycobacterium sp. KMS]	c_amazonense.gapfilled_200_mauve.fasta.1431
VFG009331[gi 118471351]	[purC] phosphoribosylaminimidazole-succinocarboxamide synthase [Purine synthesis [CVF306]] [Mycobacterium smegmatis str. MC2 155]	c_amazonense.gapfilled_200_mauve.fasta.56
VFG009376[gi 118470522]	[leuD] 3-isopropylmalate dehydratase, small subunit [Lucine synthesis [CVF309]] [Mycobacterium smegmatis str. MC2 155]	c_amazonense.gapfilled_200_mauve.fasta.2259
VFG009407[gi 145223515]	[glnA1] glutamine synthetase, type I [Glutamine synthesis [CVF311]] [Mycobacterium gilvum PPR-GCK]	c_amazonense.gapfilled_200_mauve.fasta.3113
VFG009865[gi 120405794]	[mprA] two component transcriptional regulator, winged helix family [MprA/B [CVF333]] [Mycobacterium vanbaalenii PPR-1]	c_amazonense.gapfilled_200_mauve.fasta.130
VFG009865[gi 120405794]	[mprA] two component transcriptional regulator, winged helix family [MprA/B [CVF333]] [Mycobacterium vanbaalenii PPR-1]	c_amazonense.gapfilled_200_mauve.fasta.1391
VFG009921[gi 15842122]	[relA] GTP pyrophosphokinase [[pppGpp synthesis and hydrolysis [CVF335]] [Mycobacterium tuberculosis CDC1551]	c_amazonense.gapfilled_200_mauve.fasta.3345
VFG010484[gi 54296712]	[htpB] 60 kDa chaperonin (Protein Cpn60)[groEL protein]/Heat shock protein B. [Hsp60 [CVF347]] [Legionella pneumophila str. Paris]	c_amazonense.gapfilled_200_mauve.fasta.3523
VFG010515[gb YP_095205]	[lidI] Dot/Icm type IV secretion system effector LidI [Dot/Icm [SSO47]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	c_amazonense.gapfilled_200_mauve.fasta.44
VFG010782[gi 52841485]	[virB5] LvhB5 [Lvh TASSA [SSO48]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	c_amazonense.gapfilled_200_mauve.fasta.4264
VFG010904[gi 54293730]	[iraB] di/tripeptide transporter homolog IraB [Iron acquisition/assimilation locus [CVF361]] [Legionella pneumophila str. Lens]	c_amazonense.gapfilled_200_mauve.fasta.1083
VFG010904[gi 54293730]	[iraB] di/tripeptide transporter homolog IraB [Iron acquisition/assimilation locus [CVF361]] [Legionella pneumophila str. Lens]	c_amazonense.gapfilled_200_mauve.fasta.384
VFG011154[gi 115421194]	[bpgG] probable sugar transferase [LPS [CVF380]] [Bordetella avium 197N]	c_amazonense.gapfilled_200_mauve.fasta.3611
VFG011157[gi 33599142]	[bplF] lipopolysaccharide biosynthesis protein [LPS [CVF380]] [Bordetella bronchiseptica RB50]	c_amazonense.gapfilled_200_mauve.fasta.3612
VFG011157[gi 33599142]	[bplF] lipopolysaccharide biosynthesis protein [LPS [CVF380]] [Bordetella bronchiseptica RB50]	c_amazonense.gapfilled_200_mauve.fasta.606
VFG011167[gi 33594872]	[bplC] lipopolysaccharide biosynthesis protein [LPS [CVF380]] [Bordetella parapertussis 12822]	c_amazonense.gapfilled_200_mauve.fasta.3618
VFG011175[gi 33594874]	[bplA] probable oxidoreductase [LPS [CVF380]] [Bordetella parapertussis 12822]	c_amazonense.gapfilled_200_mauve.fasta.3621
VFG011255[gi 33601532]	[fliH] flagellar biosynthetic protein FlhB [Flagella [CVF382]] [Bordetella bronchiseptica RB50]	c_amazonense.gapfilled_200_mauve.fasta.917
VFG011274[gi 33596137]	[fliG] flagellar basal body rod protein [Flagella [CVF382]] [Bordetella parapertussis 12822]	c_amazonense.gapfilled_200_mauve.fasta.2361
VFG011317[gi 33592490]	[fliR] flagellar biosynthetic protein FlhR [Flagella [CVF382]] [Bordetella pertussis Tohama I]	c_amazonense.gapfilled_200_mauve.fasta.2554

VFG011351[gi 33601561]	(fliJ) flagellar protein FliJ [Flagella (CVF382)] [Bordetella bronchiseptica R850]	c_amazonense.gapped1200_mauve.fasta.2563
VFG011355[gi 33601562]	(fliJ) flagellar-specific ATP synthase FliJ [Flagella (CVF382)] [Bordetella bronchiseptica R850]	c_amazonense.gapped1200_mauve.fasta.2564
VFG011402[gi 23502030]	(fabZ) (3R)-hydroxymyristoyl ACP dehydratase [LPS (CVF383)] [Brucella suis 1330]	c_amazonense.gapped1200_mauve.fasta.1592
VFG011430[gb NP_540392]	(acpM) acyl carrier protein [LPS (CVF383)] [Brucella melitensis bv. 1 str. 16M]	c_amazonense.gapped1200_mauve.fasta.2972
VFG011582[gi 83269014]	(virB9) Type IV secretion system CagX conjugation protein [Type IV secretion system (CVF385)] [Brucella melitensis biovar Abortus 2308]	c_amazonense.gapped1200_mauve.fasta.4206
VFG011773[gi 118475094]	(CFF8240_1403) putative heptosyltransferase III waaq [LOS (CVF396)] [Campylobacter fetus subsp. fetus 82-40]	c_amazonense.gapped1200_mauve.fasta.667
VFG011805[gi 118475485]	(CFF8240_1412) aspartate racemase [LOS (CVF396)] [Campylobacter fetus subsp. fetus 82-40]	c_amazonense.gapped1200_mauve.fasta.102
VFG011809[gi 118475685]	(CFF8240_1413) bifunctional protein HldE [LOS (CVF396)] [Campylobacter fetus subsp. fetus 82-40]	c_amazonense.gapped1200_mauve.fasta.368
VFG012080[gi 118475230]	(pgII) glycosyl transferase, group 1 family protein [N-linked protein glycosylation (CVF400)] [Campylobacter fetus subsp. fetus 82-40]	c_amazonense.gapped1200_mauve.fasta.666
VFG012165[gi 11080269]	(CPR_0433) transport protein ysiA [Hemolysin (CVF417)] [Clostridium perfringens SM101]	c_amazonense.gapped1200_mauve.fasta.3662
VFG012183[gi 150016581]	(Cbe1_1707) hemolysin A [Hemolysin (CVF417)] [Clostridium beijerinckii NCIM8 8052]	c_amazonense.gapped1200_mauve.fasta.3796
VFG012187[gi 28210321]	(CTC00586) hemolysin III [Hemolysin (CVF417)] [Clostridium tetani E88]	c_amazonense.gapped1200_mauve.fasta.2914
VFG012633[gi 26252982]	(ireA) Putative iron-regulated outer membrane virulence protein [iron-regulated element (CVF461)] [Escherichia coli CF7073]	c_amazonense.gapped1200_mauve.fasta.1319
VFG012837[gi 82524546]	(ipaH2_5) invasion plasmid antigen, fragment [Mxi-Spa TTSS effectors controlled by MxiE (CVF465)] [Shigella dysenteriae Sd197]	c_amazonense.gapped1200_mauve.fasta.4033
VFG012837[gi 82524546]	(ipaH2_5) invasion plasmid antigen, fragment [Mxi-Spa TTSS effectors controlled by MxiE (CVF465)] [Shigella dysenteriae Sd197]	c_amazonense.gapped1200_mauve.fasta.4046
VFG012837[gi 82524546]	(ipaH2_5) invasion plasmid antigen, fragment [Mxi-Spa TTSS effectors controlled by MxiE (CVF465)] [Shigella dysenteriae Sd197]	c_amazonense.gapped1200_mauve.fasta.4118
VFG012837[gi 82524546]	(ipaH2_5) invasion plasmid antigen, fragment [Mxi-Spa TTSS effectors controlled by MxiE (CVF465)] [Shigella dysenteriae Sd197]	c_amazonense.gapped1200_mauve.fasta.4122
VFG012837[gi 82524546]	(ipaH2_5) invasion plasmid antigen, fragment [Mxi-Spa TTSS effectors controlled by MxiE (CVF465)] [Shigella dysenteriae Sd197]	c_amazonense.gapped1200_mauve.fasta.4144
VFG012874[gi 30064027]	(ipaH) hypothetical protein [Mxi-Spa TTSS effectors controlled by MxiE (CVF465)] [Shigella flexneri 2a str. 24571]	c_amazonense.gapped1200_mauve.fasta.110
VFG013082[gi 82524781]	(virK) VirK [VirK (CVF483)] [Shigella boydii Sb227]	c_amazonense.gapped1200_mauve.fasta.757
VFG013147[gi 170719185]	(kdsIb) 3-deoxy-D-manno-oxulosonate cytidyltransferase [LOS (CVF494)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2916
VFG013165[gi 170717703]	(VFG012-Q-0-(3-hydroxymyristoyl) glucosamine N-acyltransferase [LOS (CVF494)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.1591
VFG013173[gi 170719107]	(rfae) rfaE bifunctional protein [LOS (CVF494)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2476
VFG013190[gi 170717479]	(hItA) extracellular solute-binding protein family 1 [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2334
VFG013191[gi 170717477]	(hItB) binding-protein-dependent transport systems inner membrane component [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2333
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.1027
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.1338
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2332
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2580
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2707
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2717
VFG013192[gi 170717476]	(hItC) ABC transporter related [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.3314
VFG013197[gi 170717931]	(hemB) Porphobilinogen synthase [Heme biosynthesis (CVF506)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.1444
VFG013198[gi 170718229]	(hemC) porphobilinogen deaminase [Heme biosynthesis (CVF506)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.34
VFG013199[gi 170718230]	(hemD) Uroporphyrinogen III synthase HEM4 [Heme biosynthesis (CVF506)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.35
VFG013203[gi 170719024]	(hemL) glutamate-1-semialdehyde-2,1-aminomutase [Heme biosynthesis (CVF506)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.2288
VFG013205[gi 170718942]	(hemM) oxygen-independent coproporphyrinogen III oxidase [Heme biosynthesis (CVF506)] [Haemophilus somnus 2336]	c_amazonense.gapped1200_mauve.fasta.3232
VFG013247[gi 113460811]	(pgII) tetraacylsaccharide 4'-kinase (Iipid-A 4'-kinase) [LOS (CVF494)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.2918
VFG013252[gi 33152665]	(mbaA) ABC transporter ATP-binding protein MbaA [LOS (CVF494)] [Haemophilus ducreyi 35000HP]	c_amazonense.gapped1200_mauve.fasta.670
VFG013265[gb NP_438428]	(orfM) deoxyribonucleotide triphosphate pyrophosphatase [LOS (CVF494)] [Haemophilus influenzae Rd KW20]	c_amazonense.gapped1200_mauve.fasta.816
VFG013324[gi 148827923]	(lpwH) UDP-2,3-diacylglycosamine hydrolase [LOS (CVF494)] [Haemophilus influenzae PittG5]	c_amazonense.gapped1200_mauve.fasta.2602
VFG013384[gb NP_439218]	(lpwB) Iipid A-disaccharide synthase [LOS (CVF494)] [Haemophilus influenzae Rd KW20]	c_amazonense.gapped1200_mauve.fasta.1594
VFG013394[gi 113461502]	(lpac) UDP-N-acetylglucosamine acyltransferase [LOS (CVF494)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.1593
VFG013407[gi 68249665]	(rfad) ADP-L-glycero-D-manno-heptose-6-epimerase [LOS (CVF494)] [Haemophilus influenzae 86-028NP]	c_amazonense.gapped1200_mauve.fasta.2474
VFG013417[gi 113460510]	(lpac) UDP-3-O-(3-hydroxymyristoyl)-N-acetylglucosamine deacetylase [LOS (CVF494)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.3836
VFG013423[gi 113461381]	(gmhA/lpCA) phosphoglycerate isomerase [LOS (CVF494)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.237
VFG013466[gi 68249928]	(kdsA) 2-dehydro-3-deoxyphosphoactonate aldolase [LOS (CVF494)] [Haemophilus influenzae 86-028NP]	c_amazonense.gapped1200_mauve.fasta.3009
VFG013470[gi 113461089]	(kdsA) 2-dehydro-3-deoxyphosphoactonate aldolase [LOS (CVF494)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.2141
VFG013515[gi 148826007]	(mrsA/glmM) predicted phosphomannomutase [Exopolysaccharide (CVF495)] [Haemophilus influenzae PittEE]	c_amazonense.gapped1200_mauve.fasta.3371
VFG013530[gi 16273471]	(pgI) glucose-6-phosphate isomerase [Exopolysaccharide (CVF495)] [Haemophilus influenzae Rd KW20]	c_amazonense.gapped1200_mauve.fasta.18
VFG013535[gi 113461081]	(pgII) glucose-6-phosphate isomerase [Exopolysaccharide (CVF495)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.1986
VFG013539[gi 113460750]	(manA) mannose-6-phosphate isomerase (phosphomannomannose isomerase) [Exopolysaccharide (CVF495)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.1104
VFG013568[gi 68248709]	(hItB) iron(III)-transport system permease protein hfbpB [Haemophilus iron transport locus (CVF501)] [Haemophilus influenzae 86-028NP]	c_amazonense.gapped1200_mauve.fasta.2693
VFG013573[gi 113460924]	(hItC) iron(III) ABC transporter, ATP-binding protein [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.1213
VFG013573[gi 113460924]	(hItC) iron(III) ABC transporter, ATP-binding protein [Haemophilus iron transport locus (CVF501)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.2459
VFG013607[gi 113460953]	(hemA) glutamyl-tRNA reductase [Heme biosynthesis (CVF506)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.3919
VFG013612[gi 113461676]	(hemE) uroporphyrinogen decarboxylase [Heme biosynthesis (CVF506)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.1048
VFG013615[gi 68249709]	(hemH) ferrochelatase [Heme biosynthesis (CVF506)] [Haemophilus influenzae 86-028NP]	c_amazonense.gapped1200_mauve.fasta.1950
VFG013618[gi 113461372]	(hemL) glutamate-1-semialdehyde aminotransferase [Heme biosynthesis (CVF506)] [Haemophilus somnus 129PT]	c_amazonense.gapped1200_mauve.fasta.28
VFG013629[gi 33152698]	(hemN) coproporphyrinogen III oxidase [Heme biosynthesis (CVF506)] [Haemophilus ducreyi 35000HP]	c_amazonense.gapped1200_mauve.fasta.817
VFG013631[gi 30995388]	(hemX) heme biosynthesis-like protein [Heme biosynthesis (CVF506)] [Haemophilus influenzae Rd KW20]	c_amazonense.gapped1200_mauve.fasta.36
VFG013794[gi 146281442]	(pilQ) type 4 pilus biogenesis protein PilQ [Type IV pilus biosynthesis (CVF518)] [Pseudomonas stutzeri A1501]	c_amazonense.gapped1200_mauve.fasta.3404
VFG013800[gi 71731545]	(pilQ) type IV pilus pilgrillin peptide PilQ [Type IV pilus biosynthesis (CVF518)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.3576
VFG013811[gi 28868044]	(pilQ) type IV pilus biogenesis protein PilQ [Type IV pilus biosynthesis (CVF518)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.2546
