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Description	RVBD0864_(moaC)_962893_963396
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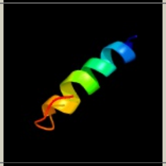
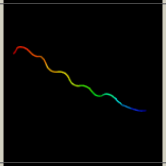
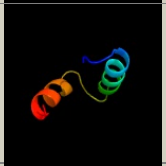
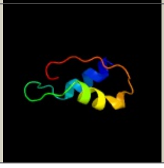
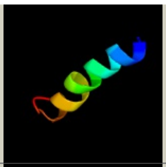
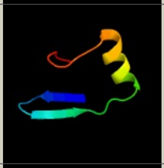
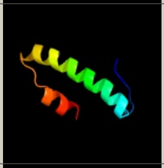
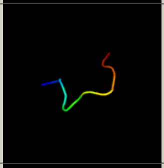
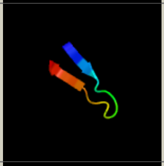
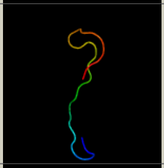
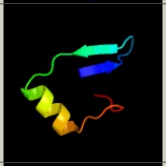
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eeyA_	Alignment		100.0	48	**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 theromophilus hb8
3	d1ekra_	Alignment		100.0	51	**Fold:**Ferredoxin-like **Superfamily:**Molybdenum cofactor biosynthesis protein C, MoaC **Family:**Molybdenum cofactor biosynthesis protein C, MoaC
4	c4fdfB_	Alignment		100.0	98	**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	47	**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		62.0	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		51.3	23	**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		36.4	36	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 27 carbohydrate binding module, CBM27
10	c6m9kD_	Alignment		31.3	31	**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	c4bhcA_	Alignment		31.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine methyltransferase; **PDBTitle:** crystal structure of the m. tuberculosis o6-methylguanine2 methyltransferase r37l variant

12	c4o9tH_	Alignment		30.3	23	**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		24.2	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
14	c3ct5A_	Alignment		18.2	18	**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	c2b5lC_	Alignment		15.9	42	**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
16	c6bbqA_	Alignment		15.5	64	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**cytohesin-3,adp-ribosylation factor 6; **PDBTitle:** model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
17	d2ia9a1	Alignment		14.5	33	**Fold:**SpoVG-like **Superfamily:**SpoVG-like **Family:**SpoVG-like
18	d1bu2a2	Alignment		14.4	47	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
19	c5ounA_	Alignment		14.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ruvb-like protein 2; **PDBTitle:** nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
20	c4zyeA_	Alignment		12.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine methyltransferase; **PDBTitle:** crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
21	d2i9xa1	Alignment	not modelled	12.2	38	**Fold:**SpoVG-like **Superfamily:**SpoVG-like **Family:**SpoVG-like
22	c2i9zB_	Alignment	not modelled	12.2	38	**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
23	c3pn1A_	Alignment	not modelled	11.9	16	**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
24	c4p96B_	Alignment	not modelled	11.5	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**fatty acid metabolism regulator protein; **PDBTitle:** fadr, fatty acid responsive transcription factor from vibrio cholerae
25	c5xyiZ_	Alignment	not modelled	11.4	38	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**uncharacterized protein; **PDBTitle:** small subunit of trichomonas vaginalis ribosome
26	d1vqon1	Alignment	not modelled	11.3	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
27	d2gp4a1	Alignment	not modelled	10.9	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
28	d2f1fa2	Alignment	not modelled	10.6	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
29	c2vqmA_	Alignment	not modelled	10.5	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34;

29	c2vgmA_	Alignment	not modelled	10.5	10	**PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
30	c5tj5P_	Alignment	not modelled	10.2	38	**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
31	c2gp4A_	Alignment	not modelled	9.2	13	**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
32	c3bdqB_	Alignment	not modelled	9.2	17	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**sterol carrier protein 2-like 2; **PDBTitle:** room tempreture crystal structure of sterol carrier protein-2 2 like-2
33	c2xuvB_	Alignment	not modelled	8.9	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hdeb; **PDBTitle:** the structure of hdeb
34	c2gp4B_	Alignment	not modelled	8.8	13	**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
35	c5z62N_	Alignment	not modelled	8.7	54	**PDB header:**electron transport **Chain:** N: **PDB Molecule:**cytochrome c oxidase subunit ndufa4; **PDBTitle:** structure of human cytochrome c oxidase
36	c1wrjA_	Alignment	not modelled	8.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** crystal structure of o6-methylguanine methyltransferase2 from sulfolobus tokodaii
37	d1pz4a_	Alignment	not modelled	8.6	18	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
38	d1ikta_	Alignment	not modelled	8.3	19	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
39	d1vlfn1	Alignment	not modelled	8.0	29	**Fold:**Prealbumin-like **Superfamily:**Cna protein B-type domain **Family:**Cna protein B-type domain
40	c4eyzB_	Alignment	not modelled	7.6	43	**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
41	c1t39A_	Alignment	not modelled	7.4	42	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** human o6-alkylguanine-dna alkyltransferase covalently2 crosslinked to dna
42	c2ketA_	Alignment	not modelled	7.2	55	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**cathelicidin-6; **PDBTitle:** solution structure of bmap-27
43	d4bcla_	Alignment	not modelled	7.0	36	**Fold:**Bacteriochlorophyll A protein **Superfamily:**Bacteriochlorophyll A protein **Family:**Bacteriochlorophyll A protein
44	d1juva_	Alignment	not modelled	6.9	9	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
45	d2pt0a1	Alignment	not modelled	6.9	27	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
46	c4lp7C_	Alignment	not modelled	6.5	53	**PDB header:**calcium binding protein **Chain:** C: **PDB Molecule:**matrix protein m; **PDBTitle:** crystal structure of the human metapneumovirus matrix protein
47	c1u00A_	Alignment	not modelled	6.1	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
48	d1dgsa3	Alignment	not modelled	6.0	15	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
49	c6gboG_	Alignment	not modelled	5.9	26	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** crystal structure of the oligomerization domain of vp35 from ebola2 virus
50	c5wlpA_	Alignment	not modelled	5.7	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**autophagy-related protein 32; **PDBTitle:** solution structure of the pseudo-receiver domain of atg32
51	c2navA_	Alignment	not modelled	5.7	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
52	c2p0xA_	Alignment	not modelled	5.6	50	**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
53	c2kc5A_	Alignment	not modelled	5.6	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase-2 operon protein hybe; **PDBTitle:** solution structure of hybe from escherichia coli
54	c2vdaB_	Alignment	not modelled	5.5	54	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
55	d1of5b_	Alignment	not modelled	5.4	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like

						Family:NTF2-like
56	c2fqcA_	Alignment	not modelled	5.3	75	**PDB header:**toxin **Chain:** A: **PDB Molecule:**conotoxin pl14a; **PDBTitle:** solution structure of conotoxin pl14a
57	c2eqgA_	Alignment	not modelled	5.2	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** solution structure of the first a20-type zinc finger domain2 from human tumor necrosis factor, alpha-induced protein3
58	d2bbya_	Alignment	not modelled	5.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding domain from rap30
59	c2kc1A_	Alignment	not modelled	5.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mkiaa1027 protein; **PDBTitle:** nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain