Supplementary Material

Table S1. Data collection and refinement statistics

Data Collection[a]	FeCu-P19 (red)	FeCu-P19 (ox)	Cu-P19 E44Q	Cu-P19 M88I	Cu-P19 D92H	Cu-FetP E46Q	Cu-FetP M90I
Resolution Range (Å)	50.00-1.55 (1.61-1.55)	33.07-1.65 (1.74-1.65)	50.00-1.90 (1.93-1.90)	50.00-2.30 (2.34-2.30)	50.00-2.50 (2.54-2.50)	33.65-1.40 (1.47-1.40)	38.34-1.53 (1.61-1.53)
Space group	$P2_12_12$	$P2_12_12$	$P2_12_12$	$P6_2$	$P3_2$	$C2$	$P2_1$
Cell dimensions (Å)	a = 53.91 b = 73.23 c = 74.93	a = 54.22 b = 73.72 c = 74.85	a = 55.35 b = 73.34 c = 78.96	a = b = 132.97 c = 104.88	a = b = 132.46 c = 104.59	a = 83.16 b = 36.54 c = 101.00 β = 106.5	a = 49.16 b = 51.61 c = 66.14 β = 93.3
Wavelength (Å)	1.000	0.979	1.542	1.542	1.542	1.000	1.000
Unique Reflections	43367	36846	25709	45287	69955	50962	52557
Completeness (%)	98.9 (97.1)	100.0 (99.4)	99.2 (88.8)	97.5 (77.8)	99.0 (97.3)	87.4 (84.8)	99.4 (96.8)
Average I/σI	29.7 (4.1)	15.0 (3.1)	24.2 (1.7)	21.6 (1.4)	12.6 (1.63)	14.9 (5.0)	19.0 (2.6)
Redundancy	6.0	8.3	6.7	10.7	4.9	3.9	3.6
R_{merge}	0.050 (0.417)	0.082 (0.639)	0.086 (0.515)	0.104 (0.833)	0.109 (0.624)	0.053 (0.235)	0.058 (0.362)
Refinement							
R_{work}	0.175	0.178	0.174	0.235	0.270	0.186	0.176
R_{free}	0.207	0.211	0.222	0.277	0.299	0.212	0.208
No. of waters	286	260	256	385	541	274	348
Average B-value (Å^2)	19.9	21.9	34.0	47.0	51.0	15.4	17.1
r.m.s.d. bond lengths (Å)	0.011	0.010	0.013	0.003	0.003	0.010	0.011
Ramachandran plot							
Most-favorable (%)	91.7	92.1	97.7	95.8	96.9	93.1	91.9
Allowed (%)	8.3	7.5	2.3	4.0	2.9	6.5	8.1
Outliers (%)	0	0.4	0	0.2	0.2	0.4	0

[a] Values for the highest resolution shell are shown in parenthesis

Table S2. Bacterial strains and plasmids used in this study.

Strains and plasmids	Relevant genotype	Reference
E. coli strains		
XL1-Blue	*recA*1, *endA*1, *gyrA*96, *thi*-1, *hsd*R17, *relA*1, *sup*E44, *lac* (F¢, *proAB*, *lacI*qZ_M15, Tn*10*)	Stratagene
BL21	*F- dcm, omp, hsd*S, ($r_B^-m_B^-$), *lon*-, *gal*λ, DE3, pLysS	Novagen
BL21-pLysS	*F- dcm, omp, hsd*S, ($r_B^-m_B^-$), *lon*-, *gal*λ, DE3	[1]
	Genomic DNA of *E. coli* strain F11	Robert Koch-Institute, S2, Wernigerode
C. jejuni strains		
81-176 wild-type reference strain		[2]
81-176Δ*p19*		[3]
81-176Δ*p19* complemented		[3]
Vectors & plasmids		
pECD1098	pASK-IBA3::*fetM*	[1]
	pASK-IBA6	IBA GmbH
pECD1138	pASK-IBA6:: *fetM*_PL	This study
pECD1101	pET22b(+)::*fetP*	[1]
pECD1128	pET22b(+)::*fetP* E46Q	This study
pECD1129	pET22b(+)::*fetP* M90I	This study

1 Koch, D. *et al.* Characterization of a dipartite iron-uptake system from uropathogenic *Escherichia coli* strain F11. *J Biol Chem* **286**, 25317-25330, doi:10.1074/jbc.M111.222745 (2011).

2 Korlath, J. A. *et al.* A point-source outbreak of campylobacteriosis associated with consumption of raw milk. *J Infect Dis* **152**, 592-596 (1985).

3 Chan, A. C. K. *et al.* Structure and function of P19, a high-affinity iron transporter of the human pathogen *Campylobacter jejuni*, *J Mol Biol* **401**, 590-604 (2010).

Table S3. Primers used in this study.

Primer	Sequence
*fetM*_PD *Bsa*I d	ATGGTAGGTCTCAGCGCACCTCGACGAATTATGCGCCTTT
*fetM*_PD *Bsa*I u	ATGGTAGGTCTCATATCAACTATAGAGCAGCAGACTCCACT
fetP E46Q d	AAAGCCGATGTTCACCTT**C**A**G**GCGGATATCCACGCTGTA
fetP E46Q u	TACAGCGTGGATATCCGC**C**T**G**AAGGTGAACATCGGCTTT
fetP M90I d	GGCACCTTCATGCCGAT**C**GTTGCCAGCGATGGC
fetP M90I u	GCCATCGCTGGCAAC**G**ATCGGCATGAAGGTGCC
p19 E44Q phos Cj	GCAGATATTCATCTA**C**AAGCTGACATTCACGC
p19 E44Q phos Rec	CTTTAGCAGATATTCACCTA**C**AAGCTGACATTCACGCAC
p19 M88I phos Cj and Rec	GGAACTTTGATGCCTAT**C**GTGGCTGATGATGG
p19 D92H phos Cj and Rec	CCTATGGTGGCTGAT**C**ATGGTCCTCACTATGGTG

Underlined: restriction endonuclease recognition site

Bold letters: altered bases leading to amino acid exchange

Table S4. Taxonomic assignment of FetP-like sequences. The number (N) of predicted protein sequences in each cluster identified from a BLAST search is shown with the taxonomic assignment. The ε value compared to the FetP sequence of least related sequence of the cluster is indicated. Changes are truncations, non-conserved amino acid residues in metal binding site (FetP numbering) and a conserved cysteine residue in the leader of the sequences from Gram-positive bacteria, which might allow anchoring of the protein in the cytoplasmic membrane. The ratio of the sequences with these changes is also indicated. The clusters are shown in Supplementary Figure S6.

Cluster	N	Min ε value	Changes	*Taxon*	*Genera*
I A	2	2.00E-70	none	*Spirochaeta*	*Spirochaeta*
I B1	1	6.00E-72	none	*δ-Proteobacteria*	*Geobacter*
I B2	1	1.00E-69	none	*α-Proteobacteria*	*Rhodospirillum*
I B3	17	6.00E-58	none	*e-Proteobacteria*	*Campylobacter, Wollinella*
I C1	1	6.00E-83	none	*g-Proteobacteria*	*Vibrio*
I C2	1	1.00E-88	E5, truncated	*g-Proteobacteria*	*Psychromonas*
I C3	2	2.00E-87	1/2=ΔLEADIH	*Chlamydia*	*Opitutaceae*
I C4	18	1.00E-88	none	*g-Proteobacteria*	*Aggregatibacter, Haemophilus, Pasteurella, Actinobacillus, Cardiobacterium*
I C5	22	4.00E-91	none	*Enterobacteriaceae*	*Escherichia, Citrobacter, Shigella, Klebsiella, Yersinia, Brenneria, Pectobacterium (=Seratia)*
II A1	9	2.00E-49	none	*Enterobacteriaceae*	*Providencia, Proteus, Morganella*
II A2	1	2.00E-50	none	*α -Proteobacteria*	*Candidatus Liberibacter solanacearum*
II A3	2	3.00E-53	none	*γ -Proteobacteria*	*Vibrio, Photobacterium*
II B1	16	3.00E-42	none	*γ -Proteobacteria*	*Pseudomonas*
II B2	1	3.00E-52	none	*α -Proteobacteria*	*Rhodopseudomonas*
II B3	48	3.00E-43	1/48 E5/truncated	*β-Proteobacteria*	*Burkholderia, Herbaspirillum*
II B4	3	2.00E-46	none	*α -Proteobacteria*	*Rhodopseudomonas. Rhodovulum*
II B5	17	2.00E-27	none	*α -Proteobacteria*	*Beijerinckia, Brucella, Rhodopseudomonas, Rhodomicrobium, Methylobacterium*
II B6	7	1.00E-44	1/7 E5/truncated	*α -Proteobacteria*	*Hyphomicrobium, Mesorhizobium, Sinorhizobium, Rhizobium*
II C1,	11	6.00E-47	none	*β -Proteobacteria*	*Achromobacter, Bordetella*
II C2	4	2.00E-45	1/4 E5D	*β -Proteobacteria*	*Pseudogulbenkiamia, Chromobacterium, Verminephrobacter*
II C3	1	4.00E-50	none	*β -Proteobacteria*	*Dechloromonas*
II C4	2	2.00E-47	none	*β -Proteobacteria*	*Aromatoleum, Azoarcus*
II C5	1	3.00E-47	none	*γ -Proteobacteria*	*gamma proteobacterium HdN1*
II C6	1	5.00E-46	none	*β -Proteobacteria*	*Dechlorosoma*
II C7	2	4.00E-37	none	*α -Proteobacteria*	*Magnetospirillum*
II C8	2	2.00E-44	none	*β -Proteobacteria*	*Rubrivivax*
III A	1	5.00E-51	none	*γ -Proteobacteria*	*gamma proteobacterium IMCC2047*
III B	1	2.00E-54	none	*Deferribacteres*	*Flexistipes*
III C	16	2.00E-13	2/16: H44, E5, E46, truncated	*Firmicutes*	*Centipeda, Selenomonas, Dialister, Pelosinus, Megasphaera,*
III D1	3	1.00E-17	1/3: H44, E5, E46; truncated	*Actinobacteria*	*Mobiluncus*
III D2	3	1.00E-27	none, Leader-Cys?	*Firmicutes*	*Parvimonas*

III D3	18	1.00E-06	Cys-Leader, 2/18 M90; 1/18 M90, H97, H127, D94	*Fusobacteria*	*Fusobacterium*
III D4	1	1.00E-21	none, leader-Cys?	*Firmicutes*	*Clostridiales genomosp. BVAB3 str. UPII9-5*
III D5	3	4.00E-25	none, Cys-Leader	*Synergistetes*	*Synergistetes, Jonquetella, Pyramidobacter*
III E1	10	6.00E-28	Cys-Leader, 1/10 H127, 1/10 M90,H97	*Actinobacteria*	*Actinomyces*
III E2,	34	3.00E-34	1/34 M90, H127, E5, D94	*Actinobacteria*	*Actinomaces, Parascardovia, Scardovia, Bifidobacterium, Gardnerella*
III E3	2	1.00E-26	none	*Firmicutes*	*Abiotrophia, Ruminococcus*
III F1	1	6.00E-44	none, leader-Cys	*Firmicutes*	*Clostridium*
III F2	3	9.00E-40	none	*Spirochaeta*	*Treponema*
III F3	7	7.00E-26	1/7: M90, H97	*Spirochaeta*	*Treponema*
III F4	11	2.00E-26	none, Leacer-Cys?	*Firmicutes*	*Filifactor, Johnsonella, Peptinophilus, Finegoldia, Anaerococcus, Stomatobaculum*
IV A	1	2.00E-46	none	*Planctomyces*	*Singulisphaera*
IV B	1	7.00E-46	none	*α-Proteobacteria*	*Phaeospirillum*
IV C	1	2.00E-55	none, TwinR-leader?	*α-Proteobacteria*	*magnetite-containing magnetic vibrio*
V A	2	8.00E-35	1/2 E5/truncated	*α-Proteobacteria*	*Magnetospirillum*
V B	1	5.00E-24	none	*BACTERIA*	*uncultured bacterium Bio2*
VI A	2	5.00E-42	none	*γ-Proteobacteria*	*Pseudomonas*
VI B	11	4.00E-29	none, Leacer-Cys?	*α-Proteobacteria*	*Gluconobacter, Acetobacter*
VII A	1	3.00E-11	H44, E5, leader too long	*Bacteroides/Chlorobi*	*Salinibacter*
VII B	1	5.00E-05	H44, E5, E46, truncated	*BACTERIA*	*uncultured marine bacterium EB0_39H12*