VFG013820[gi 146281354]	(pilE) type 4 fimbrial biogenesis protein PilE [Type IV pilus biosynthesis (CVF518)] [Pseudomonas stutzeri A1501]	c_amazonense.gapped1200_mauve.fasta.677
VFG013848[gi 152985916]	(pilN) type 4 fimbrial biogenesis protein PilN [Type IV pilus biosynthesis (CVF518)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.676
VFG013867[gi 77456635]	(pilO) Pilus assembly protein, PilO [Type IV pilus biosynthesis (CVF518)] [Pseudomonas fluorescens Pf0-1]	c_amazonense.gapped1200_mauve.fasta.675
VFG013881[gi 146305582]	(pilP) Pilus assembly protein, PilP [Type IV pilus biosynthesis (CVF518)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.674
VFG013887[gi 66043674]	(pilQ) type II and III secretion system protein:NoiW-like:NoiW-like [Type IV pilus biosynthesis (CVF518)] [Pseudomonas syringae pv. syringae B728A]	c_amazonense.gapped1200_mauve.fasta.74
VFG013907[gi 146309163]	(pilQ) twitching motility protein [Type IV pilus biosynthesis (CVF518)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.1284
VFG013912[gi 28870209]	(pilU) twitching motility protein [Type IV pilus biosynthesis (CVF518)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.3301
VFG013954[gi 146306666]	(pilZ) type IV pilus assembly PilZ [Type IV pilus biosynthesis (CVF518)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.3923
VFG014002[gi 146283959]	(pilS) two-component sensor PilS [Type IV pilus biosynthesis (CVF518)] [Pseudomonas stutzeri A1501]	c_amazonense.gapped1200_mauve.fasta.3622
VFG014099[gi 15598355]	(wbpA) probable UDP-glucose/GDP-mannose dehydrogenase WbpA [LPS O-antigen (P. aeruginosa) (CVF520)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.435
VFG014099[gi 15598355]	(wbpA) probable UDP-glucose/GDP-mannose dehydrogenase WbpA [LPS O-antigen (P. aeruginosa) (CVF520)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.503
VFG014106[gi 15598348]	(hItB) gltI aminotransferase [LPS O-antigen (P. aeruginosa) (CVF520)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.3614
VFG014109[gi 15598345]	(wbpH) probable glycosyltransferase WbpH [LPS O-antigen (P. aeruginosa) (CVF520)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.4148
VFG014116[gi 155983338]	(PA3142) hypothetical protein [LPS O-antigen (P. aeruginosa) (CVF520)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.3610
VFG014147[gi 116051137]	(wbpM) nucleotide sugar epimerase/dehydratase WbpM [LPS O-antigen (P. aeruginosa) (CVF520)] [Pseudomonas aeruginosa UCBBP-PA14]	c_amazonense.gapped1200_mauve.fasta.3437
VFG014292[gi 152985351]	(fliC) A-type Flagellin [Flagella (CVF521)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.3434
VFG014329[gi 146282226]	(fliD) flagellar capping protein FliD [Flagella (CVF521)] [Pseudomonas stutzeri A1501]	c_amazonense.gapped1200_mauve.fasta.2996
VFG014378[gi 70729027]	(fleS) sensory box histidine kinase FleS [Flagella (CVF521)] [Pseudomonas fluorescens Pf-5]	c_amazonense.gapped1200_mauve.fasta.2555
VFG014561[gi 77457777]	(fliQ) flagellar biosynthesis protein [Flagella (CVF521)] [Pseudomonas fluorescens Pf0-1]	c_amazonense.gapped1200_mauve.fasta.914
VFG014628[gi 146282909]	(fleN) flagellar motor regulator FleN [Flagella (CVF521)] [Pseudomonas stutzeri A1501]	c_amazonense.gapped1200_mauve.fasta.912
VFG014707[gb NP_250151]	(motC) flagellar motor protein [Deoxyhexose linking sugar, 209 Da capping structure (A1138)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.2726
VFG014731[gi 146307821]	(motD) OmpA/MotB domain protein [Flagella (CVF521)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.2218
VFG014894[gi 1529858001]	(algC) phosphomannomutase AlgC [Alginate biosynthesis (CVF523)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.2170
VFG014942[gi 774575914]	(algH) Sigma-E regulatory protein MuD [Alginate regulation (CVF523)] [Pseudomonas fluorescens Pf0-1]	c_amazonense.gapped1200_mauve.fasta.2169
VFG014950[gb NP_294957]	(mucD) serine protease MucD precursor [Alginate regulation (CVF523)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.2871
VFG014952[gi 116048682]	(mucD) serine protease MucD precursor [Alginate regulation (CVF523)] [Pseudomonas aeruginosa UCBBP-PA14]	c_amazonense.gapped1200_mauve.fasta.1458
VFG014966[gi 28867367]	(algR) alginate biosynthesis regulatory protein AlgR [Alginate regulation (CVF523)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.2756
VFG014966[gi 28867367]	(algR) alginate biosynthesis regulatory protein AlgR [Alginate regulation (CVF523)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.2789
VFG014966[gi 28867367]	(algR) alginate biosynthesis regulatory protein AlgR [Alginate regulation (CVF523)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.121
VFG014974[gi 146305320]	(algR) two component transcriptional regulator, LytTR family [Alginate regulation (CVF523)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.3897
VFG014981[gi 71736095]	(algZ) sensor histidine kinase FimS [Alginate regulation (CVF523)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.257
VFG015057[gi 152986918]	(lasI) autoinducer synthase protein LasI [N-(3-oxo-dodecanoyl)-L-homoserine lactone QS system (CVF526)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.1377
VFG015072[gi 71734710]	(gacS) response regulator, sensor histidine kinase component GacS [GacS/GacA two-component system (CVF529)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.2106
VFG015085[gi 71738055]	(gacA) response regulator, DNA binding component GacA [GacS/GacA two-component system (CVF529)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.781
VFG015456[gi 71735435]	(hcp1) ScpM protein [Hcp secretion island-1 encoded type VI secretion system (H-T655) (CVF535)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.785
VFG015475[gi 66048180]	(PsrY_4956) protein of unknown function DUF879 [Hcp secretion island-1 encoded type VI secretion system (H-T655) (CVF535)] [Pseudomonas syringae pv. syringae B728A]	c_amazonense.gapped1200_mauve.fasta.210
VFG015519[gi 152985181]	(phzG) phaeazine biosynthesis protein PhzG [Phaeazine biosynthesis (CVF536)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.30
VFG015521[gb NP_252906]	(phzG1) phaeazine biosynthesis protein PhzG, pyridoxamine 5'-phosphate aldolase [Phaeazines biosynthesis (CVF536)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.31
VFG015558[gi 116051721]	(lasB) elastase LasB [Elastase (CVF537)] [Pseudomonas aeruginosa UCBBP-PA14]	c_amazonense.gapped1200_mauve.fasta.1453
VFG015600[gi 152984031]	(hdsS) probable acyltransferase [Acylhomoserine lactone synthase (CVF528)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.2358
VFG015650[gi 73034944]	(fliG) flagellar basal body FlhE domain protein [Flagella (CVF521)] [Pseudomonas putida GB-1]	c_amazonense.gapped1200_mauve.fasta.1118
VFG015681[gi 70722859]	(fleR) two component, sigma54 specific, transcriptional regulator, Fis family [Flagella (CVF521)] [Pseudomonas putida W619]	c_amazonense.gapped1200_mauve.fasta.1588
VFG015774[gi 167032166]	(mucP) membrane-associated zinc metalloprotease [Alginate regulation (CVF523)] [Pseudomonas putida GB-1]	c_amazonense.gapped1200_mauve.fasta.788
VFG015806[gi 70721686]	(cnpV1) type VI secretion ATPase, CnpV1 family [Hcp secretion island-1 encoded type VI secretion system (H-T655) (CVF535)] [Pseudomonas putida W619]	c_amazonense.gapped1200_mauve.fasta.215
VFG015881[gi 28871838]	(PSPTO_4713) alanyl tRNA synthetase-related protein [Phytotoxin coronatine (CVF545)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.3331
VFG015881[gi 28871838]	(PSPTO_4713) alanyl tRNA synthetase-related protein [Phytotoxin coronatine (CVF545)] [Pseudomonas syringae pv. tomatato str. DC3000]	c_amazonense.gapped1200_mauve.fasta.2222
VFG015885[gi 71736839]	(cysC1) adenylylsulfate kinase [Phytotoxin phaseolotoxin (CVF546)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.2838
VFG015888[gi 71737277]	(PSPPH_4304) hydrolase, HAD-superfamily, subfamily IIA [Phytotoxin phaseolotoxin (CVF546)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.2187
VFG015903[gi 71735677]	(argK) phaseolotoxin-insensitive ornithine carbamoyltransferase [Phytotoxin phaseolotoxin (CVF546)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.248
VFG015903[gi 71735677]	(argK) phaseolotoxin-insensitive ornithine carbamoyltransferase [Phytotoxin phaseolotoxin (CVF546)] [Pseudomonas syringae pv. phaseolicola 1448A]	c_amazonense.gapped1200_mauve.fasta.3357
VFG015914[gi 15597389]	(hcnA) hydrogen cyanide synthase HcnA [Hydrogen cyanide production (CVF549)] [Pseudomonas aeruginosa PAO1]	c_amazonense.gapped1200_mauve.fasta.2829
VFG015925[gi 77459737]	(hcnB) BFD-like [2Fe-2S]-binding region [Hydrogen cyanide production (CVF549)] [Pseudomonas fluorescens Pf0-1]	c_amazonense.gapped1200_mauve.fasta.2830
VFG015927[gi 152985611]	(hcnC) hydrogen cyanide synthase HcnC [Hydrogen cyanide production (CVF549)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.2328
VFG015930[gi 70729947]	(hcnC) hydrogen cyanide synthase HcnC [Hydrogen cyanide production (CVF549)] [Pseudomonas fluorescens Pf-5]	c_amazonense.gapped1200_mauve.fasta.2831
VFG015972[gi 146307893]	(pvdA) Lysine/ornithine N-monooxygenase-like protein [Pyoverdine (CVF551)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.562
VFG016039[gi 152983967]	(pvdJ) thermophilic carboxylesterase EstZ [Pyoverdine (CVF551)] [Pseudomonas aeruginosa PA7]	c_amazonense.gapped1200_mauve.fasta.238
VFG016057[gi 146307890]	(pvdH) 2,4-diaminobutyrate 4-transaminase [Pyoverdine (CVF551)] [Pseudomonas mendocina ynp]	c_amazonense.gapped1200_mauve.fasta.563

VF061630(gi:15078902) (capD) gamma-glutamyltranspeptidase [Polyglutamic acid capsule (CVF566)] [Bacillus subtilis subsp. subtilis str. 168]

VF061637(gi:42784426) (galE) UDP-glucose 4-epimerase [Polysaccharide capsule (CVF567)] [Bacillus cereus ATCC 10987]

VF061639(gi:42784429) (BCE_3384) NAD dependent epimerase/dehydratase family protein [Polysaccharide capsule (CVF567)] [Bacillus cereus ATCC 10987]

VF061690(gi:4947840) (BT9727_4951) conserved hypothetical protein, possible MVN-like virulence factor [Polysaccharide capsule (CVF567)] [Bacillus thuringiensis serovar konkukian str. 97-27]

VF0616433(gi:118480317) (gtab) UTP-glucose-1-phosphate uridylyltransferase [Polysaccharide capsule (CVF567)] [Bacillus thuringiensis str. Al Hakam]

VF0616433(gi:118480317) (gtab) UTP-glucose-1-phosphate uridylyltransferase [Polysaccharide capsule (CVF567)] [Bacillus thuringiensis str. Al Hakam]

VF0616485(gi:31544430) (tuf) elongation factor Tu [EF-Tu (CVF587)] [Mycoplasma gallisepticum str. R(10w)]

VF0616485(gi:31544430) (tuf) elongation factor Tu [EF-Tu (CVF587)] [Mycoplasma gallisepticum str. R(10w)]

VF0616486(gi:54020567) (tuf) elongation factor Tu [EF-Tu (CVF587)] [Mycoplasma hyopneumoniae 232]

VF0616676(gi:9475416) (cnaB) Outer membrane arabinic acid-binding protein (A25-7) [Bartonella henselae str. Houston-1]

VF0617360(gi:153950020) (dhaA) glucose-1-phosphate cytidyl transferase [O-antigen (VF043)] [Yersinia pseudotuberculosis IP 31758]

VF0617486(gi:118462718) (nuoG) NADH-quinone oxidoreductase, chain g [nuoG (CVF620)] [Mycobacterium avium 104]

VF0617670(gi:443489219) (icl) isocitrate lyase Icl [Isocitrate lyase (CVF320)] [Mycobacterium liflandii 128FX1]

VF0617733(gi:153952077) (pebA) amino acid ABC transporter, periplasmic amino acid-binding protein PEB1 [PEB1/CBF1 (CVF388)] [Campylobacter jejuni subsp. jejuni 81116]

VF0617759(gi:153951764) (kpsF) arabinose-5-phosphate isomerase [Capsule biosynthesis and transport (CVF393)] [Campylobacter jejuni subsp. jejuni 81116]

VF0617761(gi:153952331) (kpsE) capsular polysaccharide ABC transporter [Capsule biosynthesis and transport (CVF393)] [Campylobacter jejuni subsp. jejuni 81116]

VF0617855(gi:153948767) (pilW) putative transposase [Type IV pili (CVF049)] [Yersinia pseudotuberculosis IP 31758]

VF0617855(gi:153948767) (pilW) putative transposase [Type IV pili (CVF049)] [Yersinia pseudotuberculosis IP 31758]

VF0617855(gi:153948767) (pilW) putative transposase [Type IV pili (CVF049)] [Yersinia pseudotuberculosis IP 31758]

VF0617989(gi:157415665) (CB1_1346) hypothetical protein [Capsule biosynthesis and transport (CVF393)] [Campylobacter jejuni subsp. jejuni 81116]

VF0617989(gi:157415665) (CB1_1346) hypothetical protein [Capsule biosynthesis and transport (CVF393)] [Campylobacter jejuni subsp. jejuni 81116]

VF0617989(gi:157415665) (CB1_1346) hypothetical protein [Capsule biosynthesis and transport (CVF393)] [Campylobacter jejuni subsp. jejuni 81116]

VF0618020(gi:157415415) (gmhA-1) phosphoethanol isomerase [LOS (CVF386)] [Mycobacterium avium subsp. jejuni 81116]

VF0618293(gi:161620106) (dhaB) Probable isochromatase [Bruceabactin (CVF386)] [Brucella canis ATCC 23365]

VF0618336(gi:161612541) (staB) hypothetical protein [Sta (VF019)] [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]

VF0618402(gi:1616105694) (mgfB) hypothetical protein [Mg²⁺ transport (CVF005)] [Salmonella enterica subsp. enterica serovar G24:2,3::str. RSK2980]

VF0618554(gi:1616102085) (prgK) hypothetical protein [TTSS (SPI-1 encode) (CVF031)] [Salmonella enterica subsp. enterica serovar G24:2,3::str. RSK2980]

VF0618558(gi:1616102087) (orgB) hypothetical protein [TTSS (SPI-1 encode) (CVF031)] [Salmonella enterica subsp. enterica serovar G24:2,3::str. RSK2980]

VF0618707(gi:163869212) (korB) trans-acting regulatory protein [Trw type IV secretion system (CVF604)] [Bartonella tribocorum CIP 105476]

VF0618707(gi:163869212) (korB) trans-acting regulatory protein [Trw type IV secretion system (CVF604)] [Bartonella tribocorum CIP 105476]

VF0618707(gi:163869212) (korB) trans-acting regulatory protein [Trw type IV secretion system (CVF604)] [Bartonella tribocorum CIP 105476]

VF0618806(gi:161870575) (icdE) biopolymer transport protein [Ton system (CVF202)] [Neisseria meningitidis 053442]

VF0618806(gi:161870575) (icdE) biopolymer transport protein [Ton system (CVF202)] [Neisseria meningitidis 053442]

VF0618806(gi:161870575) (icdE) biopolymer transport protein [Ton system (CVF202)] [Neisseria meningitidis 053442]

VF0619028(gi:170025406) (YPK_2189) DegT/DnaI/ErpC/Sly5 aminotransferase [O-antigen (VF043)] [Yersinia pseudotuberculosis YPIII]

VF0619252(gi:163844264) (virB4) type IV secretion/conjugial transfer ATPase, VirB4 family [Type IV secretion system (CVF385)] [Brucella suis ATCC 23445]

VF0619276(gi:163844212) (dhaB) hypothetical protein [Bruceabactin (CVF386)] [Brucella suis ATCC 23445]

VF0619334(gi:25685884) (dhcC) isochromatase synthase [Bruceabactin (CVF386)] [Brucella melitensis ATCC 23457]

VF0619335(gi:25685883) (dhbE) 2,3-dihydroxybenzoate-AMP ligase [Bruceabactin (CVF386)] [Brucella melitensis ATCC 23457]

VF0619385(gi:26224673) (bsh) conjugated bile acid hydrolase [Bile-salt hydrolase (CVF250)] [Listeria monocytogenes serotype 4b str. CLIP 80459]

VF0619431(gi:188527050) (napA) neutrophil activating protein (napA) (bacterioferritin) [Neutrophil-activating protein (HP-NAP) (CVF215)] [Helicobacter pylori Sh470]

VF0619544(gi:210134297) (fucC) alpha-1,2-fucosyltransferase [Lipopolysaccharide Lewis antigens (CVF222)] [Helicobacter pylori P12]

VF0619722(gi:194091955) (exlB) ExbB [Ton system (CVF202)] [Neisseria gonorrhoeae NGCP11945]

VF0619732(gi:196858336) (YFP15_1052) lipase-like proteins leader peptide processing enzyme [Type IV pili biosynthesis (CVF518)] [Pseudomonas fluorescens SBW25]

VF0620307(gi:160894378) (YFP15_1052) lipase-like proteins leader peptide processing enzyme [Type IV pili biosynthesis (CVF518)] [Pseudomonas fluorescens SBW25]

VF0620307(gi:160894378) (YFP15_1052) lipase-like proteins leader peptide processing enzyme [Type IV pili biosynthesis (CVF518)] [Pseudomonas fluorescens SBW25]

VF0620437(gi:194736233) (icgE) invasion protein [Invasion protein (CVF031)] [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

VF0621683(gi:197251878) (stjC) putative periplasmic chaperone protein [Stj (VF028)] [Salmonella enterica subsp. enterica serovar Agona str. SL483]

VF0621856(gi:118470693) (fxbA) Formyl transferase [exochelin (A0323)] [Mycobacterium smegmatis str. MC2 155]

VF0622587(gi:333989098) (icl) isocitrate lyase Icl [Isocitrate lyase (CVF302)] [Mycobacterium sp. JDM601]

VF0622623(gi:333992530) (panD) aspartate 1-decarboxylase precursor PanD [Pantothenate synthesis (CVF305)] [Mycobacterium sp. JDM601]

VF0622639(gi:333991835) (proC) pyrroline-5-carboxylate reductase ProC [Proline synthesis (CVF307)] [Mycobacterium sp. JDM601]

VF0622709(gi:169629208) (mbtE) putative peptide synthetase MbtE [Mycoabactin (CVF315)] [Mycobacterium abscessus ATCC 19977]

VF0622816(gi:169630604) (nirK) integral membrane nitrite extrusion protein NirK [Nitrate/nitrite transporter (CVF320)] [Mycobacterium abscessus ATCC 19977]

VF0623783(gi:332161122) (YE105_C1504) Mannose-1-phosphate guanylyltransferase, ManC protein [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(1)]

VF0623786(gi:332161126) (YE105_C1504) GDP-mannose 4,6-dehydratase [O-antigen (CVF043)] [Yersinia enterocolitica subsp. palearctica 105.5R(1)]

VF0623952(gi:315443880) (sprY) anthranilate phosphoribosyltransferase [Tryptophan synthesis (CVF308)] [Burkholderia thailandensis cnpM SpY1]

VF0624912(gi:262382190) (shvA) type IVB pilus form protein [ShvA (CVF381)] [Burkholderia thailandensis cnpM SpY1]

