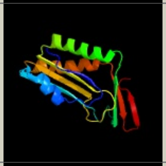
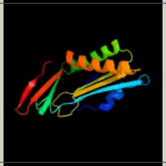
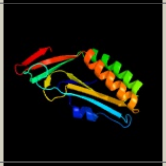
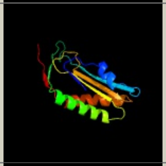
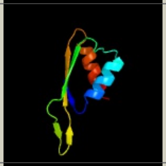
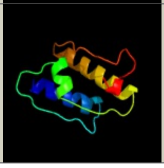
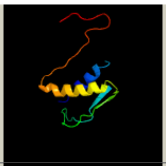
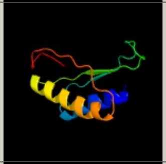
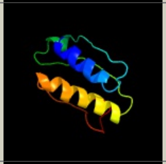
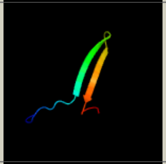
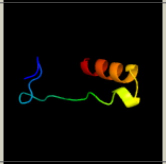
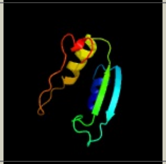
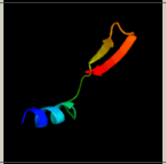
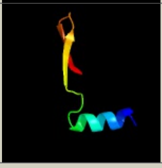
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD0866_(moaE2)_963872_964297
Date	Fri Jul 26 01:50:45 BST 2019
Unique Job ID	0308b54a876e0af2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6jbzC_	Alignment		100.0	100	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdenum cofactor biosynthesis protein e; **PDBTitle:** structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
2	c6jc0D_	Alignment		100.0	65	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative molybdenum cofactor biosynthesis protein; **PDBTitle:** structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
3	c2qieA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin-converting factor subunit 2; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex with precursor2 z
4	c2omdB_	Alignment		100.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**molybdopterin-converting factor subunit 2; **PDBTitle:** crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
5	c4ap8A_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin synthase catalytic subunit; **PDBTitle:** crystal structure of human molybdopterin synthase catalytic subunit2 (mocs2b)
6	d1fm0e_	Alignment		100.0	28	**Fold:**alpha/beta-Hammerhead **Superfamily:**Molybdopterin synthase subunit MoaE **Family:**Molybdopterin synthase subunit MoaE
7	c3rpfB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase catalytic subunit; **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
8	c2wp4A_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin-converting factor subunit 2 1; **PDBTitle:** crystal structure of rv3119 from mycobacterium tuberculosis
9	d1nvja_	Alignment		100.0	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**Molybdopterin synthase subunit MoaE **Family:**Molybdopterin synthase subunit MoaE
10	c1v8cA_	Alignment		98.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
11	c3upsA_	Alignment		76.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis

12	d1sq1a_	Alignment		56.8	14	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
13	c4wcwB_	Alignment		54.3	15	**PDB header:**translation **Chain:** B: **PDB Molecule:**ribosomal silencing factor rsfs; **PDBTitle:** ribosomal silencing factor during starvation or stationary phase2 (rsfs) from mycobacterium tuberculosis
14	d2o5aa1	Alignment		50.7	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
15	d2id1a1	Alignment		50.3	16	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
16	c4gzvH_	Alignment		45.2	18	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a lipocalin family protein (bacova_00364) from2 bacteroides ovatus atcc 8483 at 1.95 a resolution
17	c1zcoA_	Alignment		25.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
18	c5oomu_	Alignment		23.7	15	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**39s ribosomal protein l23, mitochondrial; **PDBTitle:** structure of a native assembly intermediate of the human mitochondrial2 ribosome with unfolded interfacial rrna
19	c2k8eA_	Alignment		21.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
20	c2k49A_	Alignment		21.7	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
21	c2z4tA_	Alignment	not modelled	18.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-galactoside alpha-2,6-sialyltransferase; **PDBTitle:** crystal structure of vibrionaceae photobacterium sp. jt-ish-224 2,6-2 sialyltransferase in a ternary complex with donor product cmp and3 accepter substrate lactose
22	d1m5q1_	Alignment	not modelled	15.9	13	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
23	c3lvmB_	Alignment	not modelled	15.9	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cysteine desulfurase; **PDBTitle:** crystal structure of e.coli iscs
24	c4e5sC_	Alignment	not modelled	15.7	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mccflike protein (ba_5613); **PDBTitle:** crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames
25	d1xmba2	Alignment	not modelled	15.0	19	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
26	c5usrG_	Alignment	not modelled	14.7	19	**PDB header:**transferase **Chain:** G: **PDB Molecule:**cysteine desulfurase, mitochondrial; **PDBTitle:** crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
27	d2dy1a5	Alignment	not modelled	14.1	23	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
28	c5intB_	Alignment	not modelled	14.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphopantothenate--cysteine ligase; **PDBTitle:** crystal structure of the c-terminal domain of coenzyme a biosynthesis2 bifunctional protein coabc

29	d1uwda_	Alignment	not modelled	13.3	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
30	d1p3wa_	Alignment	not modelled	13.1	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
31	d2gnoa1	Alignment	not modelled	12.8	17	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
32	c4qjiB_	Alignment	not modelled	12.7	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphopantothenate--cysteine ligase; **PDBTitle:** crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
33	c5z9aB_	Alignment	not modelled	12.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**chorismate synthase; **PDBTitle:** crystal structure of chorismate synthase from pseudomonas aeruginosa
34	d2k49a2	Alignment	not modelled	11.4	12	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
35	c4h1hB_	Alignment	not modelled	11.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo1638 protein; **PDBTitle:** crystal structure of mccf homolog from listeria monocytogenes egd-e
36	c4ikcA_	Alignment	not modelled	11.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphotidylinositol phosphatase ptprq; **PDBTitle:** crystal structure of catalytic domain of ptprq
37	c3tlgB_	Alignment	not modelled	10.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mccf; **PDBTitle:** microcin c7 self immunity protein mccf in the inactive mutant apo2 state
38	c3e7wA_	Alignment	not modelled	10.6	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--poly(phosphoribitol) ligase subunit 1; **PDBTitle:** crystal structure of dlta: implications for the reaction mechanism of2 non-ribosomal peptide synthetase (nrps) adenylation domains
39	c3d8dA_	Alignment	not modelled	10.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family b member **PDBTitle:** crystal structure of the human fe65-ptb1 domain
40	c1zrsB_	Alignment	not modelled	10.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
41	d1udsa2	Alignment	not modelled	10.1	16	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
42	c3gjzB_	Alignment	not modelled	10.1	6	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
43	c5vevB_	Alignment	not modelled	10.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from neisseria2 gonorrhoeae
44	c3okqA_	Alignment	not modelled	9.7	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
45	c5usrC_	Alignment	not modelled	9.6	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**cysteine desulfurase, mitochondrial; **PDBTitle:** crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
46	c2kouA_	Alignment	not modelled	9.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dicer-like protein 4; **PDBTitle:** dicer like protein
47	d2od6a1	Alignment	not modelled	9.4	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Marine metagenome family DABB1
48	d2burb1	Alignment	not modelled	9.4	21	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
49	c2xd4A_	Alignment	not modelled	9.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
50	c1tmxA_	Alignment	not modelled	8.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from nocardioides2 simplex 3e
51	c2boyC_	Alignment	not modelled	8.8	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from rhodococcus2 opacus 1cp
52	c6q2zB_	Alignment	not modelled	8.7	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0339 family protein; **PDBTitle:** nmr solution structure of the hvo_2922 protein from haloferax volcanii
53	c2b9kA_	Alignment	not modelled	8.7	25	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**antimicrobial peptide lci; **PDBTitle:** solution structure of lci, an amp from bacillus subtilis
54	d1rpma	Alignment	not modelled	8.6	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II

54	d1rpma_	Alignment	not modelled	8.6	14	**Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
55	d2acya_	Alignment	not modelled	7.9	10	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
56	d2dkya1	Alignment	not modelled	7.6	33	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
57	c4ra6A_	Alignment	not modelled	7.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of linker less pyrococcus furiosus l-asparaginase
58	d2k8ea1	Alignment	not modelled	7.6	7	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