Supplementary Figures

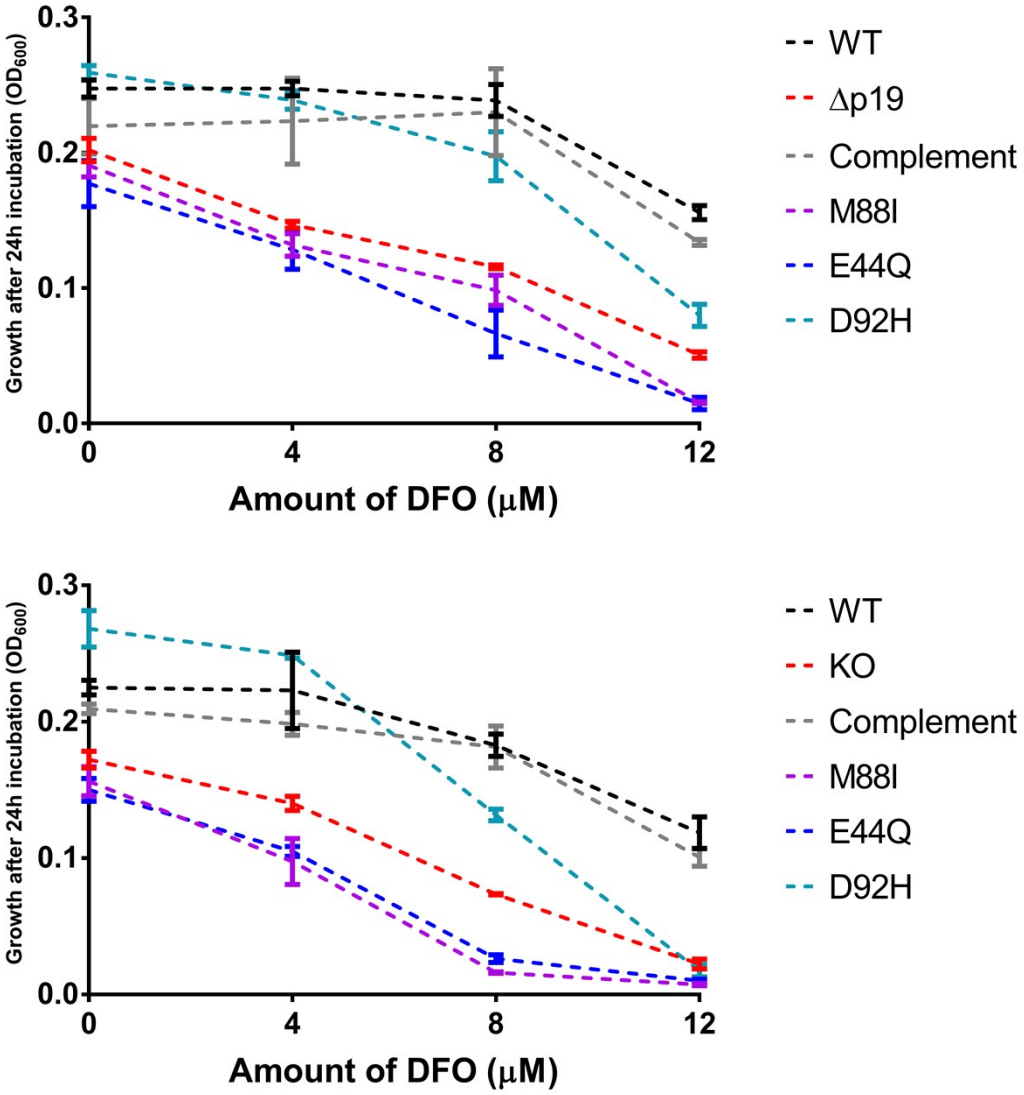


Figure S1. P19 metal site variants are unable to fully restore growth under iron limitation. *C. jejuni* wild-type 81-176, 81-176Δ*p19*, and trans-complemented strains grown under 0-12 μM DFO in a stationary 96-well plate incubated in a tri-gas incubator at 37 °C. After 24 h of growth, the plates were resuspended and OD_{600} readings were taken. The two plots here and the one in Fig. 4 represent experiments performed on three separate occasions. Plot points represent the amount of bacterial growth averaged from three separate wells with standard deviation error bars drawn.

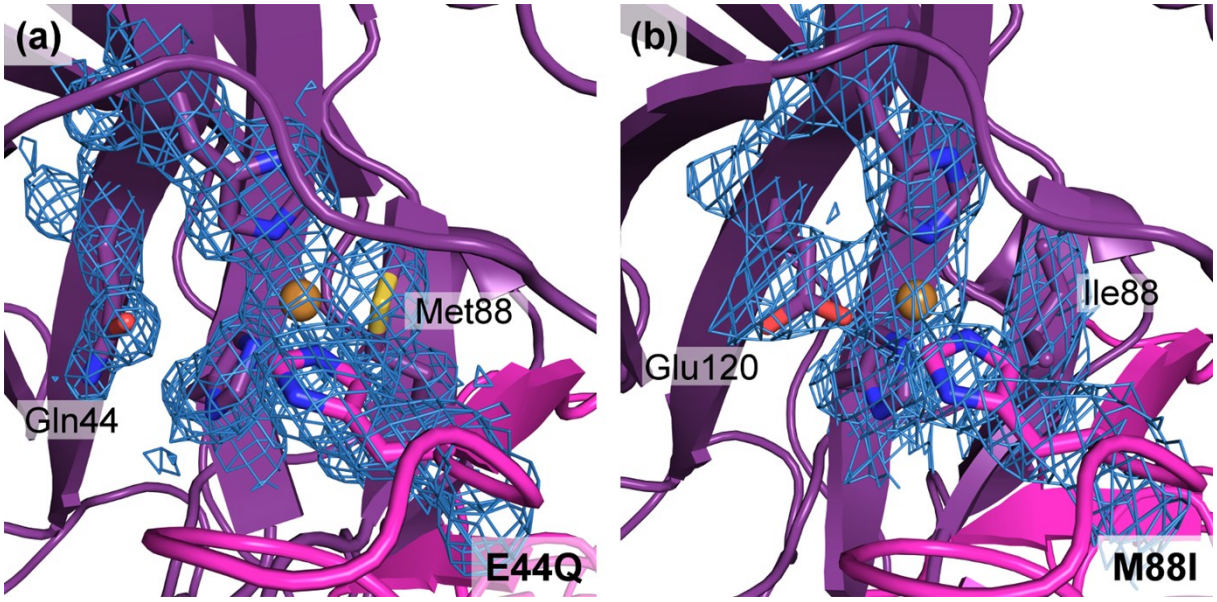


Figure S2. Cu-bound *C. jejuni* P19 (a) E44Q and (b) M88I variants do not exhibit positional plasticity. The copper cation is colored in brown. A 2Fo-Fc map contoured at 1 σ (blue) is overlaid the active site. Sulfur, oxygen and nitrogen atoms are colored yellow, red and dark blue, respectively. One protomer of the FetP dimer is shown in purple and the other in pink.

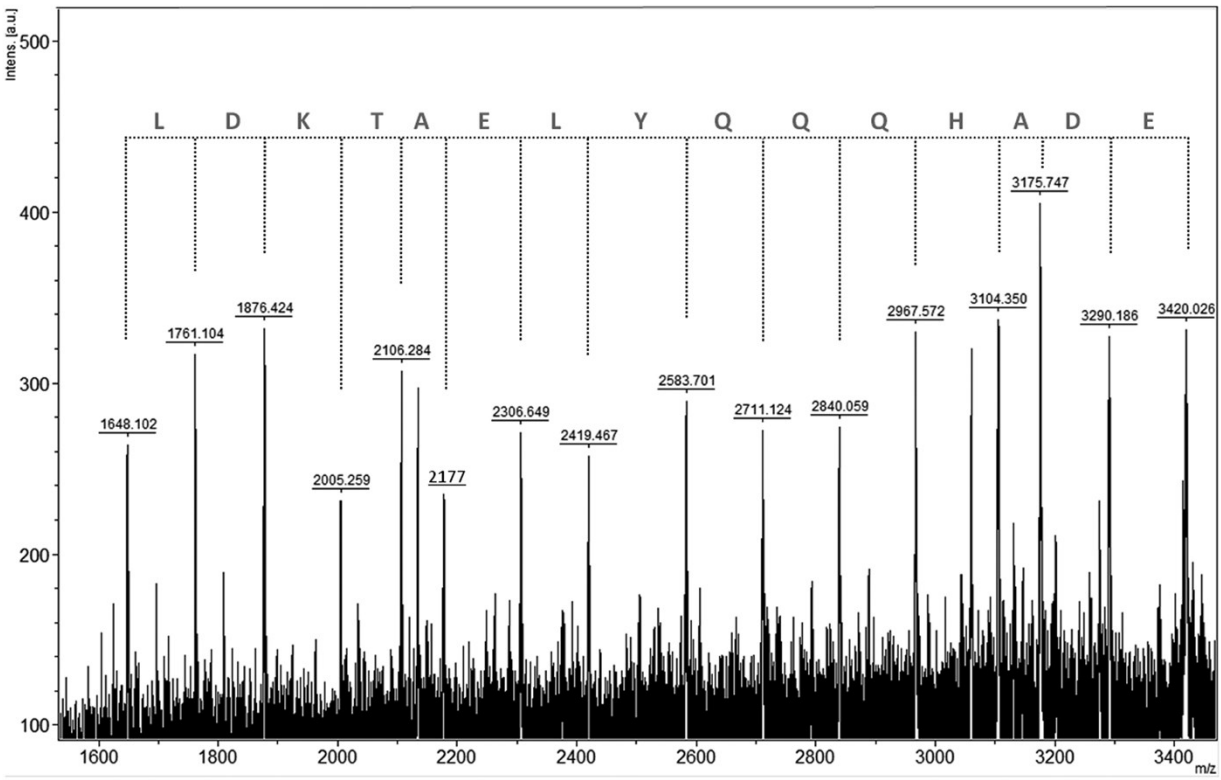


Figure S3. In source decay (ISD) MALDI-MS spectrum of ecFetM. ecFetM carrying a C-terminal strep-tag was solubilized from the membrane fraction after expression in *E. coli* and purified. In source decay led to a series of peptides and the molecular masses of these peptides (peaks) were determined with the matrix-assisted laser desorption mass spectrometer (MALDI-MS). The mass difference between the peptides identified the respective amino acid just removed from the protein with the sequence indicated above. This sequence, LDKTAELYQQQHADE, followed that of the amino acids within the smallest peptide identified with a mass of 1648.102 (left-most peak) which corresponded to the peptide STNYAPLIEDIEQR. This sequence was therefore identified as the amino-terminal sequence of the mature ecFetM-strep-tag protein as isolated from the membrane.