VF0625389(gi:53723902) (flm) flagellar motor switch protein Flm [Flagella

(fimH) long polar fimbrial protein LpfA [Type I fimbriae (CVF426)] [Escherichia coli O104:H+ str. 2009EL-2050]
(hlyD) hemolysin secretion protein D [Alpha-hemolysin (CVF453)] [Escherichia coli ABU 83972]
(hlyB) hemolysin B [Alpha-hemolysin (CVF453)] [Escherichia coli O103:H2 str. 12009]
(hlyB) hemolysin secretion protein HlyB [Alpha-hemolysin (CVF453)] [Escherichia coli ABU 83972]
(chuT) Periplasmic heme-binding protein (Hemin uptake [CVF460]) [Escherichia coli NA114]
(lbeB) copper/silver efflux system outer membrane protein CusC [Invasion of brain endothelial cells (lbes) (CFV249)] [Escherichia coli O127:H6 str. E2348/69]
(lbeB) Cation efflux system protein cusC [Invasion of brain endothelial cells (lbes) (CFV249)] [Escherichia coli O83:H1 str. LF82]
(ECO42_4530) putative type VI secretion protein [SCI-H (SS183)] [Escherichia coli Q44:H18 A04]
(ECS5989_3327) hypothetical protein [SCI-H T655 (CVF734)] [Escherichia coli S5989]
(aacC) ABC transporter ATP binding domain [ABC transporters (CVF737)] [Escherichia coli O78:H1X80 str. H10407]
(rfaP) ADP-heptose -1,5 heptosyltransferase [LOS synthesis (CVF718)] [Neisseria lactamica 020-06]
(plwI) type IV pilus biogenesis/stability protein [Type IV pili (CVF189)] [Neisseria meningitidis M01-240149]
(porB) major outer membrane protein P.IB precursor [PorB (CVF195)] [Neisseria meningitidis G2136]
(porB) major outer membrane protein P.IB precursor [PorB (CVF195)] [Neisseria meningitidis G2136]
(porB) major outer membrane protein P.IB precursor [PorB (CVF195)] [Neisseria meningitidis G2136]
(exdB) biopolymer transport protein [Ton system (CVF202)] [Neisseria lactamica 020-06]
(exdE) biopolymer transport protein [Ton system (CVF202)] [Neisseria lactamica 020-06]
(kdaA_waaA)-3 deoxy-D-manno-octulosonic acid synthesis [LOS synthesis (CVF187)] [Neisseria meningitidis alpha14]
(rfaC) lipopolysaccharide heptosyltransferase I [LOS synthesis (CVF187)] [Neisseria meningitidis Z2491]
(plvI) putative type IV pilin protein [Type IV pili (CVF189)] [Neisseria meningitidis alpha14]
(farA) efflux pump protein, fatty acid resistance [FarAB (CVF758)] [Neisseria gonorrhoeae NCCP11945]
(farA) putative efflux pump protein [FarAB (CVF758)] [Neisseria meningitidis alpha14]
(farA) multidrug resistance translocase [FarAB (CVF758)] [Neisseria lactamica 020-06]
(farA) multidrug resistance protein B [FarAB (CVF758)] [Neisseria meningitidis R013]
(farB) antibacterial fatty acid resistance protein B [FarAB (CVF758)] [Neisseria meningitidis G2136]
(farB) bacterial resistance translocase [FarAB (CVF758)] [Neisseria lactamica 020-06]
(mtrC) antibiotic resistance efflux pump component [MtrCDE (CVF759)] [Neisseria gonorrhoeae NCCP11945]
(mtrC) antibiotic resistance efflux pump component [MtrCDE (CVF759)] [Neisseria gonorrhoeae NCCP11945]
(mtrC) membrane fusion protein MtrC [MtrCDE (CVF759)] [Neisseria meningitidis M01-240355]
(mtrD) drug efflux protein [MtrCDE (CVF759)] [Neisseria meningitidis Z2491]
(mtrD) drug efflux transport protein MTrD [MtrCDE (CVF759)] [Neisseria meningitidis WuY 2594]
(mtrD) drug efflux transport protein MTrD [MtrCDE (CVF759)] [Neisseria meningitidis R013]
(mtrE) multiple transferable antibiotic resistance system protein MTR [MtrCDE (CVF759)] [Neisseria meningitidis M04-240196]
(mntA) ABC transporter ATP binding domain [Manganese transport system (CVF761)] [Neisseria gonorrhoeae FA 1090]
(mntB) putative ABC transporter membrane protein [Manganese transport system (CVF761)] [Neisseria meningitidis alpha170]
(mntC) putative periplasmic solute binding protein [Manganese transport system (CVF761)] [Neisseria meningitidis alpha14]
(msrA/B[plm]) peptide methionine sulfoxide reductase MsrA/MsrB [includes: thiorodone, peptide methionine sulfoxide reductase MsrA (protein-methionine-S-oxide reductase
(msrA/B[plm]) peptide methionine sulfoxide reductase [Methionine sulphoxide reductase (CVF762)] [Neisseria lactamica 020-06]
(reCN) DNA repair protein [Recombinational repair protein (CVF763)] [Neisseria lactamica 020-06]
(ABK1_0905) transcriptional regulator [Heme utilization (CVF769)] [Acinetobacter baumannii 1656-2]
(hemoI) heme oxygenase [Heme utilization (CVF769)] [Acinetobacter baumannii TYTH-1]
(adefR) RNA efflux transporter [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii D127979]
(adegN) RND family efflux transporter [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii AB0057]
(adegN) RND family efflux transporter [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii AB0057]
(adegN) RND family efflux transporter [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii AB0057]
(adegN) RND family efflux transporter [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii AB0057]
(adegH) Node family efflux transporter outer membrane lipoprotein [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii TYTH-1]
(adegH) Node family efflux transporter outer membrane lipoprotein [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii TYTH-1]
(adegH) Node family efflux transporter outer membrane lipoprotein [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii TYTH-1]
(adegH) Node family efflux transporter outer membrane lipoprotein [AdeFGH efflux pump/transport autoinducer (CVF773)] [Acinetobacter baumannii TYTH-1]
(lpxL) Lauryl/myristoyl acyltransferase [LPS (CVF774)] [Acinetobacter baumannii BJAB0715]
(MQ3_285) nucleoside-diphosphate sugar epimerase [Capsule (CVF775)] [Acinetobacter baumannii TYTH-1]
(A1S_0054) WbbJ protein [Capsule (CVF775)] [Acinetobacter baumannii ATCC 17978]
(A1S_0056) O-antigen translocase [Capsule (CVF775)] [Acinetobacter baumannii ATCC 17978]
(MQ3_289) Sel1 repeat protein [Capsule (CVF775)] [Acinetobacter baumannii TYTH-1]
(BJA80710_00096) putative UDP-glucose 6-dehydrogenase [Capsule (CVF775)] [Acinetobacter baumannii BJAB0710]
(ABSDF0072) polysaccharide biosynthesis protein [Capsule (CVF775)] [Acinetobacter baumannii SDP]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(ABK1_0097) transposase [Capsule (CVF775)] [Acinetobacter baumannii 1656-2]
(bfmR) putative response regulator (activator) in two-component regulatory system (OmpR family) [Two-component system (CVF778)] [Acinetobacter baumannii 1656-2]
(bfmR) putative response regulator (activator) in two-component regulatory system (OmpR family) [Two-component system (CVF778)] [Acinetobacter baumannii 1656-2]
(bfmR) putative response regulator (activator) in two-component regulatory system (OmpR family) [Two-component system (CVF778)] [Acinetobacter baumannii 1656-2]
(bfmS) sensory histidine kinase in two-component regulatory system with RstA [Two-component system (CVF778)] [Acinetobacter baumannii D127979]
(bfmS) signal transduction histidine kinase [Two-component system (CVF778)] [Acinetobacter baumannii TYTH-1]
(pbpG) D-alanyl-D-alanine endopeptidase [PbpG (CVF779)] [Acinetobacter baumannii ATCC 17978]
(fimD) fimbrial chaperone protein [Type I pili (VF0486)] [Aeromonas hydrophila ML09-119]
(tpoB) type IV pilus assembly protein [Tap type IV pili (CVF783)] [Aeromonas salmonicida subsp. salmonicida A449]
(AHA_1389) ColCo/CobM/Mind/Para family protein [Polar flagella (CVF786)] [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
(VSA_1361) SedA-like and chromosome partitioning protein [Pole flagella (CVF786)] [Aeromonas salmonicida subsp. salmonicida A449]
(AFA_1361) SedB-like and chromosome partitioning protein [Pole flagella (CVF786)] [Aeromonas salmonicida subsp. salmonicida A449]
(flaxA) flagellin [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flaxA) flagellin [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(chexV) two-component system chemotaxis response regulator CheV [Polar flagella (CVF786)] [Aeromonas salmonicida subsp. salmonicida A449]
(flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (CVF786)] [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
(flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (CVF786)] [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
(flmH) 3-oxoacyl-ACP reductase [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flmH) 3-oxoacyl-ACP reductase [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flmH) 3-oxoacyl-ACP reductase [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flmH) 3-oxoacyl-ACP reductase [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flmH) 3-oxoacyl-ACP reductase [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flmH) 3-oxoacyl-ACP reductase [Polar flagella (VF0473)] [Aeromonas hydrophila ML09-119]
(flrR) lateral flagellar biosynthetic protein Lflr [Lateral flagella (VF0474)] [Aeromonas salmonicida subsp. salmonicida A449]
(hlyA) hemolysin [Hemolysin, HlyA (CVF792)] [Aeromonas salmonicida subsp. salmonicida A449]
(hlyA) putative transporter [Hemolysin, HlyA (CVF792)] [Aeromonas veronii B565]
(rtsh) hypothetical protein [The repeat in toxin (RTX) (CVF795)] [Aeromonas hydrophila subsp. hydrophila AT