59	c5irdA_	Alignment	not modelled	7.5	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 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
60	d1n0ua5	Alignment	not modelled	7.5	16	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
61	d2k49a1	Alignment	not modelled	7.4	0	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
62	d3bida1	Alignment	not modelled	7.3	27	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
63	d2k8ea2	Alignment	not modelled	7.2	13	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
64	c3th1C_	Alignment	not modelled	7.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of chlorocatechol 1,2-dioxygenase from pseudomonas2 putida
65	c2n73B_	Alignment	not modelled	6.6	31	**PDB header:**transferase/transferase regulator **Chain:** B: **PDB Molecule:**phosphatidylinositol 4-kinase beta; **PDBTitle:** solution structure of the acbd3:pi4kb complex
66	c2bijA_	Alignment	not modelled	6.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase, non-receptor type 5; **PDBTitle:** crystal structure of the human protein tyrosine phosphatase ptpn52 (step, striatum enriched enriched phosphatase)
67	d1larb1	Alignment	not modelled	6.5	21	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
68	d2qn6b1	Alignment	not modelled	6.5	10	**Fold:**Ferredoxin-like **Superfamily:**eIF-2-alpha, C-terminal domain **Family:**eIF-2-alpha, C-terminal domain
69	c2c7sA_	Alignment	not modelled	6.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**receptor-type tyrosine-protein phosphatase kappa; **PDBTitle:** crystal structure of human protein tyrosine phosphatase kappa at 1.95a2 resolution
70	c2qdmA_	Alignment	not modelled	6.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 7; **PDBTitle:** crystal structure of the heptp catalytic domain c270s/d236a/q314a2 mutant
71	c3degC_	Alignment	not modelled	6.2	33	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
72	d2k7ia1	Alignment	not modelled	5.8	27	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
73	c2k7iB_	Alignment	not modelled	5.8	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0339 protein atu0232; **PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
74	c2h04A_	Alignment	not modelled	5.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase, receptor type, b,; **PDBTitle:** structural studies of protein tyrosine phosphatase beta catalytic2 domain in complex with inhibitors
75	c3jrlA_	Alignment	not modelled	5.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oncogenic tyrosine phosphatase shp2; **PDBTitle:** crystal structure of the oncogenic tyrosine phosphatase shp2 complexed2 with a salicylic acid-based small molecule inhibitor
76	d2h80a1	Alignment	not modelled	5.7	21	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
77	c4bnqA_	Alignment	not modelled	5.6	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** the structure of the staphylococcus aureus ham1 protein
78	c4ilvB_	Alignment	not modelled	5.5	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**intradiol ring-cleavage dioxygenase; **PDBTitle:** structure of the dioxygenase domain of sacte_2871, a novel dioxygenase2 carbohydrate-binding protein fusion from the

						cellulolytic bacterium3 streptomyces sp. sirexaa-e
79	d1jb3a_	Alignment	not modelled	5.5	25	**Fold:**OB-fold **Superfamily:**TIMP-like **Family:**The laminin-binding domain of agrin
80	c2i75A_	Alignment	not modelled	5.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 4; **PDBTitle:** crystal structure of human protein tyrosine phosphatase n4 (ptpn4)
81	c3cb4D_	Alignment	not modelled	5.4	26	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
82	d2auna2	Alignment	not modelled	5.3	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
83	d1yfoa_	Alignment	not modelled	5.2	19	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
84	d1u7za_	Alignment	not modelled	5.2	24	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
85	c4czdD_	Alignment	not modelled	5.2	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative transcriptional regulator, asnc family; **PDBTitle:** sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
86	c2w2rA_	Alignment	not modelled	5.2	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** structure of the vesicular stomatitis virus matrix protein
87	c4d56A_	Alignment	not modelled	5.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**apnaa1; **PDBTitle:** understanding bi-specificity of a-domains
88	c3eplA_	Alignment	not modelled	5.1	10	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
89	d2cu6a1	Alignment	not modelled	5.0	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like