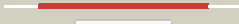



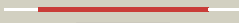






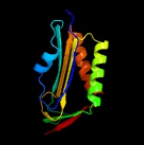
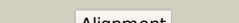








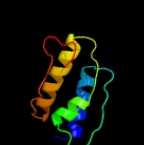


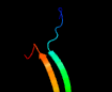


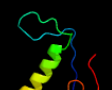


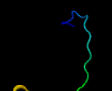


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3119\_(moaE1)\_3485129\_3485572  
 Date Thu Aug 8 16:20:30 BST 2019  
 Unique Job ID 7f5359a027445711

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qieA_</a>	 Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> staphylococcus aureus molybdopterin synthase in complex with precursor2 z
2	<a href="#">c6jzbzC_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> molybdenum cofactor biosynthesis protein e; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
3	<a href="#">c6jc0D_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> putative molybdenum cofactor biosynthesis protein; <b>PDBTitle:</b> structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
4	<a href="#">c2omdB_</a>	 Alignment		100.0	34	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2; <b>PDBTitle:</b> crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
5	<a href="#">d1fm0e_</a>	 Alignment		100.0	36	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Molybdopterin synthase subunit MoaE <b>Family:</b> Molybdopterin synthase subunit MoaE
6	<a href="#">c4ap8A_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin synthase catalytic subunit; <b>PDBTitle:</b> crystal structure of human molybdopterin synthase catalytic subunit2 (mocs2b)
7	<a href="#">c3rpfB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> molybdopterin synthase catalytic subunit; <b>PDBTitle:</b> protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
8	<a href="#">c2wp4A_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> molybdopterin-converting factor subunit 2 1; <b>PDBTitle:</b> crystal structure of rv3119 from mycobacterium tuberculosis
9	<a href="#">d1nvja_</a>	 Alignment		100.0	37	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Molybdopterin synthase subunit MoaE <b>Family:</b> Molybdopterin synthase subunit MoaE
10	<a href="#">c1v8cA_</a>	 Alignment		99.3	22	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> moad related protein; <b>PDBTitle:</b> crystal structure of moad related protein from thermus2 thermophilus hb8
11	<a href="#">c3upsA_</a>	 Alignment		77.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> iojap-like protein; <b>PDBTitle:</b> crystal structure of iojap-like protein from zymomonas mobilis

12	<a href="#">d2id1a1</a>	Alignment		63.2	16	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> lojap/YbeB-like
13	<a href="#">d2o5aa1</a>	Alignment		42.5	12	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> lojap/YbeB-like
14	<a href="#">c4gzvH_</a>	Alignment		37.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a lipocalin family protein (bacova_00364) from2 bacteroides ovatus atcc 8483 at 1.95 a resolution
15	<a href="#">c4wcvB_</a>	Alignment		36.4	15	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal silencing factor rsfs; <b>PDBTitle:</b> ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis
16	<a href="#">c5oomu_</a>	Alignment		36.1	14	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 39s ribosomal protein l23, mitochondrial; <b>PDBTitle:</b> structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rrna
17	<a href="#">d1xmba2</a>	Alignment		33.2	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Bacterial exopeptidase dimerisation domain <b>Family:</b> Bacterial exopeptidase dimerisation domain
18	<a href="#">dlsq1a_</a>	Alignment		28.9	6	<b>Fold:</b> Chorismate synthase, AroC <b>Superfamily:</b> Chorismate synthase, AroC <b>Family:</b> Chorismate synthase, AroC
19	<a href="#">c1zcoA_</a>	Alignment		22.2	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoheptonate aldolase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
20	<a href="#">d2dy1a5</a>	Alignment		18.0	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
21	<a href="#">d1n0ua5</a>	Alignment	not modelled	17.2	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
22	<a href="#">c5usrG_</a>	Alignment	not modelled	16.0	14	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
23	<a href="#">c3lvmB_</a>	Alignment	not modelled	14.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase; <b>PDBTitle:</b> crystal structure of e.coli iscs
24	<a href="#">d2h80a1</a>	Alignment	not modelled	14.6	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Variant SAM domain
25	<a href="#">c2i2xO_</a>	Alignment	not modelled	13.8	16	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> methyltransferase 1; <b>PDBTitle:</b> crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
26	<a href="#">c2kouA_</a>	Alignment	not modelled	13.5	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dicer-like protein 4; <b>PDBTitle:</b> dicer like protein
27	<a href="#">d2dkya1</a>	Alignment	not modelled	13.3	33	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> Variant SAM domain
28	<a href="#">d2burb1</a>	Alignment	not modelled	11.9	31	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
29	<a href="#">d1p3wa_</a>	Alignment	not modelled	11.3	22	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases

						<b>Family:</b> Cystathionine synthase-like
30	<a href="#">c4ikcA_</a>	Alignment	not modelled	11.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol phosphatase ptprq; <b>PDBTitle:</b> crystal structure of catalytic domain of ptprq
31	<a href="#">d2od6a1</a>	Alignment	not modelled	11.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Marine metagenome family DABB1
32	<a href="#">c5h7lB_</a>	Alignment	not modelled	10.2	11	<b>PDB header:</b> translation/ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> complex of elongation factor 2-50s ribosomal protein l12
33	<a href="#">d2gnoa1</a>	Alignment	not modelled	10.0	22	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
34	<a href="#">c4e5sC_</a>	Alignment	not modelled	9.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> mccflike protein (ba_5613); <b>PDBTitle:</b> crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames
35	<a href="#">c5vevB_</a>	Alignment	not modelled	9.5	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
36	<a href="#">d1udsa2</a>	Alignment	not modelled	9.1	20	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
37	<a href="#">c2ys6A_</a>	Alignment	not modelled	9.1	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide synthetase; <b>PDBTitle:</b> crystal structure of gar synthetase from geobacillus kaustophilus
38	<a href="#">c5usrC_</a>	Alignment	not modelled	8.8	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
39	<a href="#">d2qn6b1</a>	Alignment	not modelled	8.5	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eIF-2-alpha, C-terminal domain <b>Family:</b> eIF-2-alpha, C-terminal domain
40	<a href="#">d1v8ca2</a>	Alignment	not modelled	8.3	18	<b>Fold:</b> TBP-like <b>Superfamily:</b> MoaD-related protein, C-terminal domain <b>Family:</b> MoaD-related protein, C-terminal domain
41	<a href="#">d1m5q1_</a>	Alignment	not modelled	8.1	10	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Sm motif of small nuclear ribonucleoproteins, SNRNP
42	<a href="#">c2obaE_</a>	Alignment	not modelled	8.1	21	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> probable 6-pyruvoyl tetrahydrobiopterin synthase; <b>PDBTitle:</b> pseudomonas aeruginosa 6-pyruvoyl tetrahydrobiopterin synthase
43	<a href="#">c3okqA_</a>	Alignment	not modelled	8.0	30	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bud site selection protein 6; <b>PDBTitle:</b> crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
44	<a href="#">d1rpma_</a>	Alignment	not modelled	7.9	17	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
45	<a href="#">c2w2rA_</a>	Alignment	not modelled	7.9	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> matrix protein; <b>PDBTitle:</b> structure of the vesicular stomatitis virus matrix protein
46	<a href="#">c2xd4A_</a>	Alignment	not modelled	7.5	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
47	<a href="#">d2k49a2</a>	Alignment	not modelled	7.5	27	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
48	<a href="#">c1zrsB_</a>	Alignment	not modelled	7.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> wild-type ld-carboxypeptidase
49	<a href="#">c2n73B_</a>	Alignment	not modelled	7.4	31	<b>PDB header:</b> transferase/transferase regulator <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 4-kinase beta; <b>PDBTitle:</b> solution structure of the acbd3:pi4kb complex
50	<a href="#">c2bijA_</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase, non-receptor type 5; <b>PDBTitle:</b> crystal structure of the human protein tyrosine phosphatase ptpn52 (step, striatum enriched enriched phosphatase)
51	<a href="#">d1uwda_</a>	Alignment	not modelled	6.5	19	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
52	<a href="#">c1ceuA_</a>	Alignment	not modelled	6.4	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hiv-1 regulatory protein n-terminal) <b>PDBTitle:</b> nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
53	<a href="#">c6q2zB_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0339 family protein; <b>PDBTitle:</b> nmr solution structure of the hvo_2922 protein from haloferax volcanii
54	<a href="#">c3e7wA_</a>	Alignment	not modelled	6.3	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine--poly(phosphoribitol) ligase subunit 1; <b>PDBTitle:</b> crystal structure of dlta: implications for the reaction mechanism of 2 non-ribosomal peptide synthetase (nrps) adenylation domains

55	<a href="#">c3cb4D_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> the crystal structure of lepa
56	<a href="#">d1larb1</a>	Alignment	not modelled	6.3	24	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
57	<a href="#">c2kl8A_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> or15; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
58	<a href="#">c4bnqA_</a>	Alignment	not modelled	6.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-canonical purine ntp pyrophosphatase; <b>PDBTitle:</b> the structure of the staphylococcus aureus ham1 protein
59	<a href="#">d2k8ea1</a>	Alignment	not modelled	6.2	20	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
60	<a href="#">c4txdA_</a>	Alignment	not modelled	6.1	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> csc2; <b>PDBTitle:</b> crystal structure of thermofilum pendens csc2
61	<a href="#">d2k49a1</a>	Alignment	not modelled	6.1	13	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
62	<a href="#">c4h1hb_</a>	Alignment	not modelled	6.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1638 protein; <b>PDBTitle:</b> crystal structure of mccf homolog from listeria monocytogenes egd-e
63	<a href="#">d1b66a_</a>	Alignment	not modelled	5.9	25	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> 6-pyruvoyl tetrahydropterin synthase
64	<a href="#">c3d8dA_</a>	Alignment	not modelled	5.9	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 precursor protein-binding family b member <b>PDBTitle:</b> crystal structure of the human fe65-ptb1 domain
65	<a href="#">d1lg7a_</a>	Alignment	not modelled	5.9	31	<b>Fold:</b> VSV matrix protein <b>Superfamily:</b> VSV matrix protein <b>Family:</b> VSV matrix protein
66	<a href="#">c3tlgB_</a>	Alignment	not modelled	5.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mccf; <b>PDBTitle:</b> microcin c7 self immunity protein mccf in the inactive mutant apo2 state
67	<a href="#">d3bida1</a>	Alignment	not modelled	5.8	20	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
68	<a href="#">c4az1B_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine specific protein phosphatase; <b>PDBTitle:</b> crystal structure of the trypanosoma cruzi protein tyrosine2 phosphatase tcptp1, a potential therapeutic target for chagas'3 disease
69	<a href="#">d2k8ea2</a>	Alignment	not modelled	5.7	13	<b>Fold:</b> YegP-like <b>Superfamily:</b> YegP-like <b>Family:</b> YegP-like
70	<a href="#">d2gz1a2</a>	Alignment	not modelled	5.7	24	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
71	<a href="#">c3gjzB_</a>	Alignment	not modelled	5.7	21	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> microcin immunity protein mccf; <b>PDBTitle:</b> crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
72	<a href="#">c2h04A_</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine phosphatase, receptor type, b,; <b>PDBTitle:</b> structural studies of protein tyrosine phosphatase beta catalytic2 domain in complex with inhibitors
73	<a href="#">c5irdA_</a>	Alignment	not modelled	5.5	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytud.17486.a
74	<a href="#">c2i75A_</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 4; <b>PDBTitle:</b> crystal structure of human protein tyrosine phosphatase n4 (ptpn4)
75	<a href="#">d1q8ka2</a>	Alignment	not modelled	5.5	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> eIF-2-alpha, C-terminal domain <b>Family:</b> eIF-2-alpha, C-terminal domain
76	<a href="#">d1jlna_</a>	Alignment	not modelled	5.4	28	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Higher-molecular-weight phosphotyrosine protein phosphatases
77	<a href="#">c4ra6A_</a>	Alignment	not modelled	5.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase; <b>PDBTitle:</b> crystal structure of linker less pyrococcus furiosus l-asparaginase
78	<a href="#">c3o6qD_</a>	Alignment	not modelled	5.2	32	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> stage ii sporulation protein sb; <b>PDBTitle:</b> the structure of spoisa and spoisb, a toxin - antitoxin system
79	<a href="#">c3jrIA_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oncogenic tyrosine phosphatase shp2; <b>PDBTitle:</b> crystal structure of the oncogenic tyrosine phosphatase shp2 complexed2 with a salicylic acid-based small molecule inhibitor