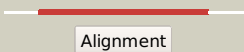

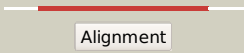



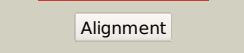



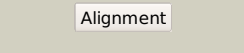

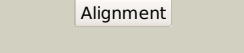



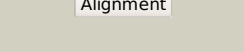

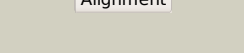

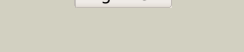





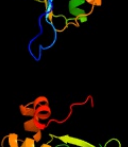



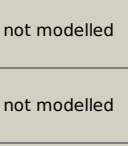


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2064_(cobG)_2321459_2322550
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	28c13beb9b2a3d7c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zj8B_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: probable ferredoxin-dependent nitrite reductase nira; PDBTitle: structure of mycobacterium tuberculosis nira protein
2	c3b0nA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: q448k mutant of assimilatory nitrite reductase (nii3) from tobacco2 leaf
3	c2akjA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nitrite reductase, chloroplast; PDBTitle: structure of spinach nitrite reductase
4	c5h92A_	 Alignment		100.0	23	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: sulfite reductase [ferredoxin], chloroplastic; PDBTitle: crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal
5	c5aopA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase hemoprotein; PDBTitle: sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
6	c2v4jE_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
7	c3c7bE_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
8	c2v4jA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
9	c3c7bA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
10	d1zj8a4	 Alignment		99.9	17	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
11	d2akja4	 Alignment		99.9	17	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like

12	d1aopa3	Alignment		99.9	13	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
13	d3c7ba3	Alignment		99.9	13	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
14	d2v4ja3	Alignment		99.9	14	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
15	d2akja2	Alignment		99.9	30	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
16	d1zj8a2	Alignment		99.9	30	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
17	d2v4jb3	Alignment		99.8	17	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
18	d3c7bb2	Alignment		99.8	22	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
19	d3c7bb3	Alignment		99.8	13	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
20	d2v4jb2	Alignment		99.8	15	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
21	d1zj8a1	Alignment	not modelled	99.8	14	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
22	d1aopa1	Alignment	not modelled	99.8	34	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
23	d1zj8a3	Alignment	not modelled	99.7	20	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
24	d2akja3	Alignment	not modelled	99.7	16	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
25	d2akja1	Alignment	not modelled	99.6	25	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
26	d1aopa2	Alignment	not modelled	99.6	19	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
27	d1aopa4	Alignment	not modelled	99.5	15	Fold: Nitrite and sulphite reductase 4Fe-4S domain-like Superfamily: Nitrite and sulphite reductase 4Fe-4S domain-like Family: Nitrite and sulphite reductase 4Fe-4S domain-like
28	c3noyA	Alignment	not modelled	99.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
29	d3c7ba2	Alignment	not modelled	98.1	17	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like

