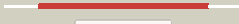



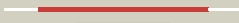












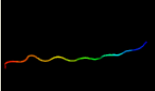


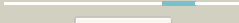

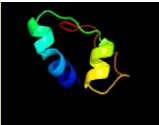


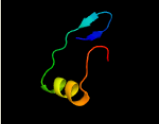



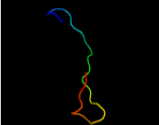
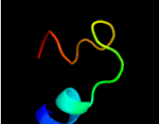


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3324c_(moaC)_3709886_3710419
 Date Thu Aug 8 16:20:53 BST 2019
 Unique Job ID 91b3b47a6f93ddb9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eeyA_	 Alignment		100.0	49	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis; PDBTitle: structure of gk0241 protein from geobacillus kaustophilus
2	c2ideE_	 Alignment		100.0	50	PDB header: biosynthetic protein Chain: E: PDB Molecule: molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus thermophilus hb8
3	d1ekra_	 Alignment		100.0	57	Fold: Ferredoxin-like Superfamily: Molybdenum cofactor biosynthesis protein C, MoaC Family: Molybdenum cofactor biosynthesis protein C, MoaC
4	c4fdFB_	 Alignment		100.0	52	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdenum cofactor biosynthesis protein c 2; PDBTitle: structural insights into putative molybdenum cofactor biosynthesis2 protein c (moac2) from mycobacterium tuberculosis h37rv
5	c2eknC_	 Alignment		100.0	45	PDB header: biosynthetic protein Chain: C: PDB Molecule: probable molybdenum cofactor biosynthesis protein c; PDBTitle: structure of ph1811 protein from pyrococcus horikoshii
6	c2ohdB_	 Alignment		100.0	42	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable molybdenum cofactor biosynthesis protein c; PDBTitle: crystal structure of hypothetical molybdenum cofactor biosynthesis2 protein c from sulfolobus tokodaii
7	c2lqjA_	 Alignment		62.3	25	PDB header: hydrolase Chain: A: PDB Molecule: mg2+ transport protein; PDBTitle: solution structure of the c-terminal domain of the mgtc protein from2 mycobacterium tuberculosis
8	c4o9uB_	 Alignment		53.0	32	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
9	d1oh4a_	 Alignment		35.9	36	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 27 carbohydrate binding module, CBM27
10	c4bhcA_	 Alignment		32.2	22	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r371 variant
11	c4o9tH_	 Alignment		32.0	32	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer

12	c1sfeA	Alignment		31.7	17	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
13	c6m9kD	Alignment		30.1	22	PDB header: hydrolase Chain: D: PDB Molecule: recombination protein bet; PDBTitle: crystal structure of lambda exonuclease in complex with the red beta2 c-terminal domain
14	c3ct5A	Alignment		23.4	25	PDB header: hydrolase Chain: A: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
15	d2cqaa1	Alignment		17.8	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
16	d1bu2a2	Alignment		15.4	53	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
17	c2b51C	Alignment		15.0	17	PDB header: protein binding/viral protein Chain: C: PDB Molecule: nonstructural protein v; PDBTitle: crystal structure of ddb1 in complex with simian virus 5 v2 protein
18	c3bdqB	Alignment		13.2	19	PDB header: lipid transport Chain: B: PDB Molecule: sterol carrier protein 2-like 2; PDBTitle: room temperature crystal structure of sterol carrier protein-2 2 like-2
19	d2ia9a1	Alignment		11.9	29	Fold: SpoVG-like Superfamily: SpoVG-like Family: SpoVG-like
20	c4zyeA	Alignment		11.8	21	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
21	d1vqon1	Alignment	not modelled	11.6	24	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
22	c5xyiZ	Alignment	not modelled	11.4	38	PDB header: ribosome Chain: Z: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
23	c2p0xA	Alignment	not modelled	11.0	63	PDB header: de novo protein Chain: A: PDB Molecule: abiotic atp-binding, folding optimized protein; PDBTitle: solution structure of a non-biological atp-binding protein
24	c6gboG	Alignment	not modelled	10.4	32	PDB header: viral protein Chain: G: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from ebola2 virus
25	d2gp4a1	Alignment	not modelled	10.4	20	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
26	d1ikta	Alignment	not modelled	10.2	17	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
27	d2i9xa1	Alignment	not modelled	10.2	43	Fold: SpoVG-like Superfamily: SpoVG-like Family: SpoVG-like
28	c2i9zB	Alignment	not modelled	10.2	43	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative septation protein spovg; PDBTitle: structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
29	c4p96B	Alignment	not modelled	10.2	18	PDB header: transcription Chain: B: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from vibrio

