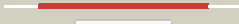



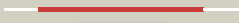



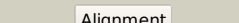



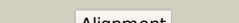


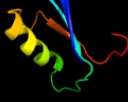







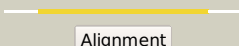

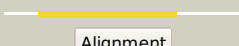
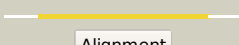
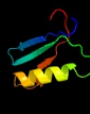
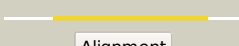

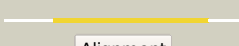

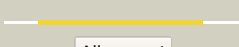

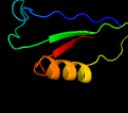
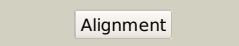
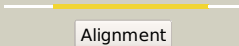
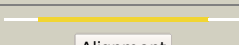
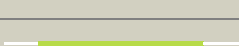
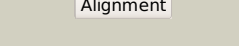
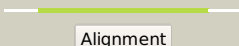
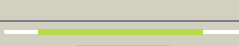


Phyre2

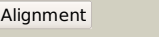
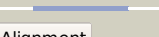
Email mdejesus@rockefeller.edu
 Description RVBD1984A_(RVBD1984A)_2228684_2228914
 Date Mon Aug 5 13:25:08 BST 2019
 Unique Job ID 7bc3db038860ed12

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yh5a1	 Alignment		99.9	21	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
2	d1jrma_	 Alignment		99.9	25	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
3	c3t5sA_	 Alignment		90.4	13	PDB header: immune system Chain: A: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: structure of macrophage migration inhibitory factor from giardia2 lamblia
4	d1ffvb2	 Alignment		89.2	18	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
5	d1t3qb2	 Alignment		88.1	20	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
6	c3hrdF_	 Alignment		88.0	17	PDB header: oxidoreductase Chain: F: PDB Molecule: nicotinate dehydrogenase medium molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
7	d1n62b2	 Alignment		86.9	15	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
8	c1n62E_	 Alignment		86.5	15	PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase large chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
9	c1ffvB_	 Alignment		85.3	18	PDB header: hydrolase Chain: B: PDB Molecule: cutl, molybdoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
10	d1v97a5	 Alignment		83.5	15	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
11	d1jrob2	 Alignment		80.7	18	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain

12	c3eubL_	 Alignment		77.8	15	PDB header: oxidoreductase Chain: L: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
13	c6cuqB_	 Alignment		77.4	13	PDB header: cytokine Chain: B: PDB Molecule: macrophage migration inhibitory factor-like protein; PDBTitle: crystal structure of macrophage migration inhibitory factor-like2 protein (ehmif) from entamoeba histolytica
14	c1t3qB_	 Alignment		77.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: quinoline 2-oxidoreductase large subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
15	d1t6aa_	 Alignment		76.5	29	Fold: TBP-like Superfamily: Rbstp2229 protein Family: Rbstp2229 protein
16	c2w54F_	 Alignment		75.1	17	PDB header: oxidoreductase Chain: F: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase from rhodobacter2 capsulatus in complex with bound inhibitor pterin-6-aldehyde
17	c1wygA_	 Alignment		74.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
18	c4uhxA_	 Alignment		73.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
19	d2gdga1	 Alignment		73.4	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
20	d1fima_	 Alignment		73.3	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
21	c1sb3D_	 Alignment	not modelled	73.1	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa reductase alpha subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
22	d1rm6a2	 Alignment	not modelled	72.0	16	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
23	c3zyvA_	 Alignment	not modelled	70.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
24	c4zohA_	 Alignment	not modelled	70.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase molybdopterin-binding subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
25	c3b64A_	 Alignment	not modelled	68.6	11	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major
26	c5g5hC_	 Alignment	not modelled	67.4	17	PDB header: oxidoreductase Chain: C: PDB Molecule: putative xanthine dehydrogenase yagr molybdenum-binding PDBTitle: escherichia coli periplasmic aldehyde oxidase r440h mutant
27	d1gd0a_	 Alignment	not modelled	62.8	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
28	c2vcaA_	 Alignment	not modelled	62.8	12	PDB header: immune system Chain: A: PDB Molecule: possible at1s1-like light-inducible protein;

