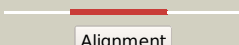

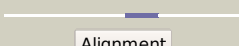

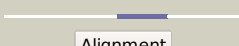


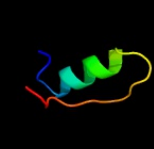





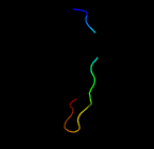

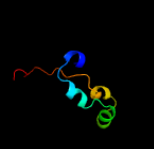

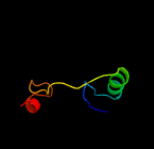

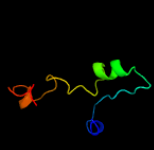

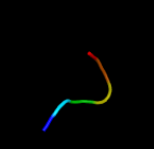


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3862c_(whiB6)_4338349_4338699
 Date Sat Aug 10 22:05:04 BST 2019
 Unique Job ID 84653757c4df0b19

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oayA_	 Alignment		97.8	29	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional regulator whib1; PDBTitle: m. tuberculosis [4fe-4s] protein whib1 is a four-helix bundle that2 forms a no-sensitive complex with sigmaa and regulates the major3 virulence factor esx-1
2	c3shgB_	 Alignment		15.0	44	PDB header: transferase/protein binding Chain: B: PDB Molecule: vbha; PDBTitle: vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin
3	c1fjnA_	 Alignment		14.5	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin mgd-1; PDBTitle: solution structure and activity of the four disulfide bond2 mediterranean mussel defensin mgd-1
4	d1fjna_	 Alignment		14.5	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Defensin MGD-1
5	d1vmda_	 Alignment		13.6	32	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
6	c5m73D_	 Alignment		12.8	80	PDB header: rna binding protein Chain: D: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
7	c3u2aA_	 Alignment		11.3	53	PDB header: hydrolase Chain: A: PDB Molecule: ggdef family protein; PDBTitle: adaptor dependent degradation of a cell-cycle regulator reveals2 diversity in substrate architectures
8	c4b2nB_	 Alignment		10.0	24	PDB header: electron transport Chain: B: PDB Molecule: 70 kda protein; PDBTitle: latex oxygenase roxa
9	c2hg4A_	 Alignment		9.7	26	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
10	c6c8vA_	 Alignment		9.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
11	c2pcoA_	 Alignment		8.6	33	PDB header: toxin Chain: A: PDB Molecule: latarcin-1; PDBTitle: spatial structure and membrane permeabilization for2 latarcin-1, a spider antimicrobial peptide

12	c1y7nA_	Alignment		8.2	31	PDB header: protein transport Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding family PDBTitle: solution structure of the second pdz domain of the human2 neuronal adaptor x11alpha
13	d1bm8a_	Alignment		8.1	33	Fold: DNA-binding domain of Mlu1-box binding protein MBP1 Superfamily: DNA-binding domain of Mlu1-box binding protein MBP1 Family: DNA-binding domain of Mlu1-box binding protein MBP1
14	d1prtc1	Alignment		7.4	39	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
15	c5m73H_	Alignment		7.2	60	PDB header: rna binding protein Chain: H: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
16	c3p8cD_	Alignment		7.1	40	PDB header: protein binding Chain: D: PDB Molecule: wiskott-aldrich syndrome protein family member 1; PDBTitle: structure and control of the actin regulatory wave complex
17	c4jvyA_	Alignment		7.0	35	PDB header: rna binding protein Chain: A: PDB Molecule: female germline-specific tumor suppressor gld-1; PDBTitle: structure of the star (signal transduction and activation of rna)2 domain of gld-1 bound to rna
18	c2ksnA_	Alignment		6.7	18	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin domain-containing protein 2; PDBTitle: solution structure of the n-terminal domain of dc-ubp/ubtd2
19	d2nx2a1	Alignment		6.5	29	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like
20	c3fptC_	Alignment		6.2	50	PDB header: immune system Chain: C: PDB Molecule: evasin-1; PDBTitle: the crystal structure of the complex between evasin-1 and2 ccl3
21	c4jvhA_	Alignment	not modelled	6.2	43	PDB header: rna binding protein Chain: A: PDB Molecule: protein quaking; PDBTitle: structure of the star domain of quaking protein in complex with rna
22	c1ihqA_	Alignment	not modelled	6.1	50	PDB header: de novo protein Chain: A: PDB Molecule: chimeric peptide glytm1bzip: tropomyosin alpha PDBTitle: glytm1bzip: a chimeric peptide model of the n-terminus of a2 rat short alpha tropomyosin with the n-terminus encoded by3 exon 1b
23	d1ra0a1	Alignment	not modelled	5.7	71	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Cytosine deaminase
24	c3danA_	Alignment	not modelled	5.7	20	PDB header: lyase Chain: A: PDB Molecule: cytochrome p450 74a2; PDBTitle: crystal structure of allene oxide synthase
25	d1u3ba2	Alignment	not modelled	5.6	31	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
26	c3kopB_	Alignment	not modelled	5.5	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
27	d1ixda_	Alignment	not modelled	5.3	16	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
28	c3c00B_	Alignment	not modelled	5.1	27	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: escu; PDBTitle: crystal structural of the mutated g247t escu/spas c-terminal domain PDB header: oxidoreductase

29	c3awmA_	Alignment	not modelled	5.1	26	Chain: A: PDB Molecule: fatty acid alpha-hydroxylase; PDBTitle: cytochrome p450sp alpha (cyp152b1) wild-type with palmitic acid
30	c2rrIA_	Alignment	not modelled	5.1	28	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik