
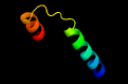

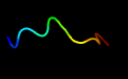



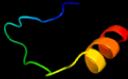




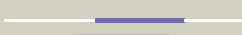








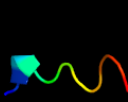
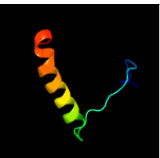
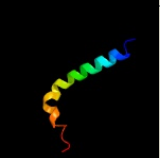
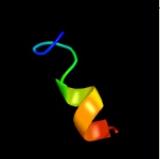
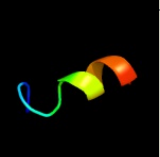
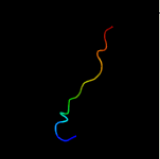
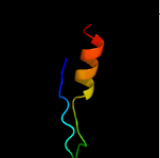
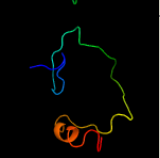
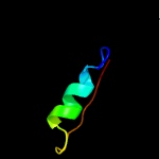



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3831 (-) _4305935_4306417
Date	Fri Aug 9 18:20:54 BST 2019
Unique Job ID	605419fa27242b88

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xvjB_	 Alignment		45.3	26	PDB header: gene regulation Chain: B: PDB Molecule: phd finger protein alfin-like 7; PDBTitle: crystal structure of al7 pal domain
2	c5lnkn_	 Alignment		29.2	55	PDB header: oxidoreductase Chain: N: PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
3	c3ug9A_	 Alignment		28.4	15	PDB header: membrane protein Chain: A: PDB Molecule: archaeal-type opsin 1, archaeal-type opsin 2; PDBTitle: crystal structure of the closed state of channelrhodopsin
4	c4h41B_	 Alignment		27.1	19	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of a putative alpha-l-fucosidase (bt_0435) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
5	c1ug9A_	 Alignment		19.6	63	PDB header: hydrolase Chain: A: PDB Molecule: glucodextranase; PDBTitle: crystal structure of glucodextranase from arthrobacter globiformis i42
6	c2eapA_	 Alignment		16.2	38	PDB header: signaling protein Chain: A: PDB Molecule: lymphocyte cytosolic protein 2; PDBTitle: solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
7	c4k90A_	 Alignment		15.7	26	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
8	d1cdoal	 Alignment		14.4	16	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
9	c5hr4J_	 Alignment		13.3	12	PDB header: hydrolase/dna Chain: J: PDB Molecule: mmei; PDBTitle: structure of type iii restriction-modification enzyme mmei in complex2 with dna has implications for engineering of new specificities
10	c2vovA_	 Alignment		13.3	55	PDB header: metal-binding protein Chain: A: PDB Molecule: surface-associated protein; PDBTitle: an oxidized tryptophan facilitates copper-binding in2 methylococcus capsulatus secreted protein mope. the3 structure of wild-type mope to 1.35aa
11	c2xnXM_	 Alignment		13.1	64	PDB header: cell adhesion Chain: M: PDB Molecule: im protein; PDBTitle: bc1 fragment of streptococcal m1 protein in complex with human2 fibrinogen

12	c3tixB	Alignment		12.6	32	PDB header: gene regulation/protein binding Chain: B: PDB Molecule: chromo domain-containing protein 1; PDBTitle: crystal structure of the chp1-tas3 complex core
13	c5id3C	Alignment		12.6	19	PDB header: transport protein Chain: C: PDB Molecule: mitochondrial calcium uniporter; PDBTitle: solution structure of the pore-forming region of c. elegans2 mitochondrial calcium uniporter (mcu)
14	c6hu9L	Alignment		12.4	42	PDB header: oxidoreductase/electron transport Chain: L: PDB Molecule: cytochrome b-c1 complex subunit 1, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
15	c6hu9X	Alignment		12.0	42	PDB header: oxidoreductase/electron transport Chain: X: PDB Molecule: PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
16	d1prta	Alignment		11.9	40	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
17	c6etzA	Alignment		10.4	37	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: cold-adapted beta-d-galactosidase from arthrobacter sp. 32cb
18	d1d1ta1	Alignment		9.4	13	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
19	c2plwA	Alignment		9.0	29	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna methyltransferase, putative; PDBTitle: crystal structure of a ribosomal rna methyltransferase, putative, from2 plasmodium falciparum (pf13_0052).
20	c2otoD	Alignment		8.7	64	PDB header: surface active protein, toxin Chain: D: PDB Molecule: m protein; PDBTitle: n-terminal fragment of streptococcus pyogenes m1 protein
21	d1j7na1	Alignment	not modelled	8.6	50	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Anthrax toxin lethal factor, N- and C-terminal domains
22	c4n48A	Alignment	not modelled	8.5	67	PDB header: transferase/rna Chain: A: PDB Molecule: cap-specific rna (nucleoside-2'-o-)-methyltransferase 1; PDBTitle: cap-specific rna (nucleoside-2'-o-)-methyltransferase 1 protein in2 complex with capped rna fragment
23	c6igkB	Alignment	not modelled	8.4	56	PDB header: signaling protein/protein binding Chain: B: PDB Molecule: endothelin-3; PDBTitle: crystal structure of human etb receptor in complex with endothelin-3
24	c3kwvF	Alignment	not modelled	8.3	50	PDB header: toxin/protein transport Chain: F: PDB Molecule: lethal factor; PDBTitle: structural basis for the unfolding of anthrax lethal factor by2 protective antigen oligomers
25	d1w36c3	Alignment	not modelled	8.2	32	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecC), C-terminal domain
26	c6eznG	Alignment	not modelled	8.2	27	PDB header: membrane protein Chain: G: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
27	c3j4bB	Alignment	not modelled	7.5	83	PDB header: viral protein Chain: B: PDB Molecule: tail tubular protein a; PDBTitle: structure of t7 gatekeeper protein (gp11)
28	c4akaA	Alignment	not modelled	7.3	46	PDB header: immune system Chain: A: PDB Molecule: il-4-inducing protein; PDBTitle: ipse alpha-1, an ige-binding crystallin

29	d1cwva5	Alignment	not modelled	6.9	35	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Invasin/intimin cell-adhesion fragment, C-terminal domain
30	d1h2ba1	Alignment	not modelled	6.7	13	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
31	c2a3dA	Alignment	not modelled	6.7	83	PDB header: three-helix bundle Chain: A: PDB Molecule: protein (de novo three-helix bundle); PDBTitle: solution structure of a de novo designed single chain three-2 helix bundle (a3d)
32	c4yk2B	Alignment	not modelled	6.6	27	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
33	c2bn5A	Alignment	not modelled	6.6	63	PDB header: nuclear protein Chain: A: PDB Molecule: psi; PDBTitle: p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
34	c5mu4A	Alignment	not modelled	6.4	36	PDB header: viral protein Chain: A: PDB Molecule: tail tubular protein a; PDBTitle: tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
35	d1u3wa1	Alignment	not modelled	6.4	16	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
36	c2bn6A	Alignment	not modelled	6.3	63	PDB header: nuclear protein Chain: A: PDB Molecule: psi; PDBTitle: p-element somatic inhibitor protein
37	d2outa2	Alignment	not modelled	5.7	57	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: YqbF N-terminal domain-like
38	c2outA	Alignment	not modelled	5.5	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mu-like prophage flumu protein gp35, protein PDBTitle: solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
39	c5lskP	Alignment	not modelled	5.4	67	PDB header: cell cycle Chain: P: PDB Molecule: centromere protein c; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
40	d1vf5b	Alignment	not modelled	5.4	19	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
41	c2k3oA	Alignment	not modelled	5.2	50	PDB header: structural protein Chain: A: PDB Molecule: tusp1; PDBTitle: solution structure of the type 2 repetitive domain (tusp1-2 rp2) of the egg case silk from nephila antipodiana
42	c5zihA	Alignment	not modelled	5.2	11	PDB header: membrane protein Chain: A: PDB Molecule: sensory opsin a,chromson; PDBTitle: crystal structure of the red light-activated channelrhodopsin2 chromson.
43	c5lo9B	Alignment	not modelled	5.1	75	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: thiosulfate dehydrogenase (tsdba) from marichromatium purpuratum - "as2 isolated" form
44	c4rymA	Alignment	not modelled	5.0	5	PDB header: membrane protein Chain: A: PDB Molecule: integral membrane protein; PDBTitle: crystal structure of bctspo iodo type1 monomer