VFG041139(gi:206558740) [bcsC] periplasmic solute-binding protein [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041142(gi:206558743) [tsiA/bcsP] putative type VI secretion system protein TsiA [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041143(gi:206558744) [tsiB/bcsO] putative type VI secretion system protein TsiB [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041146(gi:206558747) [tsiB/bcsC] putative type VI secretion system protein TsiB [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041147(gi:206558748) [tsiC/bcsK] putative type VI secretion system protein TsiC [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041149(gi:206558750) [tsiE/bcsC] putative type VI secretion system protein TsiE [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041156(gi:206558757) [tsiM/cmf/bcsB] putative type VI secretion system protein TsiM [T6SS [SS193]] [Burkholderia cenocepacia J2315]

VFG041184(gi:269139780) [evpG] type VI secretion system protein EvpG [EVP (E. tarda virulent protein) (SS189)] [Edwardsiella tarda EIB202]

VFG041188(gi:269139784) [evpK] type VI secretion system protein EvpK [EVP (E. tarda virulent protein) (SS189)] [Edwardsiella tarda EIB202]

VFG041304(gb|YP_095978) [lirB] Dot/Icm type IV secretion system effector LirB [Dot/Icm (SS047)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]

VFG041304(gb|YP_095978) [lirB] Dot/Icm type IV secretion system effector LirB [Dot/Icm (SS047)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]

VFG041317(gi:88600055) [virB9-1] type IV secretion system protein VirB9 [T4SS [SS055]] [Neorickettsia sennetsu str. Miyayama]

VFG041571(gi:283784668) [nleK] hypothetical protein [T3SS [SS022]] [Citrobacter rodentium ICC168]

VFG041575(gi:269138242) [esrB] two-component response regulator EsrB, LuxR family [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041577(gi:269138241) [esrA] two-component sensor/regulator EsrA [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041578(gi:269138240) [ETAe_0884] putative transglycosylase signal peptide protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041579(gi:269138239) [esalU] type III secretion apparatus protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041580(gi:269138237) [esalS] type III secretion apparatus [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041581(gi:269138238) [esalT] type III secretion apparatus protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041582(gi:269138235) [esalM] type III secretion apparatus protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041583(gi:269138236) [esalR] type three secretion apparatus protein R [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041584(gi:269138233) [esalN] type III secretion system ATPase [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041585(gi:269138234) [esalV] type III secretion protein, HrcV family [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041586(gi:269138230) [esalQ] translocation protein in type III secretion [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041587(gi:269138231) [esalP] putative major facilitator family transporter [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041588(gi:269138232) [esalO] type III secretion system ATPase [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041589(gi:269138227) [esalC] type III secretion low calcium response chaperone [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041590(gi:269138228) [esdB] EspA family secreted protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041590(gi:269138228) [esdB] EspA family secreted protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041591(gi:269138229) [esdC] hypothetical protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041592(gi:269138224) [esdE] type III secretion system effector protein E [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041593(gi:269138225) [esdD] type III secretion system effector protein D [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041594(gi:269138226) [esdC] type III secretion system effector protein C [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041595(gi:269138223) [esdB] type III secretion system chaperone protein B [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041596(gi:269138221) [esalB] hypothetical protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041598(gi:269138220) [esalC] type II secretory pathway, component PulD like protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041599(gi:269138218) [ETAe_0862] hypothetical protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041600(gi:269138219) [esalD] type-III secretion protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041601(gi:269138213) [esalI] putative type III secretion system apparatus lipoprotein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041602(gi:269138214) [esalI] putative type III secretion apparatus [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041604(gi:269138216) [esalG] putative type III secretion system needle protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041605(gi:269138217) [esrC] putative transcriptional regulator EsrC [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041606(gi:269138212) [ETAe_0856] hypothetical protein [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041607(gi:269138211) [esalK] putative type III secretion apparatus [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041609(gi:269138210) [esalL] putative type III secretion apparatus [T3SS [SS025]] [Edwardsiella tarda EIB202]

VFG041721(gi:206563884) [virB1] type III secretion system protein [T3SS [SS015]] [Burkholderia cenocepacia J2315]

VFG041722(gi:206563885) [BCAM2044] putative asparagine synthetase [T3SS [SS015]] [Burkholderia cenocepacia J2315]

VFG041839(gi:34498095) [cila] invasion protein regulator [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041842(gi:34498090) [armR] two-component response regulator [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041843(gi:34498093) [CV_2638] hypothetical protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041844(gi:34498087) [cviG] invasion protein -outer membrane [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041845(gi:34498086) [cviE] invasion protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041846(gi:34498085) [cviA] invasion protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041847(gi:34498084) [cviB] surface presentation of antigens, secretory protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041849(gi:34498083) [cviC] ATP synthase SpaI [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041852(gi:34498079) [cpaP] surface presentation of antigens protein SpaP [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041853(gi:34498076) [cpaS] surface presentation of antigens protein SpaS [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041854(gi:34498077) [cpaR] surface presentation of antigens secretory protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041855(gi:34498078) [cpaQ] surface presentation of antigens secretory protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041856(gi:34498075) [cviA] surface presentation of antigens secretory protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041857(gi:34498074) [cviB] cell invasion protein [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG041881(gi:34498047) [cpbD] carbohydrate-binding protein [Cpi-2 encoded T3SS (SPI-2 like) (SS013)] [Chromobacterium violaceum ATCC 12472]

VFG041902(gi:34497876) [cpfI] cell invasion protein - cytoplasmic [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG042099(gi:3475322) [mfeG361] hypothetical protein [T3SS [SS026]] [Mesorhizobium loti MAFF303099]