						cholerae
30	c3pn1A_	Alignment	not modelled	10.1	19	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: dna ligase; PDBTitle: novel bacterial nad ⁺ -dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
31	c5tj5P_	Alignment	not modelled	9.4	63	PDB header: motor protein Chain: P: PDB Molecule: v-type proton atpase subunit d; PDBTitle: atomic model for the membrane-embedded motor of a eukaryotic v-atpase
32	c5ounA_	Alignment	not modelled	9.1	16	PDB header: hydrolase Chain: A: PDB Molecule: rvvb-like protein 2; PDBTitle: nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
33	c2gp4A_	Alignment	not modelled	8.6	20	PDB header: lyase Chain: A: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
34	c4bjjA_	Alignment	not modelled	8.5	29	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau subunit sfc1; PDBTitle: sfc1-sfc7 dimerization module
35	c2p09A_	Alignment	not modelled	8.4	63	PDB header: de novo protein Chain: A: PDB Molecule: a non-biological atp binding protein with two mutations PDBTitle: structural insights into the evolution of a non-biological protein
36	d1pz4a_	Alignment	not modelled	8.4	14	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
37	d1j2ga2	Alignment	not modelled	8.3	10	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
38	d2ibaa2	Alignment	not modelled	8.2	25	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
39	c1u00A_	Alignment	not modelled	7.9	25	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein hsca; PDBTitle: hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkhhc
40	c5z62N_	Alignment	not modelled	7.6	54	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
41	c6gbrA_	Alignment	not modelled	7.5	21	PDB header: viral protein Chain: A: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
42	d1uufa2	Alignment	not modelled	7.3	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
43	c2xuvB_	Alignment	not modelled	7.3	22	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
44	c4zv3B_	Alignment	not modelled	7.0	11	PDB header: hydrolase Chain: B: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of the n- and c-terminal domains of mouse acyl-coa2 thioesterase 7
45	c2ketA_	Alignment	not modelled	7.0	45	PDB header: antibiotic Chain: A: PDB Molecule: cathelicidin-6; PDBTitle: solution structure of bmap-27
46	c2xskA_	Alignment	not modelled	7.0	24	PDB header: chaperone Chain: A: PDB Molecule: csgc; PDBTitle: e. coli curli protein csgc - secys
47	c2gp4B_	Alignment	not modelled	6.9	20	PDB header: lyase Chain: B: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
48	d1vlfn1	Alignment	not modelled	6.9	24	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
49	d2yzca2	Alignment	not modelled	6.7	33	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
50	c2kc5A_	Alignment	not modelled	6.5	20	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase-2 operon protein hybe; PDBTitle: solution structure of hybe from escherichia coli
51	c6a4mA_	Alignment	not modelled	6.4	20	PDB header: hydrolase Chain: A: PDB Molecule: uric acid degradation bifunctional protein pucl; PDBTitle: structure of urate oxidase from bacillus subtilis 168
52	c4lp7C_	Alignment	not modelled	6.1	40	PDB header: calcium binding protein Chain: C: PDB Molecule: matrix protein m; PDBTitle: crystal structure of the human metapneumovirus matrix protein
53	d1cq3a_	Alignment	not modelled	6.0	67	Fold: Soluble secreted chemokine inhibitor, VCCI Superfamily: Soluble secreted chemokine inhibitor, VCCI Family: Soluble secreted chemokine inhibitor, VCCI
54	c5wlpA_	Alignment	not modelled	5.9	31	PDB header: protein transport Chain: A: PDB Molecule: autophagy-related protein 32; PDBTitle: solution structure of the pseudo-receiver domain of atg32
55	d4bcia_	Alignment	not modelled	5.8	23	Fold: Bacteriochlorophyll A protein Superfamily: Bacteriochlorophyll A protein Family: Bacteriochlorophyll A protein

56	d1vpba_	Alignment	not modelled	5.6	12	Fold: Putative modulator of DNA gyrase, PmbA/TldD Superfamily: Putative modulator of DNA gyrase, PmbA/TldD Family: Putative modulator of DNA gyrase, PmbA/TldD
57	c1yx3A_	Alignment	not modelled	5.6	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrc; PDBTitle: nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
58	d1juva_	Alignment	not modelled	5.4	5	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
59	c2vdaB_	Alignment	not modelled	5.4	46	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
60	d1dkza2	Alignment	not modelled	5.3	17	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
61	c2fqcA_	Alignment	not modelled	5.3	75	PDB header: toxin Chain: A: PDB Molecule: conotoxin pl14a; PDBTitle: solution structure of conotoxin pl14a
62	c2navA_	Alignment	not modelled	5.3	75	PDB header: toxin Chain: A: PDB Molecule: exendin-4, alpha/kappa-conotoxin pl14a chimera; PDBTitle: nmr solution structure of ex-4[1-16]/pl14a
63	c2mtpB_	Alignment	not modelled	5.2	17	PDB header: protein binding/cell adhesion Chain: B: PDB Molecule: integrin alpha-iib; PDBTitle: the structure of filamin repeat 21 bound to integrin
64	c1s4wA_	Alignment	not modelled	5.2	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: nmr structure of the cytoplasmic domain of integrin aiib in2 dpc micelles
65	c1dpkA_	Alignment	not modelled	5.2	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib subunit; PDBTitle: solution structure of the cytoplasmic domain of the2 integrin alpha-iib subunit
66	c1m8oA_	Alignment	not modelled	5.2	17	PDB header: membrane protein Chain: A: PDB Molecule: platelet integrin alfa-iib subunit: cytoplasmic PDBTitle: platelet integrin alfa-iib-beta3 cytoplasmic domain