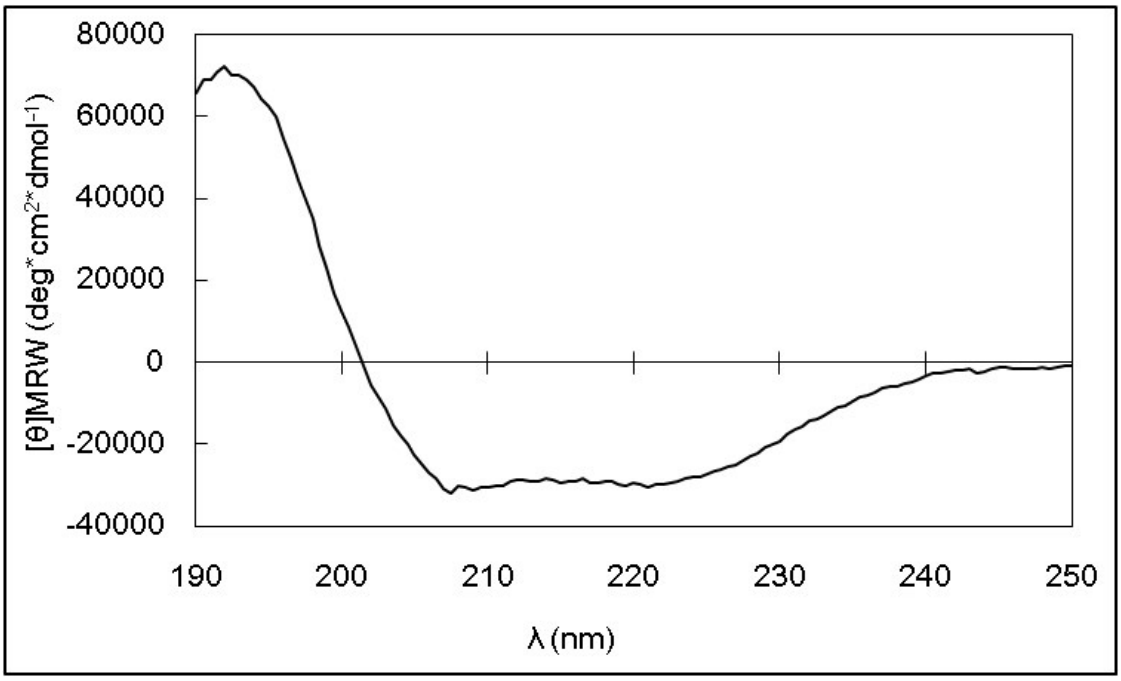


Figure S4. CD spectrum of ecFetM-PD. A circular dichroism spectrum (θ_{MRW}) of the purified periplasmic region of ecFetM, ecFetM-PD, is shown. Protein concentration was 15 µM in 25 mM Bis-Tris/HCl, pH 7.2, 25°C. Shown is a difference spectrum plus vs. minus protein.

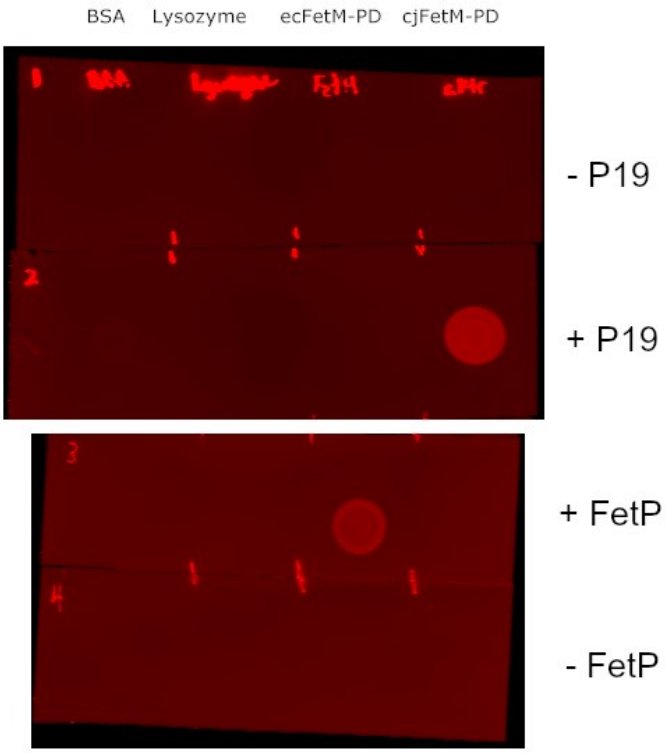


Figure S5. Original Far western blots of ecFetM-PD-FetP and cjFetM-PD-P19 interactions. Control blots (e.g. –P19) were prepared alongside non-controls (e.g. +P19) and were imaged together. The P19 and FetP experiments were performed separately.

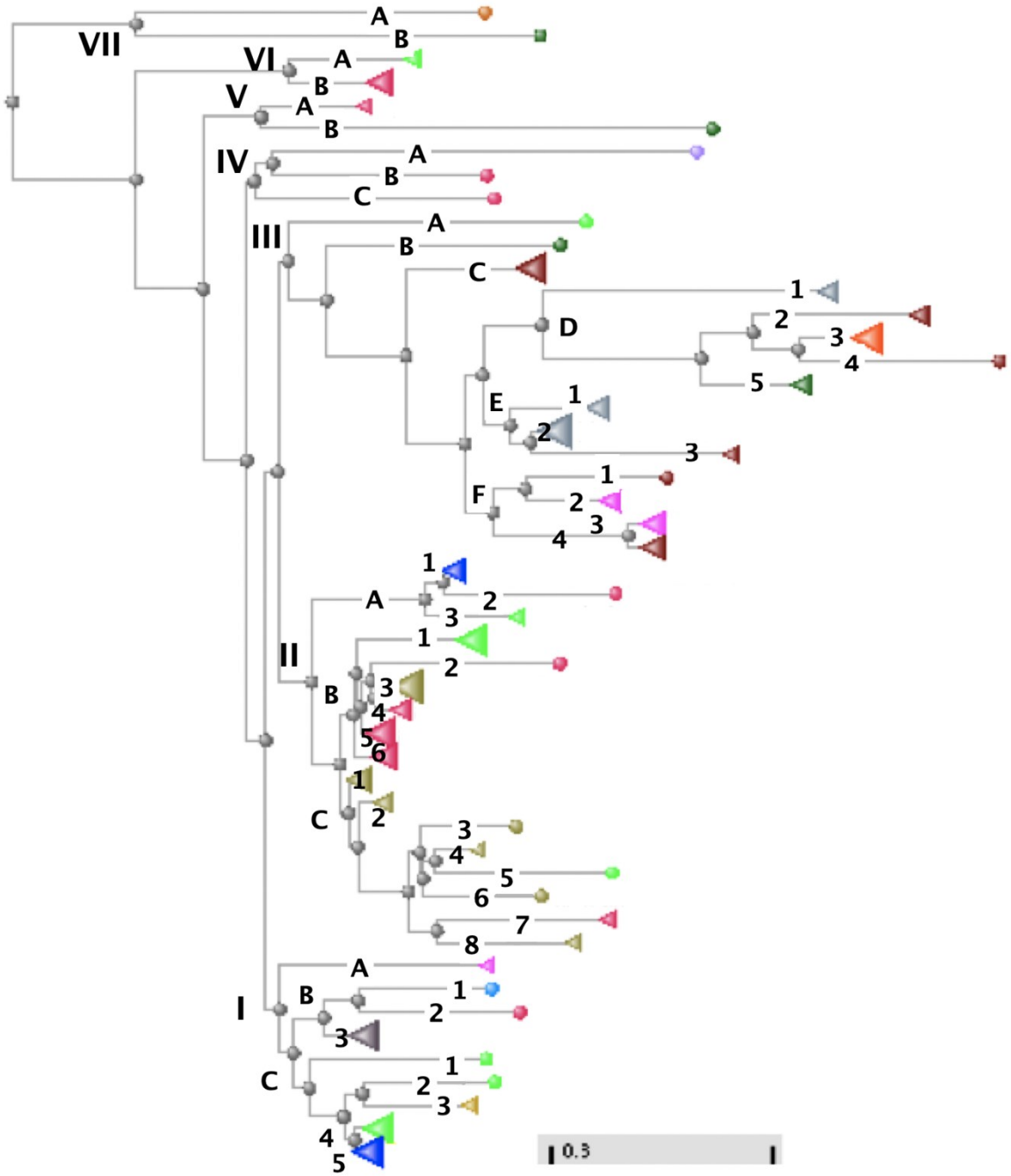
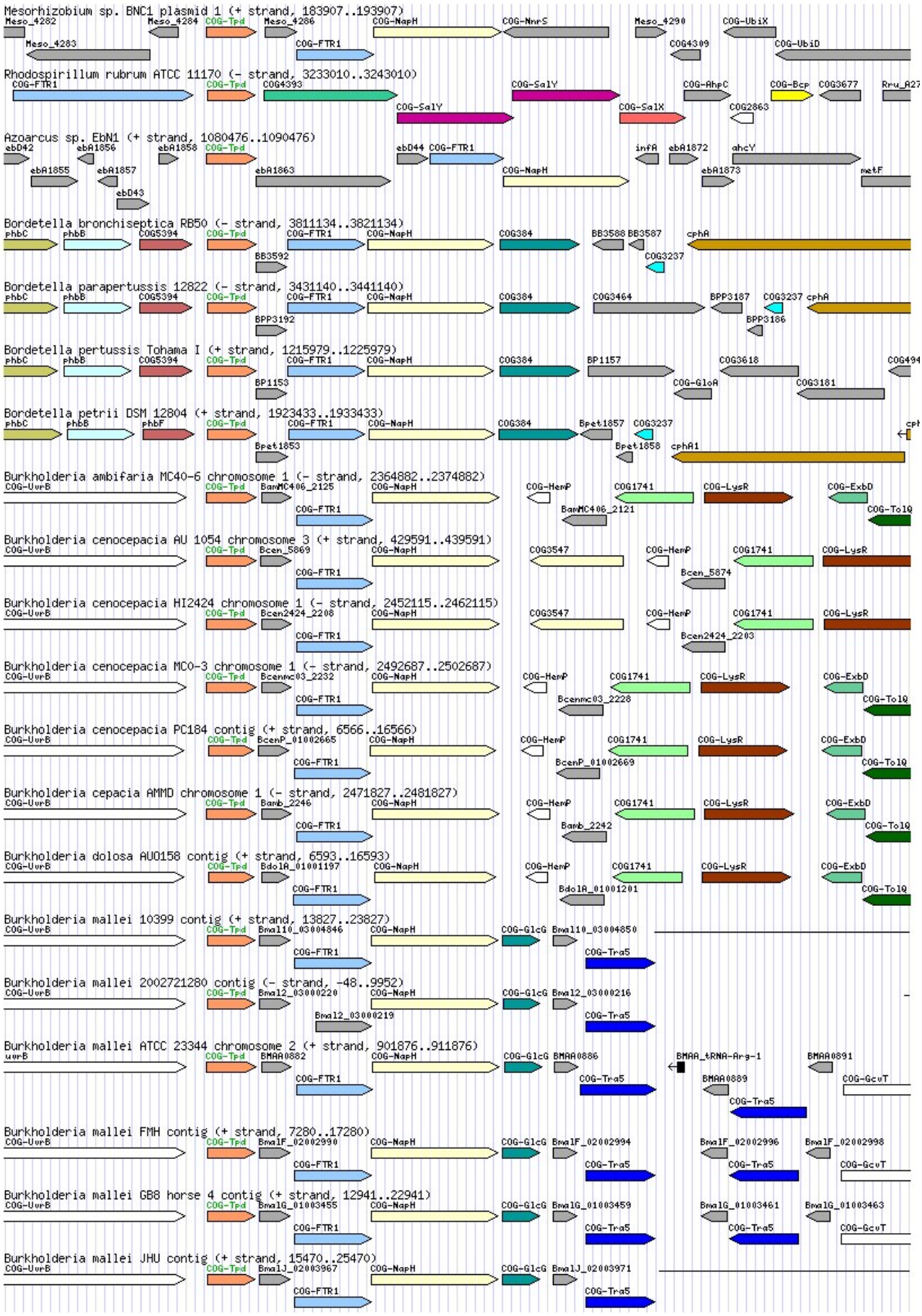


Figure S6. Clusters of FetP-like sequences. The data resulting from a BLAST search (1) was further analyzed by COBALT (2) and Geneious (www.geneious.com) to sort the sequences into clusters (I to VII), sub-clusters (A, B, C,…) and sub-sub-clusters (1, 2, 3, …). The predicted FetP-like proteins within each sub-sub-cluster are listed in Table S4. Filled circles and squares are single sequences, arrowheads are two or more sequences with the size of the arrowhead indicating the number of sequences. Enterobacteria in dark blue, γ-proteobacteria in green, α-proteobacteria in red, β-proteobacteria in yellow, spirochetes in magenta, actinobacteria in grey and firmicutes in brown.

1. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucl Acid Res 25:3389-3402.
2. Papadopoulos JS, Agarwala R. 2007. COBALT: constraint-based alignment tool for multiple protein sequences. Bioinformatics 23:1073-1079.

Figure S7. Genomic environment of genes encoding P19-like proteins (orange, 'COG-Tpd') and genes encoding FetM-like transporters (light blue, 'COG-FTR1'). The scale is in kbp and the organism is indicated above the gene symbols, which are in the direction of transcription.


Mesorhizobium sp. BNC1 plasmid 1 (+ strand, 183907..193907)
Meso_4282
Meso_4284
COG-Tpd
Meso_4286
COG-NapH
COG-NnrS
Meso_4290
COG-UbiX
Meso_4283
COG-FTR1
COG4309
COG-UbiD
Rhodospirillum rubrum ATCC 11170 (- strand, 3233010..3243010)
COG-FTR1
COG-Tpd
COG4393
COG-SalY
COG-AhpC
COG-Bcp
COG3677
Rru_A27
COG-SalY
COG-SalX
COG2863
Azoarcus sp. EbN1 (+ strand, 1080476..1090476)
ebD42
ebA1856
ebA1858
COG-Tpd
ebD44
COG-FTR1
infA
ebA1872
ahcY
ebA1855
ebA1857
ebA1863
COG-NapH
ebA1873
metF
ebD43
Bordetella bronchiseptica RB50 (- strand, 3811134..3821134)
phbC
phbB
COG5394
COG-Tpd
COG-FTR1
COG-NapH
COG384
BB3588
BB3587
cphA
BB3592
COG3237
Bordetella parapertussis 12822 (- strand, 3431140..3441140)
phbC
phbB
COG5394
COG-Tpd
COG-FTR1
COG-NapH
COG384
COG3464
BPP3187
COG3237
cphA
BPP3192
BPP3186
Bordetella pertussis Tohama I (+ strand, 1215979..1225979)
phbC
phbB
COG5394
COG-Tpd
COG-FTR1
COG-NapH
COG384
BP1157
COG3618
BP1153
COG-GloA
COG3181
Bordetella petrii DSM 12804 (+ strand, 1923433..1933433)
phbC
phbB
phbF
COG-Tpd
COG-FTR1
COG-NapH
COG384
Bpet1857
COG3237
Bpet1853
Bpet1858
cphA1
Burkholderia ambifaria MC40-6 chromosome 1 (- strand, 2364882..2374882)
COG-UvrB
COG-Tpd
BamMC406_2125
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BamMC406_2121
COG-TolQ
Burkholderia cenocepacia AU 1054 chromosome 3 (+ strand, 429591..439591)
COG-UvrB
COG-Tpd
Bcen_5869
COG-NapH
COG3547
COG-HemP
COG1741
COG-LysR
COG-FTR1
Bcen_5874
Burkholderia cenocepacia HI2424 chromosome 1 (- strand, 2452115..2462115)
COG-UvrB
COG-Tpd
Bcen2424_2208
COG-NapH
COG3547
COG-HemP
COG1741
COG-LysR
COG-FTR1
Bcen2424_2203
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COG-ExbD
COG-FTR1
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COG-HemP
COG1741
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COG-FTR1
BcenP_01002669
COG-TolQ
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COG-Tpd
Bamb_2246
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COG1741
COG-LysR
COG-ExbD
COG-FTR1
Bamb_2242
COG-TolQ
Burkholderia dolosa AUO158 contig (+ strand, 6593..16593)
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COG-NapH
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COG-ExbD
COG-FTR1
BdolA_01001201
COG-TolQ
Burkholderia mallei 10399 contig (+ strand, 13827..23827)
COG-UvrB
COG-Tpd
Bmal10_03004846
COG-NapH
COG-GlcG
Bmal10_03004850
COG-FTR1
COG-Tra5
Burkholderia mallei 2002721280 contig (- strand, -48..9952)
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COG-Tpd
Bmal2_03000220
COG-NapH
COG-GlcG
Bmal2_03000216
Bmal2_03000219
COG-Tra5
Burkholderia mallei ATCC 23344 chromosome 2 (+ strand, 901876..911876)
uvrB
COG-Tpd
BMAA0882
COG-NapH
COG-GlcG
BMAA0886
BMAA_tRNA-Arg-1
BMAA0891
COG-FTR1
COG-Tra5
BMAA0889
COG-GcvT
COG-Tra5
Burkholderia mallei FMH contig (+ strand, 7280..17280)
COG-UvrB
COG-Tpd
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COG-GlcG
BmalF_02002994
BmalF_02002996
BmalF_02002998
COG-FTR1
COG-Tra5
COG-Tra5
COG-GcvT
Burkholderia mallei GB8 horse 4 contig (+ strand, 12941..22941)
COG-UvrB
COG-Tpd
BmalG_01003455
COG-NapH
COG-GlcG
BmalG_01003459
BmalG_01003461
BmalG_01003463
COG-FTR1
COG-Tra5
COG-Tra5
COG-GcvT
Burkholderia mallei JHU contig (+ strand, 15470..25470)
COG-UvrB
COG-Tpd
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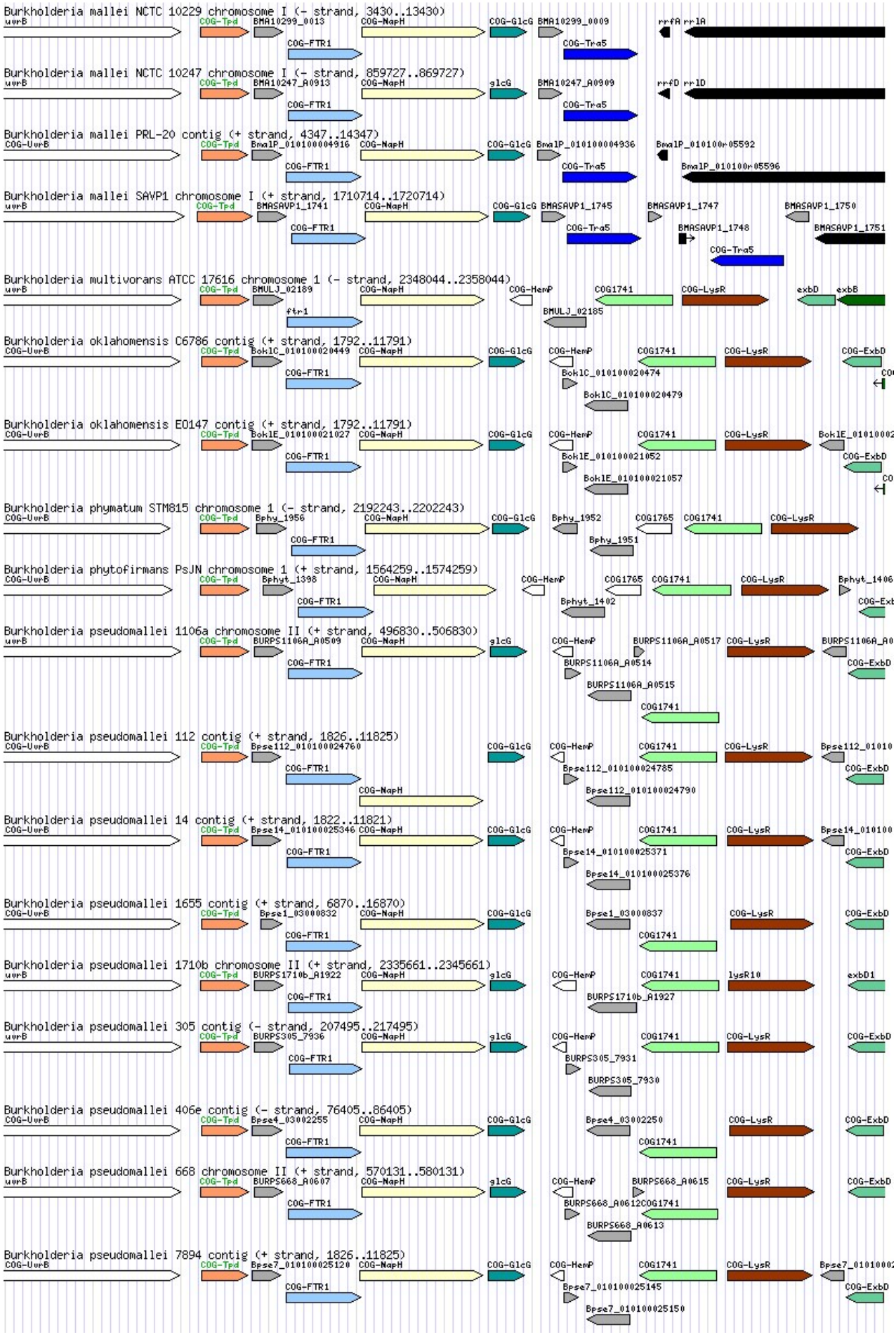
COG-NapH
COG-GlcG
BmalJ_02003971
COG-FTR1
COG-Tra5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COG-Tpd
BMA10299_0013
COG-NapH
COG-GlcG
BMA10299_0009
rrfA
rrlA
COG-FTR1
COG-Tra5
Burkholderia mallei NCTC 10247 chromosome I (- strand, 859727..869727)
uvrB
COG-Tpd
BMA10247_A0913
COG-NapH
glcG
BMA10247_A0909
rrfD
rrlD
COG-FTR1
COG-Tra5
Burkholderia mallei PRL-20 contig (+ strand, 4347..14347)
COG-UvrB
COG-Tpd
BmalP_010100004916
COG-NapH