VFG042228(gi:82470754) [AB877406] unknown [T3SS [SS007]] [Pantoea stewartii subsp. stewartii str. SS104]

VFG042313(gi:17673947) [STM0570] outer membrane esterase [ApoE [SS104]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG042316(gi:34497372) [CV_1917] hemolysin activator protein [ShIA-ShIB [SS143]] [Chromobacterium violaceum ATCC 12472]

VFG042317(gi:34497373) [CV_1918] hemolysin [ShIA-ShIB [SS143]] [Chromobacterium violaceum ATCC 12472]

VFG042569(gi:26247121) [focO] putative regulatory protein [F1C pilI [A1043]] [Escherichia coli CFT073]

VFG042619(gi:197284434) [ucaA] major fimbrial subunit [uroepithelial cell adhesion (UCA) [A1071]] [Proteus mirabilis HI4320]

VFG042633(gi:15042709) [mrfC] MrfC [mannose-resistant fimbriae, mrf [A1073]] [Photobacterium luminescens str. K122]

VFG042701(gi:15599279) [cupB3] usher CupB3 [CupB fimbriae [A1066]] [Pseudomonas aeruginosa PAO1]

VFG042736(gi:15599658) [rpoN] RNA polymerase factor sigma-54 [type IV pili [A1097]] [Pseudomonas aeruginosa PAO1]

VFG042739(gi:15600525) [crcC] catabolite repression control protein [type IV pili [A1097]] [Pseudomonas aeruginosa PAO1]

VFG042789(gi:215276199) [bfpD] nucleotide binding protein [bundle-forming pili, Bfp [A1011]] [Escherichia coli O127:H6 str. E2348/69]

VFG042931(gi:146329004) [cpfI] cell invasion protein - cytoplasmic [Cpi-1a + Cpi-1 (SPI-1 like) (SS016)] [Chromobacterium violaceum ATCC 12472]

VFG042955(gi:28199570) [pilM] fimbrial assembly membrane protein [type IV pili [A1181]] [Xylella fastidiosa Temecula1]

VFG043018(gi:15598545) [cheV] chemotaxis protein [Deoxyhexose linking sugar, 209 Da capping structure [A1138]] [Pseudomonas aeruginosa PAO1]

VFG043018(gi:15598545) [cheV] chemotaxis protein [Deoxyhexose linking sugar, 209 Da capping structure [A1138]] [Pseudomonas aeruginosa PAO1]

VFG043028(gi:17674536) [flgH] flagellar basal body L-ring protein [peritrichous flagella [A1139]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG043039(gi:17676260) [cheR] chemotaxis methyltransferase CheR [peritrichous flagella [A1139]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG043041(gi:17676262) [cheW] purine-binding chemotaxis protein [peritrichous flagella [A1139]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG043047(gi:17676292) [flvY] cystine transporter subunit [peritrichous flagella [A1139]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG043047(gi:17676292) [flvY] cystine transporter subunit [peritrichous flagella [A1139]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG043066(gi:17676317) [flpI] flagellar biosynthesis protein FlpI [peritrichous flagella [A1139]] [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

VFG043099(gi:15802355) [flvY] cystine transporter subunit [peritrichous flagella [A1140]] [Escherichia coli O157:H7 str. EDL933]

VFG043099(gi:15802355) [flvY] cystine transporter subunit [peritrichous flagella [A1140]] [Escherichia coli O157:H7 str. EDL933]

VFG043099(gi:15802355) [flvY] cystine transporter subunit [peritrichous flagella [A1140]] [Escherichia coli O157:H7 str. EDL933]

VFG043103(gi:15802359) [flvI] flagellar capping protein [peritrichous flagella [A1140]] [Escherichia coli O157:H7 str. EDL933]

VFG043113(gi:15802379) [flvI] flagellar basal body-associated protein FlvI [peritrichous flagella [A1140]] [Escherichia coli O157:H7 str. EDL933]

VFG043131(gi:28900123) [flgF] putative flagellar basal-body rod protein [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043133(gi:28900125) [flgH] flagellar basal body L-ring protein [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043136(gi:28900128) [flgK] putative flagellar hook-associated protein [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043137(gi:28900129) [flgL] flagellar hook-associated protein FlgI [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043146(gi:28901391) [flfI] flagellar MS-ring protein [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043152(gi:28901397) [flpI] flagellar biosynthesis protein FlpI [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043157(gi:28901403) [lafA] lateral flagellin LafA [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043158(gi:28901405) [lafB] flagellar distal capping protein LafB [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043159(gi:28901406) [lafC] LaC protein [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043164(gi:28901411) [motA] flagellar motor protein MotA [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043165(gi:28901412) [lafU] flagellar motor switch protein LafU [lateral flagella [A1142]] [Vibrio parahaemolyticus RIMD 2210633]

VFG043167(gi:74101639) [flhN] FlhN [ND [A1143]] [Aeromonas hydrophila str. AH-3]

VFG043172(gi:74101644) [flhA] FlhA [ND [A1143]] [Aeromonas hydrophila str. AH-3]

VFG043183(gi:74101655) [flgB] FlgB [ND [A1143]] [Aeromonas hydrophila str. AH-3]

VFG043184(gi:74101656) [flgC] FlgC [ND [A1143]] [Aeromonas hydrophila str. AH-3]

VFG043186(gi:74101658) [flgE] FlgE [ND [A1143]] [Aeromonas hydrophila str. AH-3]

VFG043206(gb|YP_001006774) [cheY] chemotaxis regulatory protein CheY [peritrichous flagella [A1145]] [Yersinia enterocolitica subsp. enterocolitica 8081]

VFG043207(gb|YP_001006775) [cheB] chemotaxis-specific methyltransferase CheB [peritrichous flagella [A1145]] [Yersinia enterocolitica subsp. enterocolitica 8081]

VFG043207(gb|YP_001006775) [cheB] chemotaxis-specific methyltransferase CheB [peritrichous flagella [A1145]] [Yersinia enterocolitica subsp. enterocolitica 8081]

VFG043211(gb|YP_001006780) [cheA] chemotaxis protein CheA [peritrichous flagella [A1145]] [Yersinia enterocolitica subsp. enterocolitica 8081]

VFG043211(gb|YP_001006780) [cheA] chemotaxis protein CheA [peritrichous flagella [A1145]] [Yersinia enterocolitica subsp. enterocolitica 8081]

VFG043212(gb|YP_001006781) [motB] flagellar motor protein MotB [peritrichous flagella [A1145]] [Yersinia enterocolitica subsp. enterocolitica 8081]

VFG043214(gi:218927893) [flhB] flagellar biosynthesis protein FlhB [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043214(gi:218927893) [flhB] flagellar biosynthesis protein FlhB [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043224(gi:218927903) [flhH] flagellar assembly protein H [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043225(gi:218927904) [flhI] flagellum-specific ATP synthase [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043229(gi:218927911) [flgD] flagellar basal body rod modification protein [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043231(gi:218927914) [flgG] flagellar basal body rod protein FlgG [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043233(gi:218927916) [flgI] flagellar basal body P-ring protein [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043244(gi:218927931) [flhA] flagellar biosynthesis sigma factor [lateral flagella [A1146]] [Yersinia pestis CO92]

VFG043297(gi:126697822) [flhI] flagellum-specific ATP synthase [HexNAc [A1148]] [Clostridium difficile 630]

VFG043435(gb|YP_095788) [fler/flrC] sigma 54-dependent response regulator [polar flagella [A1149]] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]

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