						Family: DsrA/DsrB N-terminal-domain-like
30	c2y0fD	Alignment	not modelled	96.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispq) from thermus thermophilus hb27
31	d2v4ja2	Alignment	not modelled	95.9	17	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
32	c3w9zA	Alignment	not modelled	49.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
33	c4qboA	Alignment	not modelled	46.2	14	PDB header: hydrolase Chain: A: PDB Molecule: nuclease; PDBTitle: vrr_nuc domain
34	c5hcdD	Alignment	not modelled	43.5	44	PDB header: immune system Chain: D: PDB Molecule: rhipicephalus microplus raci2; PDBTitle: ternary complex of human complement c5 with ornithodoros moubata omci2 and rhipicephalus microplus raci2
35	d1n7ka	Alignment	not modelled	38.1	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
36	c1b8hA	Alignment	not modelled	32.8	25	PDB header: transferase Chain: A: PDB Molecule: dna polymerase processivity component; PDBTitle: sliding clamp, dna polymerase
37	c1r1gA	Alignment	not modelled	31.9	43	PDB header: toxin Chain: A: PDB Molecule: neurotoxin bmk37; PDBTitle: crystal structure of the scorpion toxin bmbktx1
38	d1r1ga	Alignment	not modelled	31.9	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
39	c1r1gB	Alignment	not modelled	31.9	43	PDB header: toxin Chain: B: PDB Molecule: neurotoxin bmk37; PDBTitle: crystal structure of the scorpion toxin bmbktx1
40	c6gcsH	Alignment	not modelled	29.6	18	PDB header: oxidoreductase Chain: H: PDB Molecule: 24-kda subunit (nuhm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
41	d1tx2a	Alignment	not modelled	29.4	22	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
42	c1tx2A	Alignment	not modelled	29.4	22	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
43	c5lnk2	Alignment	not modelled	28.7	18	PDB header: oxidoreductase Chain: 2: PDB Molecule: mitochondrial complex i, 24 kda subunit; PDBTitle: entire ovine respiratory complex i
44	c5hccD	Alignment	not modelled	26.6	43	PDB header: immune system Chain: D: PDB Molecule: dermacentor andersoni raci3; PDBTitle: ternary complex of human complement c5 with ornithodoros moubata omci2 and dermacentor andersoni raci3.
45	c4qbnA	Alignment	not modelled	25.5	11	PDB header: hydrolase Chain: A: PDB Molecule: nuclease; PDBTitle: vrr_nuc domain
46	c5iecA	Alignment	not modelled	23.6	44	PDB header: blood clotting Chain: A: PDB Molecule: raci2; PDBTitle: structural basis for therapeutic inhibition of complement c5
47	d1olta	Alignment	not modelled	20.3	19	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
48	d1czda2	Alignment	not modelled	18.7	27	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
49	c4xbsA	Alignment	not modelled	18.0	11	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
50	d1pvza	Alignment	not modelled	17.2	36	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
51	c1pvzA	Alignment	not modelled	17.2	36	PDB header: toxin Chain: A: PDB Molecule: k+ toxin-like peptide; PDBTitle: solution structure of bmp07, a novel potassium channel blocker from2 scorpion buthus martensi karsch, 15 structures
52	d1ad1a	Alignment	not modelled	17.2	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
53	c2h9aB	Alignment	not modelled	16.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
54	d1qnta2	Alignment	not modelled	15.4	30	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
55	d1r8na	Alignment	not modelled	15.4	9	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
56	c5lc5E	Alignment	not modelled	14.7	19	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2,

					PDBTitle: structure of mammalian respiratory complex i, class2
57	d1b77a2	Alignment	not modelled	14.3	27 Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
58	d1xwva	Alignment	not modelled	14.0	19 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: ML domain
59	c5abrB	Alignment	not modelled	13.9	20 PDB header: electron transport Chain: B: PDB Molecule: ferredoxin, 2fe-2s; PDBTitle: structure of fesi protein from azotobacter vinelandii
60	d1tg7a5	Alignment	not modelled	13.2	22 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Glycosyl hydrolases family 35 catalytic domain
61	d2fug21	Alignment	not modelled	13.1	15 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
62	c3nqoB	Alignment	not modelled	12.9	16 PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
63	c4e8cA	Alignment	not modelled	12.8	17 PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 35; PDBTitle: crystal structure of streptococcal beta-galactosidase in complex with2 galactose
64	d1ffgb	Alignment	not modelled	12.6	21 Fold: Ferredoxin-like Superfamily: CheY-binding domain of CheA Family: CheY-binding domain of CheA
65	c6cluC	Alignment	not modelled	12.2	13 PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
66	d1p4xa2	Alignment	not modelled	12.1	14 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
67	d2j5pa1	Alignment	not modelled	11.7	21 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
68	c2h90A	Alignment	not modelled	11.6	14 PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
69	d1ktja	Alignment	not modelled	11.4	15 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: ML domain
70	c4z9rA	Alignment	not modelled	11.3	8 PDB header: oxidoreductase Chain: A: PDB Molecule: omega-3 polyunsaturated fatty acid synthase subunit pfad; PDBTitle: crystal structure of pfad from shewanella oneidensis in complex with2 nad+ determined by in-situ diffraction.
71	c4qblF	Alignment	not modelled	11.2	21 PDB header: hydrolase Chain: F: PDB Molecule: vrr-nuc; PDBTitle: vrr_nuc domain protein
72	d1mzha	Alignment	not modelled	11.2	3 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
73	d1hpca	Alignment	not modelled	10.7	18 Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
74	c3k13A	Alignment	not modelled	10.4	13 PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
75	d1ub3a	Alignment	not modelled	10.4	23 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
76	c5dbul	Alignment	not modelled	10.2	9 PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
77	c3lf4A	Alignment	not modelled	10.0	17 PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent timer precursor blue102; PDBTitle: crystal structure of fluorescent timer precursor blue102
78	c2a56A	Alignment	not modelled	9.8	8 PDB header: luminescent protein Chain: A: PDB Molecule: gfp-like non-fluorescent chromoprotein fp595 chain 1; PDBTitle: fluorescent protein asfp595, a143s, on-state, 5min irradiation
79	c4yn3B	Alignment	not modelled	9.7	19 PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin complex with pro-peptide
80	d1yaaa	Alignment	not modelled	9.4	14 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
81	d1ludka	Alignment	not modelled	9.4	33 Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Elafin-like Family: Elafin-like
82	d2gca1	Alignment	not modelled	9.3	21 Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like

