












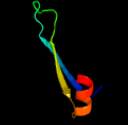

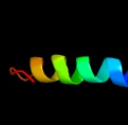

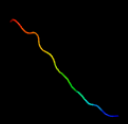
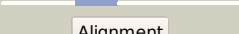

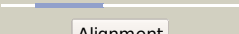



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3111_(moaC)_3479168_3479680
 Date Thu Aug 8 16:20:29 BST 2019
 Unique Job ID 945e74257daa43a8

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	51	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	59	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	43	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	43	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		65.5	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		45.2	27	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		30.6	29	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 27 carbohydrate binding module, CBM27
10	c6m9kD_	 Alignment		24.0	25	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
11	c3ct5A_	 Alignment		20.2	28	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

12	c4o9tH_	Alignment		19.7	27	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
13	d2cqaa1	Alignment		15.9	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
14	d1bu2a2	Alignment		12.9	47	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
15	c4bhca_	Alignment		11.2	16	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r37l variant
16	c1sfeA_	Alignment		10.6	37	PDB header: dna-binding protein Chain: A: PDB Molecule: ada o6-methylguanine-dna methyltransferase; PDBTitle: ada o6-methylguanine-dna methyltransferase from escherichia coli
17	c4zycA_	Alignment		10.5	21	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine methyltransferase; PDBTitle: crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
18	c2b51C_	Alignment		9.8	31	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
19	d1vqon1	Alignment		9.7	21	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
20	c2xskA_	Alignment		8.9	38	PDB header: chaperone Chain: A: PDB Molecule: csgc; PDBTitle: e. coli curli protein csgc - secys
21	c5xyiZ_	Alignment	not modelled	8.8	46	PDB header: ribosome Chain: Z: PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
22	c5tj5P_	Alignment	not modelled	8.6	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
23	d1j2ga2	Alignment	not modelled	8.4	15	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
24	c4p96B_	Alignment	not modelled	8.2	18	PDB header: transcription Chain: B: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from vibrio cholerae
25	c3pn1A_	Alignment	not modelled	8.2	22	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
26	c4bjjA_	Alignment	not modelled	8.1	29	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau subunit sfc1; PDBTitle: sfc1-sfc7 dimerization module
27	c3bdqB_	Alignment	not modelled	8.0	24	PDB header: lipid transport Chain: B: PDB Molecule: sterol carrier protein 2-like 2; PDBTitle: room temperture crystal structure of sterol carrier protein-2 2 like-2
28	d1uufa2	Alignment	not modelled	7.6	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
						Fold: T-fold

29	d2ibaa2	Alignment	not modelled	7.6	25	Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
30	d1ikta	Alignment	not modelled	7.5	18	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
31	c5ounA	Alignment	not modelled	7.4	13	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like protein 2; PDBTitle: nmr solution structure of the external dii domain of ruvb2 from2 saccharomyces cerevisiae
32	d2yzca2	Alignment	not modelled	7.3	40	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
33	c2kc5A	Alignment	not modelled	7.3	20	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase-2 operon protein hybe; PDBTitle: solution structure of hybe from escherichia coli
34	c1wrjA	Alignment	not modelled	7.2	21	PDB header: transferase Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
35	d2gp4a1	Alignment	not modelled	6.7	25	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
36	c2p0xA	Alignment	not modelled	6.7	75	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
37	c2ketA	Alignment	not modelled	6.6	45	PDB header: antibiotic Chain: A: PDB Molecule: cathelicidin-6; PDBTitle: solution structure of bmap-27
38	c6a4mA	Alignment	not modelled	6.4	15	PDB header: hydrolase Chain: A: PDB Molecule: uric acid degradation bifunctional protein pucl; PDBTitle: structure of urate oxidase from bacillus subtilis 168
39	c5z62N	Alignment	not modelled	6.4	54	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
40	c1t39A	Alignment	not modelled	6.3	32	PDB header: transferase/dna Chain: A: PDB Molecule: methylated-dna--protein-cysteine PDBTitle: human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
41	c4eyzB	Alignment	not modelled	6.3	36	PDB header: hydrolase Chain: B: PDB Molecule: cellulosome-related protein module from ruminococcus PDBTitle: crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases
42	c2vdaB	Alignment	not modelled	5.9	38	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
43	d1pz4a	Alignment	not modelled	5.8	18	Fold: SCP-like Superfamily: SCP-like Family: Sterol carrier protein, SCP
44	c2xuvB	Alignment	not modelled	5.7	22	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
45	c2vgmA	Alignment	not modelled	5.7	12	PDB header: cell cycle Chain: A: PDB Molecule: dom34; PDBTitle: structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
46	d1vfn1	Alignment	not modelled	5.6	24	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
47	d4bcla	Alignment	not modelled	5.5	23	Fold: Bacteriochlorophyll A protein Superfamily: Bacteriochlorophyll A protein Family: Bacteriochlorophyll A protein
48	c6gboG	Alignment	not modelled	5.5	26	PDB header: viral protein Chain: G: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from ebola2 virus
49	c2gp4A	Alignment	not modelled	5.5	25	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
50	d1of5b	Alignment	not modelled	5.2	7	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like