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BmalP_010100004936
BmalP_010100r05592
COG-FTR1
COG-Tra5
BmalP_010100r05596
Burkholderia mallei SAVP1 chromosome I (+ strand, 1710714..1720714)
uvrB
COG-Tpd
BMASAVP1_1741
COG-NapH
COG-GlcG
BMASAVP1_1745
BMASAVP1_1747
BMASAVP1_1750
COG-FTR1
COG-Tra5
BMASAVP1_1748
BMASAVP1_1751
COG-Tra5
Burkholderia multivorans ATCC 17616 chromosome 1 (- strand, 2348044..2358044)
uvrB
COG-Tpd
BMULJ_02189
COG-NapH
COG-HemP
COG1741
COG-LysR
exbD
exbB
ftr1
BMULJ_02185
Burkholderia oklahomensis C6786 contig (+ strand, 1792..11791)
COG-UvrB
COG-Tpd
Bok1C_010100020449
COG-NapH
COG-GlcG
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
Bok1C_010100020474
Bok1C_010100020479
Burkholderia oklahomensis E0147 contig (+ strand, 1792..11791)
COG-UvrB
COG-Tpd
Bok1E_010100021027
COG-NapH
COG-GlcG
COG-HemP
COG1741
COG-LysR
COG-FTR1
Bok1E_010100021052
COG-ExbD
Bok1E_010100021057
Burkholderia phymatum STM815 chromosome 1 (- strand, 2192243..2202243)
COG-UvrB
COG-Tpd
Bphy_1956
COG-NapH
COG-GlcG
Bphy_1952
COG1765
COG1741
COG-LysR
COG-FTR1
Bphy_1951
Burkholderia phytofirmans PsJN chromosome 1 (+ strand, 1564259..1574259)
COG-UvrB
COG-Tpd
Bphyt_1398
COG-NapH
COG-HemP
COG1765
COG1741
COG-LysR
Bphyt_1406
COG-FTR1
Bphyt_1402
Burkholderia pseudomallei 1106a chromosome II (+ strand, 496830..506830)
uvrB
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BURPS1106A_A0509
COG-NapH
glcG
COG-HemP
BURPS1106A_A0517
COG-LysR
COG-FTR1
BURPS1106A_A0514
COG-ExbD
BURPS1106A_A0515
COG1741
Burkholderia pseudomallei 112 contig (+ strand, 1826..11825)
COG-UvrB
COG-Tpd
Bpse112_010100024760
COG-GlcG
COG-HemP
COG1741
COG-LysR
COG-FTR1
Bpse112_010100024785
COG-ExbD
COG-NapH
Bpse112_010100024790
Burkholderia pseudomallei 14 contig (+ strand, 1822..11821)
COG-UvrB
COG-Tpd
Bpse14_010100025346
COG-NapH
COG-GlcG
COG-HemP
COG1741
COG-LysR
COG-FTR1
Bpse14_010100025371
COG-ExbD
Bpse14_010100025376
Burkholderia pseudomallei 1655 contig (+ strand, 6870..16870)
COG-UvrB
COG-Tpd
Bpse1_03000832
COG-NapH
COG-GlcG
Bpse1_03000837
COG-LysR
COG-ExbD
COG-FTR1
COG1741
Burkholderia pseudomallei 1710b chromosome II (+ strand, 2335661..2345661)
uvrB
COG-Tpd
BURPS1710b_A1922
COG-NapH
glcG
COG-HemP
COG1741
lysR10
exbD1
COG-FTR1
BURPS1710b_A1927
Burkholderia pseudomallei 305 contig (- strand, 207495..217495)
uvrB
COG-Tpd
BURPS305_7936
COG-NapH
glcG
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BURPS305_7931
BURPS305_7930
Burkholderia pseudomallei 406e contig (- strand, 76405..86405)
COG-UvrB
COG-Tpd
Bpse4_03002255
COG-NapH
COG-GlcG
Bpse4_03002250
COG-LysR
COG-ExbD
COG-FTR1
COG1741
Burkholderia pseudomallei 668 chromosome II (+ strand, 570131..580131)
uvrB
COG-Tpd
BURPS668_A0607
COG-NapH
glcG
COG-HemP
BURPS668_A0615
COG-LysR
COG-ExbD
COG-FTR1
BURPS668_A0612
COG1741
BURPS668_A0613
Burkholderia pseudomallei 7894 contig (+ strand, 1826..11825)
COG-UvrB
COG-Tpd
Bpse7_010100025120
COG-NapH
COG-GlcG
COG-HemP
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COG-LysR
COG-FTR1
Bpse7_010100025145
COG-ExbD
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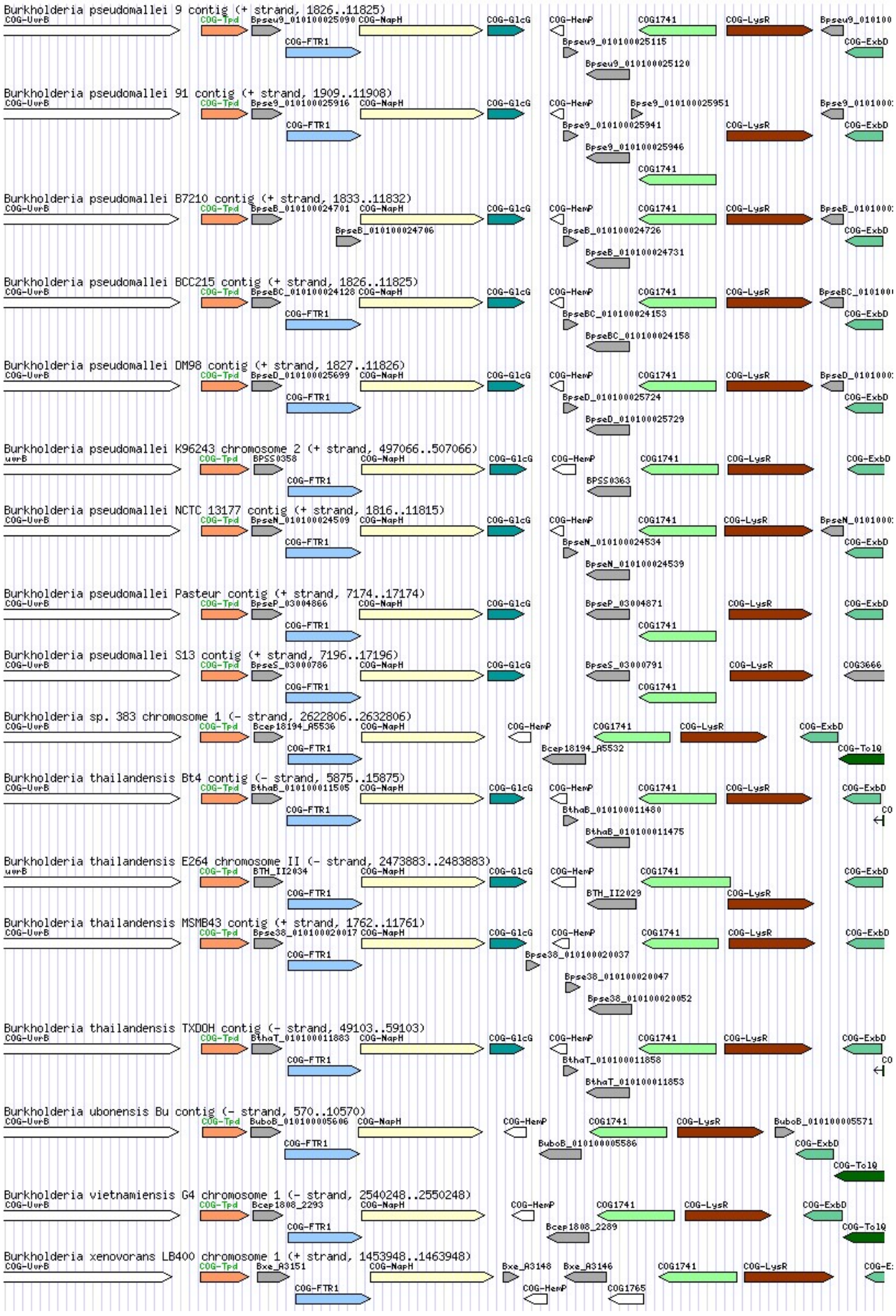
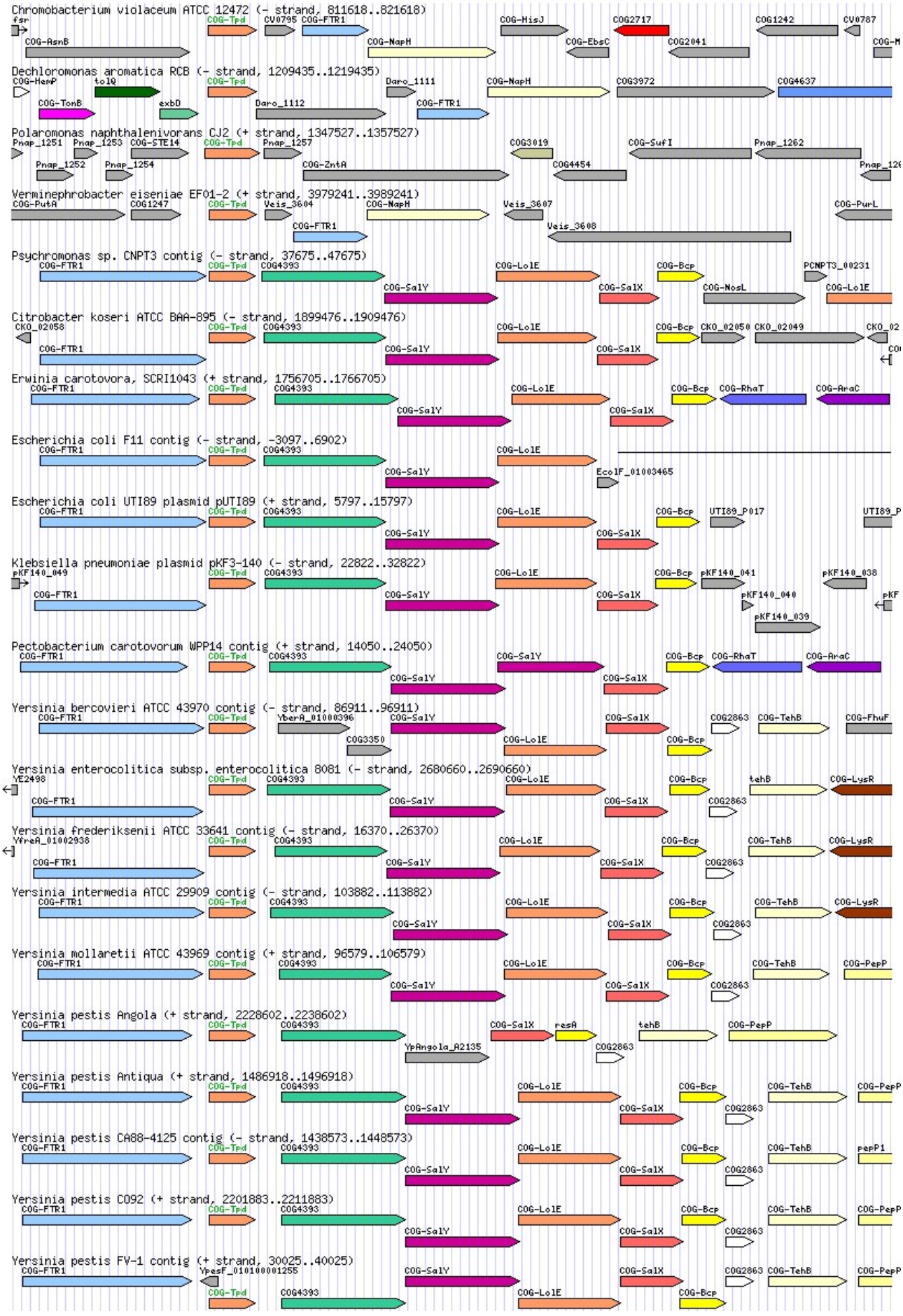

Burkholderia pseudomallei 9 contig (+ strand, 1826..11825)
Burkholderia pseudomallei 91 contig (+ strand, 1909..11908)
Burkholderia pseudomallei B7210 contig (+ strand, 1833..11832)
Burkholderia pseudomallei BCC215 contig (+ strand, 1826..11825)
Burkholderia pseudomallei DM98 contig (+ strand, 1827..11826)
Burkholderia pseudomallei K96243 chromosome 2 (+ strand, 497066..507066)
Burkholderia pseudomallei NCTC 13177 contig (+ strand, 1816..11815)
Burkholderia pseudomallei Pasteur contig (+ strand, 7174..17174)
Burkholderia pseudomallei S13 contig (+ strand, 7196..17196)
Burkholderia sp. 383 chromosome 1 (- strand, 2622806..2632806)
Burkholderia thailandensis Bt4 contig (- strand, 5875..15875)
Burkholderia thailandensis E264 chromosome II (- strand, 2473883..2483883)
Burkholderia thailandensis MSMB43 contig (+ strand, 1762..11761)
Burkholderia thailandensis TXDOH contig (- strand, 49103..59103)
Burkholderia ubonensis Bu contig (- strand, 570..10570)
Burkholderia vietnamiensis G4 chromosome 1 (- strand, 2540248..2550248)
Burkholderia xenovorans LB400 chromosome 1 (+ strand, 1453948..1463948)


