


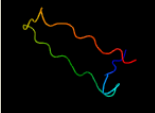






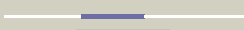
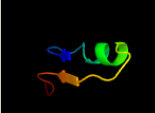



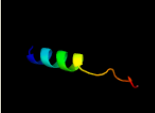



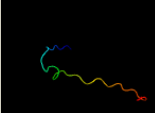

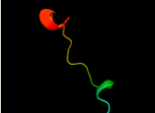


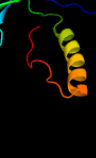





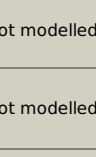


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1290A (-) _1445064_1445378
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	cf923f5b2a19c72a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6amgA_	 Alignment		23.5	26	PDB header: metal binding protein Chain: A; PDB Molecule: cytochrome p460; PDBTitle: cyt p460 of nitrosomonas sp. al212
2	c3sc0A_	 Alignment		18.9	30	PDB header: oxidoreductase Chain: A; PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
3	c1kn7A_	 Alignment		11.8	78	PDB header: membrane protein Chain: A; PDB Molecule: voltage-gated potassium channel protein kv1.4; PDBTitle: solution structure of the tandem inactivation domain2 (residues 1-75) of potassium channel rck4 (kv1.4)
4	c4blgB_	 Alignment		11.6	45	PDB header: viral protein Chain: B; PDB Molecule: latency-associated nuclear antigen; PDBTitle: crystal structure of mhv-68 latency-associated nuclear antigen (lana)2 c-terminal dna binding domain
5	c4k2jB_	 Alignment		11.1	64	PDB header: dna binding protein, viral protein Chain: B; PDB Molecule: kshv (hhv-8) latency-associated nuclear antigen (lana); PDBTitle: decameric ring structure of kshv (hhv-8) latency-associated nuclear2 antigen (lana) dna binding domain
6	c3cvoA_	 Alignment		10.7	31	PDB header: transferase Chain: A; PDB Molecule: methyltransferase-like protein of unknown function; PDBTitle: crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
7	c6db1A_	 Alignment		10.3	33	PDB header: transferase Chain: A; PDB Molecule: putative methyl-accepting chemotaxis protein; PDBTitle: 2.0 angstrom resolution crystal structure of n-terminal ligand-binding2 domain of putative methyl-accepting chemotaxis protein from3 salmonella enterica
8	c4wl2F_	 Alignment		10.1	33	PDB header: hydrolase Chain: F; PDB Molecule: putative exported choloylglycine hydrolase; PDBTitle: structure of penicillin v acylase from pectobacterium atrosepticum
9	c2rkqA_	 Alignment		10.0	19	PDB header: immune system Chain: A; PDB Molecule: peptidoglycan-recognition protein-sd; PDBTitle: crystal structure of drosophila peptidoglycan recognition2 protein sd (pgrp-sd)
10	c2yuyA_	 Alignment		9.4	21	PDB header: signaling protein Chain: A; PDB Molecule: rho gtpase activating protein 21; PDBTitle: solution structure of pdz domain of rho gtpase activating2 protein 21
11	c6hiuA_	 Alignment		9.1	26	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from methylococcus capsulatus (bath)

12	c3oc3B_	Alignment		7.7	54	PDB header: hydrolase/transcription Chain: B: PDB Molecule: helicase mot1; PDBTitle: crystal structure of the mot1 n-terminal domain in complex with tbp
13	d16vpa_	Alignment		7.6	55	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
14	c4h7wA_	Alignment		7.4	19	PDB header: unknown function Chain: A: PDB Molecule: upf0406 protein c16orf57; PDBTitle: crystal structure of human c16orf57
15	c6gw6A_	Alignment		7.3	60	PDB header: toxin Chain: A: PDB Molecule: res toxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
16	d2bopa_	Alignment		7.1	33	Fold: Ferredoxin-like Superfamily: Viral DNA-binding domain Family: Viral DNA-binding domain
17	d2ia9a1	Alignment		6.9	20	Fold: SpoVG-like Superfamily: SpoVG-like Family: SpoVG-like
18	c3somO_	Alignment		6.7	35	PDB header: oxidoreductase Chain: O: PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of human mmachc
19	c1i26A_	Alignment		6.5	44	PDB header: toxin Chain: A: PDB Molecule: ptu-1; PDBTitle: solution structure of ptu-1, a toxin from the assassin bugs2 peirates turpis that blocks the voltage sensitive calcium3 channel n-type
20	d1gpqa_	Alignment		6.4	50	Fold: Inhibitor of vertebrate lysozyme, Ivy Superfamily: Inhibitor of vertebrate lysozyme, Ivy Family: Inhibitor of vertebrate lysozyme, Ivy
21	d1nixa_	Alignment	not modelled	6.3	55	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
22	c6gftA_	Alignment	not modelled	6.0	55	PDB header: toxin Chain: A: PDB Molecule: cyriotoxin-1a; PDBTitle: antinociceptive evaluation of cyriotoxin-1a, the first toxin purified2 from cyriopagopus schioedtei spider venom
23	c4je3B_	Alignment	not modelled	5.9	50	PDB header: cell cycle Chain: B: PDB Molecule: central kinetochore subunit ch14; PDBTitle: an im13-ch14 heterodimer links the core centromere to factors required2 for accurate chromosome segregation
24	c4xa6C_	Alignment	not modelled	5.7	70	PDB header: motor protein Chain: C: PDB Molecule: gp7-myh7(1777-1855)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 4 of myh7
25	c4xa6B_	Alignment	not modelled	5.6	70	PDB header: motor protein Chain: B: PDB Molecule: gp7-myh7(1777-1855)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 4 of myh7
26	c5j9hA_	Alignment	not modelled	5.4	36	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)
27	c6fcxA_	Alignment	not modelled	5.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: methylenetetrahydrofolate reductase; PDBTitle: structure of human 5,10-methylenetetrahydrofolate reductase (mthfr)
28	c3nctC_	Alignment	not modelled	5.4	25	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor

					psib, a2 negative regulator of reca
29	c5zk4D_	Alignment	not modelled	5.1	24 PDB header: transferase Chain: D: PDB Molecule: disa protein; PDBTitle: the structure of dszs acyltransferase with carrier protein
30	c5m9eA_	Alignment	not modelled	5.1	55 PDB header: cell cycle Chain: A: PDB Molecule: microtubule integrity protein mal3; PDBTitle: interactions between the mal3 eb1-like domain and dis1
31	c2n3pA_	Alignment	not modelled	5.1	63 PDB header: toxin Chain: A: PDB Molecule: asteropsin_g; PDBTitle: solution nmr structure of asteropsin g from marine sponge asteropus