28	c2at2A	Alignment	not modelled	62.8	12	PDBTitle: crystal structure of macrophage migration inhibitory factor homologue2 from prochlorococcus marinus PDB header: cytokine
29	c3fwtA	Alignment	not modelled	62.8	7	Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
30	c5y6qC	Alignment	not modelled	59.2	12	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde oxidase large subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
31	c3gacD	Alignment	not modelled	58.9	18	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
32	c4dh4A	Alignment	not modelled	56.6	20	PDB header: isomerase Chain: A: PDB Molecule: mif; PDBTitle: macrophage migration inhibitory factor toxoplasma gondii
33	d1hfoa	Alignment	not modelled	52.6	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
34	d1dpta	Alignment	not modelled	49.8	20	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
35	c2os5C	Alignment	not modelled	49.2	21	PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum
36	d1uiza	Alignment	not modelled	47.2	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
37	d1b24a1	Alignment	not modelled	45.8	26	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Group I mobile intron endonuclease
38	c3hrdE	Alignment	not modelled	45.7	20	PDB header: oxidoreductase Chain: E: PDB Molecule: nicotinate dehydrogenase large molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
39	d1vlba4	Alignment	not modelled	38.5	11	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
40	c4fdxB	Alignment	not modelled	37.7	19	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
41	c4fazB	Alignment	not modelled	36.6	24	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate isomerase protein; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
42	d1otfa	Alignment	not modelled	35.7	29	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
43	c3abfB	Alignment	not modelled	35.4	19	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
44	d1bjpa	Alignment	not modelled	33.5	19	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
45	c3mb2G	Alignment	not modelled	31.9	29	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
46	c5uifC	Alignment	not modelled	31.4	19	PDB header: hydrolase Chain: C: PDB Molecule: ps01740; PDBTitle: crystal structure of native ps01740
47	d5mdha2	Alignment	not modelled	30.5	18	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
48	c3m20A	Alignment	not modelled	30.3	14	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpl from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
49	d1y7ta2	Alignment	not modelled	30.1	21	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
50	d2aala1	Alignment	not modelled	29.9	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like
51	c2op8A	Alignment	not modelled	29.6	10	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
52	c1vlbA	Alignment	not modelled	29.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
53	d1dgja4	Alignment	not modelled	29.1	17	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain

54	c4lkbA	 Alignment	not modelled	29.0	0	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein alr4568/putative 4-oxalocrotonate PDBTitle: crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120
55	d1mwwa	 Alignment	not modelled	28.6	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein H11388.1
56	c3ry0A	 Alignment	not modelled	28.3	24	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
57	c5un4C	 Alignment	not modelled	27.9	17	PDB header: hydrolase Chain: C: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of native fused 4-ot
58	d1gyxa	 Alignment	not modelled	27.7	19	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
59	c3p1tB	 Alignment	not modelled	27.2	33	PDB header: transferase Chain: B: PDB Molecule: putative histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
60	c2l0kA	 Alignment	not modelled	27.0	25	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
61	c2x4kB	 Alignment	not modelled	26.7	14	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
62	c3fkdC	 Alignment	not modelled	26.4	23	PDB header: lyase Chain: C: PDB Molecule: l-threonine-o-3-phosphate decarboxylase; PDBTitle: the crystal structure of l-threonine-o-3-phosphate decarboxylase from2 porphyromonas gingivalis
63	d7mdha2	 Alignment	not modelled	25.7	15	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
64	c5unqF	 Alignment	not modelled	25.0	19	PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of pt0534 inactivated by 2-oxo-3-pentynoate
65	c2ormA	 Alignment	not modelled	24.2	19	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpI2 from helicobacter pylori.
66	c6dcsB	 Alignment	not modelled	23.4	10	PDB header: protein transport Chain: B: PDB Molecule: stage iii sporulation protein af; PDBTitle: stage iii sporulation protein af (spoiiaf)
67	c1dgiA	 Alignment	not modelled	23.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
68	d1xdpa2	 Alignment	not modelled	22.5	14	Fold: PHP14-like Superfamily: PHP14-like Family: PPK middle domain-like
69	c1z2zB	 Alignment	not modelled	22.4	25	PDB header: lyase Chain: B: PDB Molecule: probable trna pseudouridine synthase d; PDBTitle: crystal structure of the putative trna pseudouridine synthase d (trud)2 from methanosarcina maezi, northeast structural genomics target mar1
70	d1szwa	 Alignment	not modelled	21.7	22	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: tRNA pseudouridine synthase TruD
71	c2pmpA	 Alignment	not modelled	21.6	16	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
72	d1w55a2	 Alignment	not modelled	21.6	16	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
73	c1sb7A	 Alignment	not modelled	20.8	22	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase d; PDBTitle: crystal structure of the e.coli pseudouridine synthase trud
74	c3n4dF	 Alignment	not modelled	20.7	24	PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
75	c3re3B	 Alignment	not modelled	20.2	13	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
76	c5kkaA	 Alignment	not modelled	20.0	13	PDB header: isomerase Chain: A: PDB Molecule: pseudouridylate synthase 7; PDBTitle: crystal structure of human pseudouridylate synthase 7
77	d1qbjc	 Alignment	not modelled	19.9	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
78	c2fl7C	 Alignment	not modelled	19.8	4	PDB header: hydrolase Chain: C: PDB Molecule: cis-3-chloroacrylic acid dehalogenase;

78	c2h2C_	Alignment	not modelled	19.8	4	PDBTitle: the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site PDB header: protein binding Chain: A; PDB Molecule: ubiquitin carboxyl-terminal hydrolase 7;
79	c2kvrA_	Alignment	not modelled	19.6	11	PDBTitle: solution nmr structure of human ubiquitin specific protease usp7 ubl2 domain (residues 537-664). nesg target hr4395c/sgc-toronto
80	d1gx1a_	Alignment	not modelled	19.6	10	Fold: Bacillus chorismate mutase-like Superfamily: !psF-like Family: !psF-like
81	c2oghA_	Alignment	not modelled	19.1	25	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor eif-1; PDBTitle: solution structure of yeast eif1
82	d1civa2	Alignment	not modelled	19.1	15	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
83	d2gxba1	Alignment	not modelled	18.9	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
84	d1vh8a_	Alignment	not modelled	18.9	19	Fold: Bacillus chorismate mutase-like Superfamily: !psF-like Family: !psF-like
85	d1qgpa_	Alignment	not modelled	18.7	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
86	c3b6nA_	Alignment	not modelled	18.5	19	PDB header: lyase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase pv003920 from plasmodium vivax
87	d1iv3a_	Alignment	not modelled	18.3	23	Fold: Bacillus chorismate mutase-like Superfamily: !psF-like Family: !psF-like
88	c3f0gA_	Alignment	not modelled	18.2	29	PDB header: lyase Chain: A; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
89	d1b8pa2	Alignment	not modelled	18.1	24	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
90	d1hyha2	Alignment	not modelled	16.7	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
91	c1b8vA_	Alignment	not modelled	16.7	24	PDB header: oxidoreductase Chain: A; PDB Molecule: protein (malate dehydrogenase); PDBTitle: malate dehydrogenase from aquaspirillum arcticum
92	d1t2da2	Alignment	not modelled	16.7	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
93	c3vp7A_	Alignment	not modelled	16.6	22	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
94	c2l9fA_	Alignment	not modelled	16.2	21	PDB header: transferase Chain: A; PDB Molecule: cale8; PDBTitle: nmr solution structure of meacp
95	d1t0aa_	Alignment	not modelled	15.8	13	Fold: Bacillus chorismate mutase-like Superfamily: !psF-like Family: !psF-like
96	c5iwyD_	Alignment	not modelled	15.7	13	PDB header: lyase Chain: D; PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from bacillus subtilis complexed with cmp and mg2+
97	c5nufA_	Alignment	not modelled	15.7	21	PDB header: oxidoreductase Chain: A; PDB Molecule: malate dehydrogenase 1, cytoplasmic; PDBTitle: cytosolic malate dehydrogenase 1
98	d2bgxa2	Alignment	not modelled	15.6	14	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
99	c4uupB_	Alignment	not modelled	15.3	27	PDB header: oxidoreductase Chain: B; PDB Molecule: malate dehydrogenase; PDBTitle: reconstructed ancestral trichomonad malate dehydrogenase in2 complex with nadh, so4, and po4