83	c4nm6A_	Alignment	not modelled	9.3	31	PDB header: oxidoreductase/dna Chain: A: PDB Molecule: methylcytosine dioxygenase tet2; PDBTitle: crystal structure of tet2-dna complex
84	d3broa1	Alignment	not modelled	9.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
85	d1u5ka1	Alignment	not modelled	9.2	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RecO N-terminal domain-like
86	d3c8ya1	Alignment	not modelled	9.1	24	Fold: Fe-only hydrogenase Superfamily: Fe-only hydrogenase Family: Fe-only hydrogenase
87	c6feyK_	Alignment	not modelled	9.0	25	PDB header: peptide binding protein Chain: K: PDB Molecule: probable insulin-like peptide 5; PDBTitle: crystal structure of drosophila neural ectodermal development factor2 imp-l2 with drosophila dilp5 insulin
88	d2okqa1	Alignment	not modelled	8.9	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YbaA-like
89	c2k9oA_	Alignment	not modelled	8.9	50	PDB header: toxin Chain: A: PDB Molecule: vm24 scorpion toxin; PDBTitle: solution structure of vm24 synthetic scorpion toxin
90	c3d3jA_	Alignment	not modelled	8.9	35	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
91	c3d3kD_	Alignment	not modelled	8.9	35	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
92	c3ngjC_	Alignment	not modelled	8.8	9	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
93	c3t18D_	Alignment	not modelled	8.7	5	PDB header: transferase Chain: D: PDB Molecule: aminotransferase class i and ii; PDBTitle: crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
94	c5dleD_	Alignment	not modelled	8.7	6	PDB header: transferase Chain: D: PDB Molecule: pts system, fructose-specific iiabc component; PDBTitle: crystal structure from a domain (thr161-f265) from fructose-specific2 iiabc component (pts system) from borrelia burgdorferi
95	c6h12C_	Alignment	not modelled	8.7	15	PDB header: electron transport Chain: C: PDB Molecule: nadh-quinone oxidoreductase subunit e; PDBTitle: wild-type nuoef from aquifex aeolicus - oxidized form
96	d2ve8a1	Alignment	not modelled	8.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
97	c1a0oH_	Alignment	not modelled	8.5	21	PDB header: chemotaxis Chain: H: PDB Molecule: chea; PDBTitle: chey-binding domain of chea in complex with chey
98	d1fxda_	Alignment	not modelled	8.5	25	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
99	d1vmfa_	Alignment	not modelled	8.5	39	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like