Chromobacterium violaceum ATCC 12472 (- strand, 811618..821618)
fsr
COG-Tpd
CV0795
COG-FTR1
COG-HisJ
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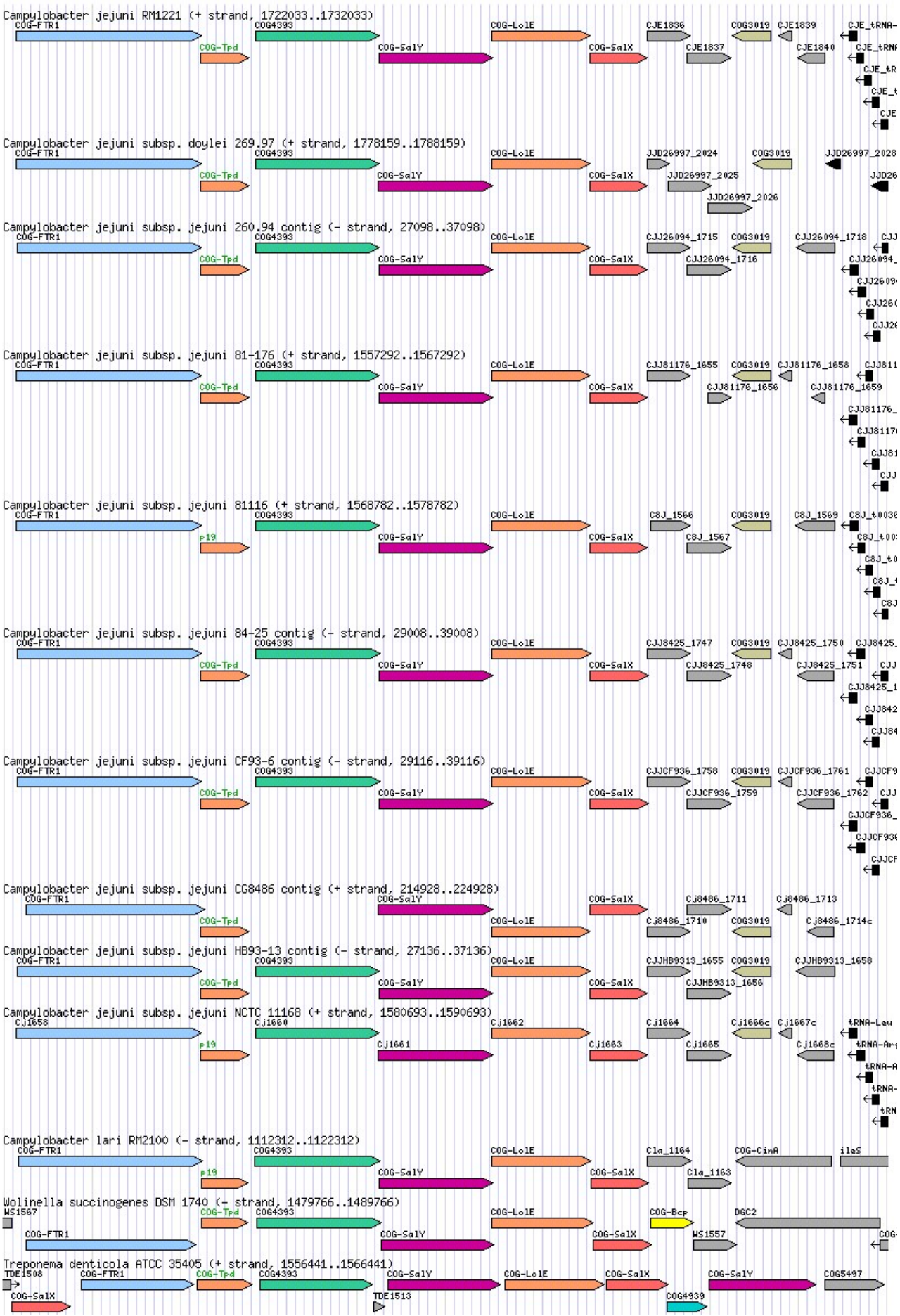
COG1242
CV0787
COG-AsnB
COG-NapH
COG-EbsC
COG2041
Dechloromonas aromatica RCB (- strand, 1209435..1219435)
COG-HemP
tolQ
COG-Tpd
Daro_1111
COG-NapH
COG3972
COG4637
COG-TonB
exbD
Daro_1112
COG-FTR1
Polaromonas naphthalenivorans CJ2 (+ strand, 1347527..1357527)
Pnap_1251
Pnap_1253
COG-STE14
COG-Tpd
Pnap_1257
COG3019
COG-SufI
Pnap_1262
Pnap_1252
Pnap_1254
COG-ZntA
COG4454
Verminephrobacter eiseniae EF01-2 (+ strand, 3979241..3989241)
COG-PutA
COG1247
COG-Tpd
Veis_3604
COG-NapH
Veis_3607
COG-PurL
COG-FTR1
Veis_3608
Psychromonas sp. CNPT3 contig (- strand, 37675..47675)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
PCNPT3_00231
COG-SalY
COG-SalX
COG-NosL
COG-LolE
Citrobacter koseri ATCC BAA-895 (- strand, 1899476..1909476)
CKO_02058
COG-Tpd
COG4393
COG-LolE
COG-Bcp
CKO_02050
CKO_02049
COG-FTR1
COG-SalY
COG-SalX
Erwinia carotovora, SCRI1043 (+ strand, 1756705..1766705)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-RhaT
COG-AraC
COG-SalY
COG-SalX
Escherichia coli F11 contig (- strand, -3097..6902)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-SalY
EcolF_01003465
Escherichia coli UTI89 plasmid pUTI89 (+ strand, 5797..15797)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
UTI89_P017
COG-SalY
COG-SalX
Klebsiella pneumoniae plasmid pKF3-140 (- strand, 22822..32822)
pKF140_049
COG-Tpd
COG4393
COG-LolE
COG-Bcp
pKF140_041
pKF140_038
COG-FTR1
COG-SalY
COG-SalX
pKF140_040
pKF140_039
Pectobacterium carotovorum WPP14 contig (+ strand, 14050..24050)
COG-FTR1
COG-Tpd
COG4393
COG-SalY
COG-Bcp
COG-RhaT
COG-AraC
COG-SalY
COG-SalX
Yersinia bercovieri ATCC 43970 contig (- strand, 86911..96911)
COG-FTR1
COG-Tpd
YberA_01000396
COG-SalY
COG-SalX
COG2863
COG-TehB
COG-FhuF
COG3350
COG-LolE
COG-Bcp
Yersinia enterocolitica subsp. enterocolitica 8081 (- strand, 2680660..2690660)
YE2498
COG-Tpd
COG4393
COG-LolE
COG-Bcp
tehB
COG-LysR
COG-FTR1
COG-SalY
COG-SalX
COG2863
Yersinia frederiksenii ATCC 33641 contig (- strand, 16370..26370)
YfreA_01002938
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-TehB
COG-LysR
COG-FTR1
COG-SalY
COG-SalX
COG2863
Yersinia intermedia ATCC 29909 contig (- strand, 103882..113882)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-TehB
COG-LysR
COG-SalY
COG-SalX
COG2863
Yersinia mollaretii ATCC 43969 contig (+ strand, 96579..106579)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-TehB
COG-PepP
COG-SalY
COG-SalX
COG2863
Yersinia pestis Angola (+ strand, 2228602..2238602)
COG-FTR1
COG-Tpd
COG4393
COG-SalX
resA
tehB
COG-PepP
YpAngola_A2135
COG2863
Yersinia pestis Antiqua (+ strand, 1486918..1496918)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-TehB
COG-PepP
COG-SalY
COG-SalX
COG2863
Yersinia pestis CA88-4125 contig (- strand, 1438573..1448573)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-TehB
pepP1
COG-SalY
COG-SalX
COG2863
Yersinia pestis C092 (+ strand, 2201883..2211883)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-TehB
COG-PepP
COG-SalY
COG-SalX
COG2863
Yersinia pestis FV-1 contig (+ strand, 30025..40025)
COG-FTR1
YpesF_01010001255
COG-SalY
COG-SalX
COG2863
COG-TehB
COG-PepP
COG-Tpd
COG4393
COG-LolE
COG-Bcp


Yersinia pestis KIM (- strand, 2604913..2614913)
COG-FTR1
y2369
COG4393
COG-SalY
COG-Bcp
tehB
hmsH
COG-Tpd
COG-SalX
COG2863
Yersinia pestis Pestoides F (- strand, 1322985..1332985)
YPDSF_1182
YPDSF_1181
COG-LolE
COG-TehB
COG-PepP
Yersinia pestis biovar Antiqua str. B42003004 contig (+ strand, 222707..232707)
resA
YpB42003
Yersinia pestis biovar Antiqua str. E1979001 contig (+ strand, 30465..40465)
Yersinia pestis biovar Antiqua str. UG05-0454 contig (- strand, 41954..51954)
Yersinia pestis biovar Medievalis 91001 (+ strand, 1858645..1868645)
YP1684
fTR12
trxA1
phnL4
pepP1
Yersinia pestis biovar Orientalis str. F1991016 contig (+ strand, 30437..40437)
YpF1991016_3889
YpF1991016_3894
Yersinia pestis biovar Orientalis str. MG05-1020 contig (- strand, 345065..355065)
Yersinia pseudotuberculosis IP 31758 (- strand, 2453663..2463663)
Yersinia pseudotuberculosis IP 32953 (+ strand, 2280264..2290264)
Actinobacillus succinogenes 130Z (+ strand, 1825638..1835638)
COG1999
Asuc_R0071
COG177
COG-GutQ
Pasteurella multocida subsp. multocida str. Pm70 (- strand, 518685..528685)
pepE
COG3100
PM044
PM0445
minC
Pseudomonas stutzeri A1501 (+ strand, 3792268..3802268)
PST_3501
COG-Pfl A
PST_3508
dnrS
COG4273
PST_3502
PST_3504
COG-NapH
COG-NrdD
Photobacterium sp. SKA34 contig (+ strand, 77..10076)
SKA34_07738
SKA34_07748
SKA34_07758
COG2822
COG-FabG
SKA34_07783
COG-IolE
COG-FTR1
COG2837
SKA34_07788
Vibrio shilonii AK1 contig (- strand, 136811..146811)
COG-NqrC
VSAK1_19979
COG2847
COG-LimK
Campylobacter coli RM2228 contig (+ strand, 44717..54717)
CCC0149
obg
rpmA
COG-TrxA
rplU
Campylobacter concisus 13826 (+ strand, 305359..315359)
sodB
CCC13826_0769
cynT
CCC1382
CCC13826_0770
Campylobacter curvus 525.92 (- strand, 1685278..1695278)
COG-HybA
proP
nuoL
CCV52592_0427
COG-CirA
CCV52592_0426
Campylobacter fetus subsp. fetus 82-40 (+ strand, 529696..539696)
flgG
CFF8240_0530
COG-MMT1
COG2957
COG388
Campylobacter hominis ATCC BAA-381 (- strand, 397942..407942)
CHAB381_0444
COG-FeoA
CHAB381_0443
feoB


Campylobacter jejuni RM1221 (+ strand, 1722033..1732033)
COG-FTR1
COG4393
COG-LolE
CJE1836
COG3019
CJE1839
COG-Tpd
COG-SalY
COG-SalX
CJE1837
CJE1840
Campylobacter jejuni subsp. doylei 269.97 (+ strand, 1778159..1788159)
JJD26997_2024
JJD26997_2025
JJD26997_2026
Campylobacter jejuni subsp. jejuni 260.94 contig (- strand, 27098..37098)
CJJ26094_1715
CJJ26094_1716
CJJ26094_1718
Campylobacter jejuni subsp. jejuni 81-176 (+ strand, 1557292..1567292)
CJJ81176_1655
CJJ81176_1656
CJJ81176_1658
CJJ81176_1659
Campylobacter jejuni subsp. jejuni 81116 (+ strand, 1568782..1578782)
p19
C8J_1566
C8J_1567
C8J_1569
Campylobacter jejuni subsp. jejuni 84-25 contig (- strand, 29008..39008)
CJJ8425_1747
CJJ8425_1748
CJJ8425_1750
CJJ8425_1751
Campylobacter jejuni subsp. jejuni CF93-6 contig (- strand, 29116..39116)
CJJCF936_1758
CJJCF936_1759
CJJCF936_1761
CJJCF936_1762
Campylobacter jejuni subsp. jejuni CG8486 contig (+ strand, 214928..224928)
Cj8486_1710
Cj8486_1711
Cj8486_1713
Cj8486_1714c
Campylobacter jejuni subsp. jejuni HB93-13 contig (- strand, 27136..37136)
CJJHB9313_1655
CJJHB9313_1656
CJJHB9313_1658
Campylobacter jejuni subsp. jejuni NCTC 11168 (+ strand, 1580693..1590693)
Cj1658
Cj1660
Cj1661
Cj1662
Cj1663
Cj1664
Cj1665
Cj1666c
Cj1667c
Cj1668c
tRNA-Leu
Campylobacter lari RM2100 (- strand, 1112312..1122312)
Cla_1163
Cla_1164
COG-CinA
ileS
Wolinella succinogenes DSM 1740 (- strand, 1479766..1489766)
WS1567
COG-Bcp
DGC2
WS1557
Treponema denticola ATCC 35405 (+ strand, 1556441..1566441)
TDE1508
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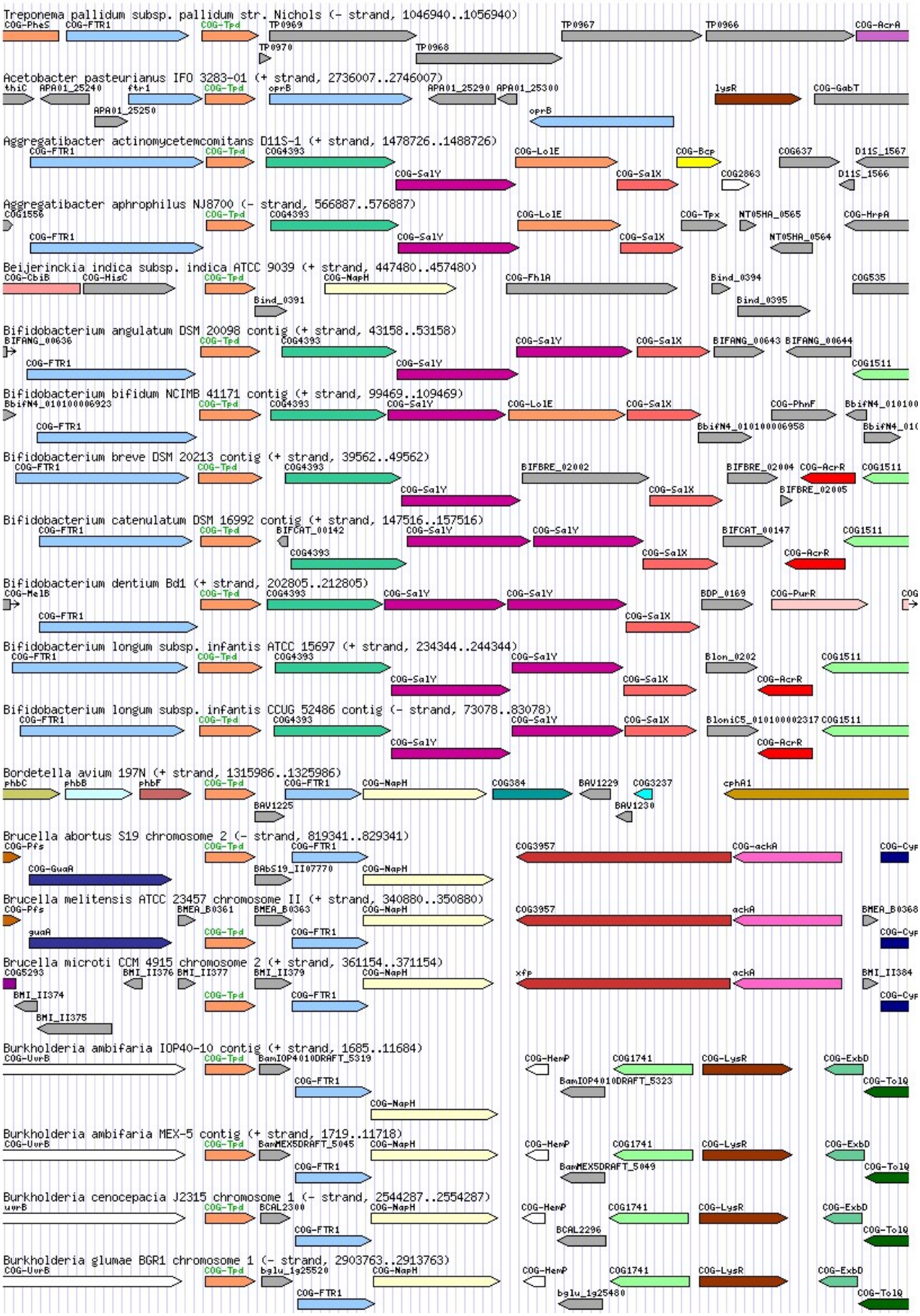
COG4939


Treponema pallidum subsp. pallidum str. Nichols (- strand, 1046940..1056940)
COG-PheS
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COG-Tpd
TP0969
TP0967
TP0966
COG-AcrA
TP0970
TP0968
Acetobacter pasteurianus IFO 3283-01 (+ strand, 2736007..2746007)
thiC
APA01_25240
ftr1
COG-Tpd
oprB
APA01_25290
APA01_25300
lysR
COG-GabT
APA01_25250
oprB
Aggregatibacter actinomycetemcomitans D11S-1 (+ strand, 1478726..1488726)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG637
D11S_1567
COG-SalY
COG-SalX
COG2863
D11S_1566
Aggregatibacter aphrophilus NJ8700 (- strand, 566887..576887)
COG1556
COG-Tpd
COG4393
COG-LolE
COG-Tpx
NT05HA_0565
COG-HrpA
COG-FTR1
COG-SalY
COG-SalX
NT05HA_0564
Beijerinckia indica subsp. indica ATCC 9039 (+ strand, 447480..457480)
COG-CbiB
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COG-FhlA
Bind_0394
COG535
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Bind_0395
Bifidobacterium angulatum DSM 20098 contig (+ strand, 43158..53158)
BIFANG_00636
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COG-SalY
COG-SalX
BIFANG_00643
BIFANG_00644
COG-FTR1
COG-SalY
COG1511
Bifidobacterium bifidum NCIMB 41171 contig (+ strand, 99469..109469)
BbifN4_010100006923
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COG-LolE
COG-SalX
COG-PhnF
BbifN4_010100
COG-FTR1
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BbifN4_010
Bifidobacterium breve DSM 20213 contig (+ strand, 39562..49562)
COG-FTR1
COG-Tpd
COG4393
BIFBRE_02002
BIFBRE_02004
COG-AcrR
COG1511
COG-SalY
COG-SalX
BIFBRE_02005
Bifidobacterium catenulatum DSM 16992 contig (+ strand, 147516..157516)
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COG-Tpd
BIFCAT_00142
COG-SalY
COG-SalY
BIFCAT_00147
COG1511
COG4393
COG-SalX
COG-AcrR
Bifidobacterium dentium Bd1 (+ strand, 202805..212805)
COG-MelB
COG-Tpd
COG4393
COG-SalY
COG-SalY
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COG
COG-FTR1
COG-SalX
Bifidobacterium longum subsp. infantis ATCC 15697 (+ strand, 234344..244344)
COG-FTR1
COG-Tpd
COG4393
COG-SalY
Blon_0202
COG1511
COG-SalY
COG-SalX
COG-AcrR
Bifidobacterium longum subsp. infantis CCUG 52486 contig (- strand, 73078..83078)
COG-FTR1
COG-Tpd
COG4393
COG-SalY
COG-SalX
BlomiC5_010100002317
COG1511
COG-SalY
COG-AcrR
Bordetella avium 197N (+ strand, 1315986..1325986)
phbC
phbB
phbF
COG-Tpd
COG-FTR1
COG-NapH
COG384
BAV1229
COG3237
cphA1
BAV1225
BAV1230
Brucella abortus S19 chromosome 2 (- strand, 819341..829341)
COG-Pfs
COG-Tpd
COG-FTR1
COG3957
COG-ackA
COG-Cyp
COG-GuaA
BAbS19_II07770
COG-NapH
Brucella melitensis ATCC 23457 chromosome II (+ strand, 340880..350880)
COG-Pfs
BMEA_B0361
BMEA_B0363
COG-NapH
COG3957
ackA
BMEA_B0368
guaA
COG-Tpd
COG-FTR1
COG-Cyp
Brucella microti CCM 4915 chromosome 2 (+ strand, 361154..371154)
COG5293
BMI_II376
BMI_II377
BMI_II379
COG-NapH
xfp
ackA
BMI_II384
BMI_II374
COG-Tpd
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BMI_II375
Burkholderia ambifaria IOP40-10 contig (+ strand, 1685..11684)
COG-UvrB
COG-Tpd
BamIOP4010DRAFT_5319
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BamIOP4010DRAFT_5323
COG-TolQ
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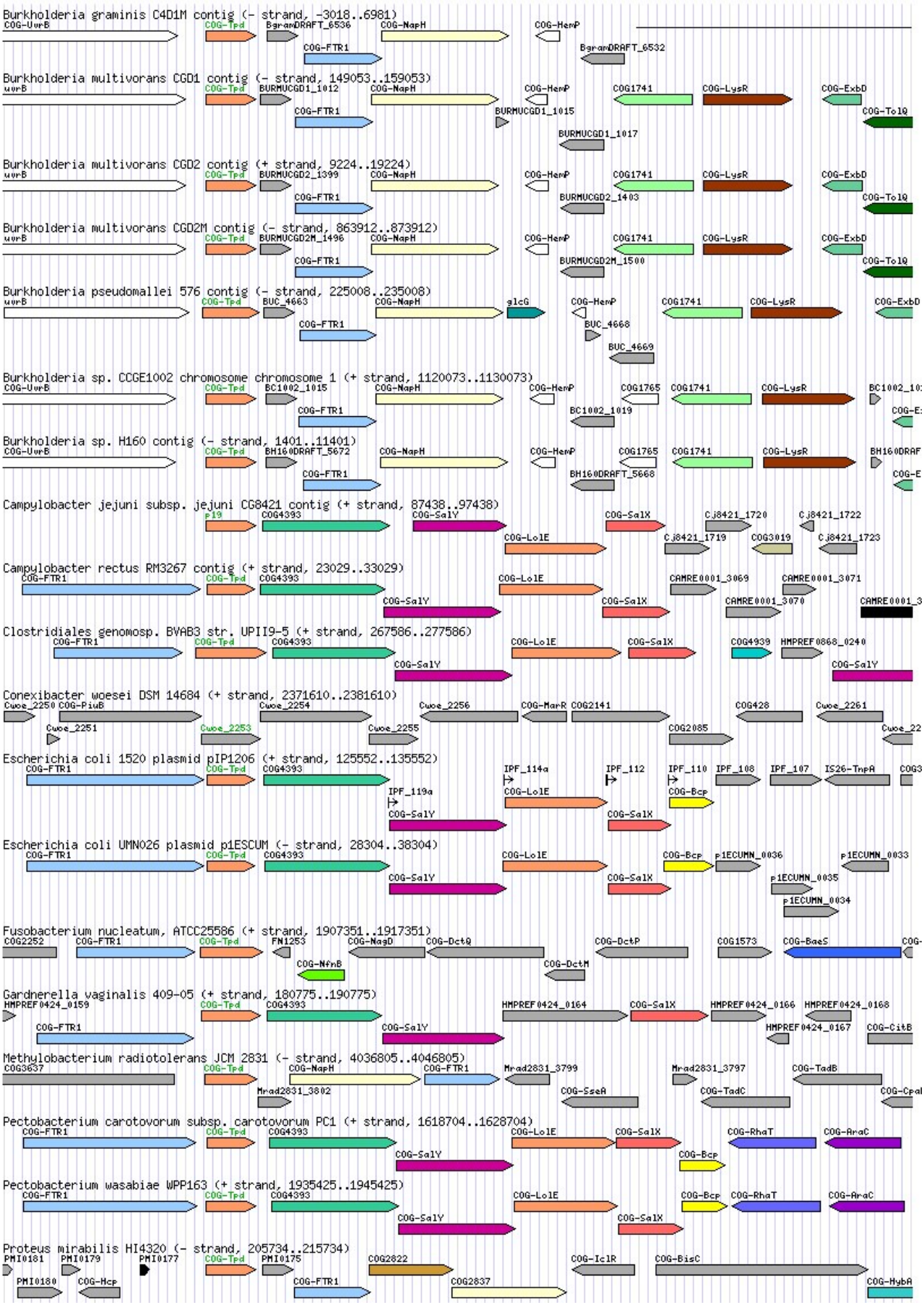
Burkholderia ambifaria MEX-5 contig (+ strand, 1719..11718)
COG-UvrB
COG-Tpd
BamMEX5DRAFT_5045
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BamMEX5DRAFT_5049
COG-TolQ
Burkholderia cenocepacia J2315 chromosome 1 (- strand, 2544287..2554287)
uvrB
COG-Tpd
BCAL2300
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BCAL2296
COG-TolQ
Burkholderia glumae BGR1 chromosome 1 (- strand, 2903763..2913763)
COG-UvrB
COG-Tpd
bglu_1g25520
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
bglu_1g25480
COG-TolQ


Burkholderia graminis C4D1M contig (- strand, -3018..6981)
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COG-FTR1
BgramDRAFT_6532
Burkholderia multivorans CGD1 contig (- strand, 149053..159053)
uvrB
COG-Tpd
BURMUCGD1_1012
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BURMUCGD1_1015
COG-TolQ
BURMUCGD1_1017
Burkholderia multivorans CGD2 contig (+ strand, 9224..19224)
uvrB
COG-Tpd
BURMUCGD2_1399
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BURMUCGD2_1403
COG-TolQ
Burkholderia multivorans CGD2M contig (- strand, 863912..873912)
uvrB
COG-Tpd
BURMUCGD2M_1496
COG-NapH
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BURMUCGD2M_1500
COG-TolQ
Burkholderia pseudomallei 576 contig (- strand, 225008..235008)
uvrB
COG-Tpd
BUC_4663
COG-NapH
glcG
COG-HemP
COG1741
COG-LysR
COG-ExbD
COG-FTR1
BUC_4668
BUC_4669
Burkholderia sp. CCGE1002 chromosome chromosome 1 (+ strand, 1120073..1130073)
COG-UvrB
COG-Tpd
BC1002_1015
COG-NapH
COG-HemP
COG1765
COG1741
COG-LysR
COG-FTR1
BC1002_1019
Burkholderia sp. H160 contig (- strand, 1401..11401)
COG-UvrB
COG-Tpd
BH160DRAFT_5672
COG-NapH
COG-HemP
COG1765
COG1741
COG-LysR
COG-FTR1
BH160DRAFT_5668
Campylobacter jejuni subsp. jejuni CG8421 contig (+ strand, 87438..97438)
p19
COG4393
COG-SalY
COG-SalX
Cj8421_1720
Cj8421_1722
COG-LolE
Cj8421_1719
COG3019
Cj8421_1723
Campylobacter rectus RM3267 contig (+ strand, 23029..33029)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
CAMRE0001_3069
CAMRE0001_3071
COG-SalY
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Clostridiales genomosp. BVAB3 str. UPII9-5 (+ strand, 267586..277586)
COG-FTR1
COG-Tpd
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COG-LolE
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COG-SalY
Conexibacter woesei DSM 14684 (+ strand, 2371610..2381610)
Cwoe_2250
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Cwoe_2254
Cwoe_2256
COG-MarR
COG2141
COG428
Cwoe_2261
Cwoe_2251
Cwoe_2253
Cwoe_2255
COG2085
Escherichia coli 1520 plasmid pIP1206 (+ strand, 125552..135552)
COG-FTR1
COG-Tpd
COG4393
IPF_114a
IPF_112
IPF_110
IPF_108
IPF_107
IS26-TnpA
IPF_119a
COG-LolE
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COG-SalY
COG-SalX
Escherichia coli UMN026 plasmid p1ESCUM (- strand, 28304..38304)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
p1ECUMN_0036
p1ECUMN_0033
COG-SalY
COG-SalX
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Fusobacterium nucleatum, ATCC25586 (+ strand, 1907351..1917351)
COG2252
COG-FTR1
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FN1253
COG-NagD
COG-DctQ
COG-DctP
COG1573
COG-BaeS
COG-NfnB
COG-DctM
Gardnerella vaginalis 409-05 (+ strand, 180775..190775)
HMPREF0424_0159
COG-Tpd
COG4393
HMPREF0424_0164
COG-SalX
HMPREF0424_0166
HMPREF0424_0168
COG-FTR1
COG-SalY
HMPREF0424_0167
COG-CitB
Methylobacterium radiotolerans JCM 2831 (- strand, 4036805..4046805)
COG3637
COG-Tpd
COG-NapH
COG-FTR1
Mrad2831_3799
Mrad2831_3797
COG-TadB
Mrad2831_3802
COG-SseA
COG-TadC
COG-CpaI
Pectobacterium carotovorum subsp. carotovorum PC1 (+ strand, 1618704..1628704)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-SalX
COG-RhaT
COG-AraC
COG-SalY
COG-Bcp
Pectobacterium wasabiae WPP163 (+ strand, 1935425..1945425)
COG-FTR1
COG-Tpd
COG4393
COG-LolE
COG-Bcp
COG-RhaT
COG-AraC
COG-SalY
COG-SalX
Proteus mirabilis HI4320 (- strand, 205734..215734)
PMI0181
PMI0179
PMI0177
COG-Tpd
PMI0175
COG2822
COG-IclR
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COG-FTR1
COG2837
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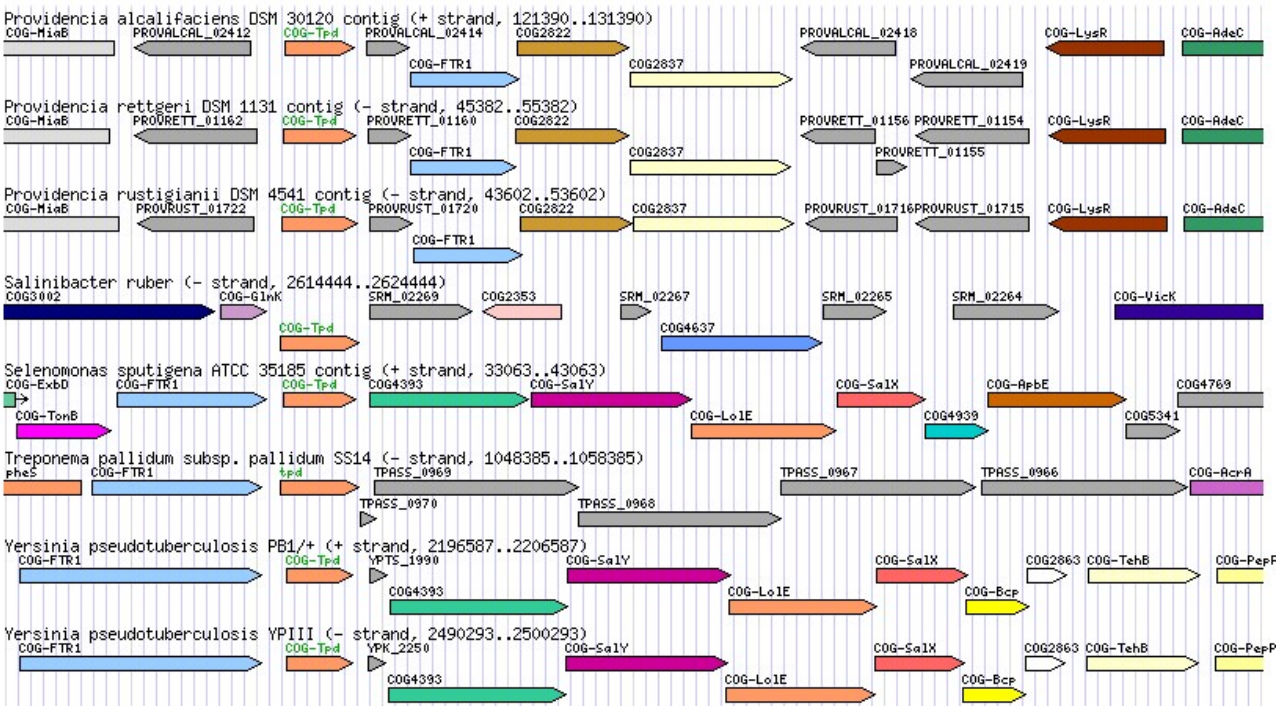
Providencia alcalifaciens DSM 30120 contig (+ strand, 121390..131390)
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COG-LysR
COG-AdeC
COG-FTR1
COG2837
PROVALCAL_02419
Providencia rettgeri DSM 1131 contig (- strand, 45382..55382)
COG-MiaB
PROVRETT_01162
COG-Tpd
PROVRETT_01160
COG2822
PROVRETT_01156
PROVRETT_01154
COG-LysR
COG-AdeC
COG-FTR1
COG2837
PROVRETT_01155
Providencia rustigianii DSM 4541 contig (- strand, 43602..53602)
COG-MiaB
PROVRUST_01722
COG-Tpd
PROVRUST_01720
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PROVRUST_01715
COG-LysR
COG-AdeC
COG-FTR1
Salinibacter ruber (- strand, 2614444..2624444)
COG3002
COG-GlnK
SRM_02269
COG2353
SRM_02267
SRM_02265
SRM_02264
COG-VicK
COG-Tpd
COG4637
Selenomonas sputigena ATCC 35185 contig (+ strand, 33063..43063)
COG-ExbD
COG-FTR1
COG-Tpd
COG4393
COG-SalY
COG-SalX
COG-ApbE
COG4769
COG-TonB
COG-LolE
COG4939
COG5341
Treponema pallidum subsp. pallidum SS14 (- strand, 1048385..1058385)
pheS
COG-FTR1
tpd
TPASS_0969
TPASS_0967
TPASS_0966
COG-AcrA
TPASS_0970
TPASS_0968
Yersinia pseudotuberculosis PB1/+ (+ strand, 2196587..2206587)
COG-FTR1
COG-Tpd
YPTS_1990
COG-SalY
COG-SalX
COG2863
COG-TehB
COG4393
COG-LolE
COG-Bcp
Yersinia pseudotuberculosis YPIII (- strand, 2490293..2500293)
COG-FTR1
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YPK_2250
COG-SalY
COG-SalX
COG2863
COG-TehB
COG4393
COG-LolE
COG-Bcp