


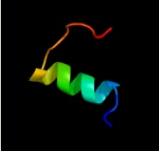
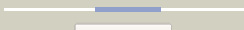
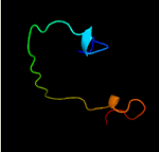



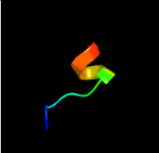

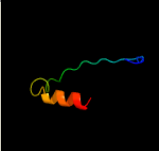

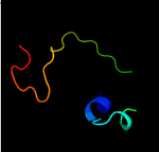

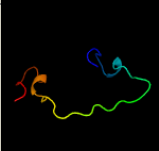



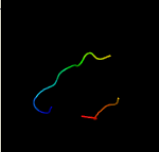

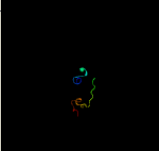

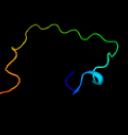
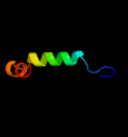


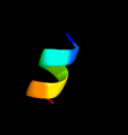

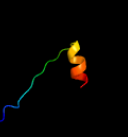



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1573_(-)_1779320_1779730
Date	Fri Aug 2 13:30:16 BST 2019
Unique Job ID	0fb598a71c849dff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2az0a1	 Alignment		25.6	44	Fold: ROP-like Superfamily: FHV B2 protein-like Family: FHV B2 protein-like
2	c2mmpA	 Alignment		22.2	32	PDB header: ribosomal protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a ribosomal protein
3	d1yq2a4	 Alignment		21.7	24	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: beta-Galactosidase, domain 5
4	d1eexa	 Alignment		21.3	73	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
5	d1iwpa	 Alignment		20.6	73	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
6	c4gs1A	 Alignment		20.1	29	PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase; PDBTitle: crystal structure of dyp-type peroxidase from thermobifida2 cellulolytica
7	c3bgaB	 Alignment		18.5	33	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
8	c3obaA	 Alignment		15.8	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: structure of the beta-galactosidase from kluveromyces lactis
9	d1jz8a4	 Alignment		14.9	26	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: beta-Galactosidase, domain 5
10	c5doiF	 Alignment		14.2	59	PDB header: dna binding protein Chain: F: PDB Molecule: telomerase associated protein p45; PDBTitle: crystal structure of tetrahymena p45n and p19
11	c1yq2C	 Alignment		13.8	22	PDB header: hydrolase Chain: C: PDB Molecule: beta-galactosidase; PDBTitle: beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2-2-1)

12	c3fubA_	Alignment		12.1	19	PDB header: hormone Chain: A: PDB Molecule: gdnf family receptor alpha-1; PDBTitle: crystal structure of gdnf-gfralpha1 complex
13	c6etzA_	Alignment		11.0	27	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: cold-adapted beta-d-galactosidase from arthrobacter sp. 32cb
14	c2v5eA_	Alignment		10.7	19	PDB header: receptor/glycoprotein complex Chain: A: PDB Molecule: gdnf family receptor alpha-1; PDBTitle: the structure of the gdnf:coreceptor complex: insights2 into ret signalling and heparin binding.
15	c5u1sA_	Alignment		10.1	39	PDB header: hydrolase Chain: A: PDB Molecule: separin; PDBTitle: crystal structure of the saccharomyces cerevisiae separase-securin2 complex at 3.0 angstrom resolution
16	c3wknG_	Alignment		7.7	63	PDB header: immune system Chain: G: PDB Molecule: affinger p17; PDBTitle: crystal structure of the artificial protein affinger p17 (af.p17)2 complexed with fc fragment of human igg
17	c3gd9A_	Alignment		7.5	44	PDB header: hydrolase Chain: A: PDB Molecule: laminaripentaose-producing beta-1,3-guluaase PDBTitle: crystal structure of laminaripentaose-producing beta-1,3-2 glucanase in complex with laminaritetraose
18	d2pnwa1	Alignment		7.4	50	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
19	c2kg4A_	Alignment		7.0	17	PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible protein gadd45 PDBTitle: three-dimensional structure of human gadd45alpha in solution by nmr
20	c5h9xA_	Alignment		6.8	67	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,3-glucanase; PDBTitle: crystal structure of gh family 64 laminaripentaose-producing beta-1,3-2 glucanase from paenibacillus barengoltzii
21	c5h4eA_	Alignment	not modelled	6.6	56	PDB header: hydrolase Chain: A: PDB Molecule: beta 1-3 glucanase; PDBTitle: crystal structure of a beta-1,3-glucanase domain (gh64) from2 clostridium beijerinckii
22	c2myxA_	Alignment	not modelled	6.6	28	PDB header: ubiquitin-binding protein Chain: A: PDB Molecule: coupling of ubiquitin conjugation to er degradation protein PDBTitle: structure of the cue domain of yeast cue1
23	c3m0zD_	Alignment	not modelled	6.4	50	PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from klebsiella pneumoniae.
24	c6c3aB_	Alignment	not modelled	6.3	23	PDB header: biosynthetic protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: o2-, plp-dependent l-arginine hydroxylase rohp 4-hydroxy-2-2 ketoarginine complex
25	c3s7xC_	Alignment	not modelled	6.2	22	PDB header: viral protein Chain: C: PDB Molecule: major capsid protein vp1; PDBTitle: unassembled washington university polyomavirus vp1 pentamer r198k2 mutant
26	c1zkaA_	Alignment	not modelled	6.2	42	PDB header: transcription Chain: A: PDB Molecule: transcription factor relb; PDBTitle: nf-kb relb forms an intertwined homodimer, y300s mutant
27	c5tdyC_	Alignment	not modelled	6.0	41	PDB header: motor protein Chain: C: PDB Molecule: flagellar m-ring protein; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
28	d2g7oa1	Alignment	not modelled	5.9	29	Fold: TraM-like Superfamily: TraM-like Family: TraM-like PDB header: ligase

29	c6mn8A_	Alignment	not modelled	5.7	23	Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of prolyl-trna synthetase from onchocerca volvulus2 with bound halofuginone and nucleotide
30	c3bn8A_	Alignment	not modelled	5.6	22	PDB header: transport protein Chain: A; PDB Molecule: putative sterol carrier protein 2; PDBTitle: crystal structure of a putative sterol carrier protein type 2 (af1534)2 from archaeoglobus fulgidus dsm 4304 at 2.11 a resolution
31	c2dhyA_	Alignment	not modelled	5.4	19	PDB header: immune system Chain: A; PDB Molecule: cue domain-containing protein 1; PDBTitle: solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
32	d1g5ha1	Alignment	not modelled	5.4	20	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
33	d2g5da1	Alignment	not modelled	5.4	28	Fold: Double psi beta-barrel Superfamily: Barwin-like endoglucanases Family: MLTA-like
34	c2ejsA_	Alignment	not modelled	5.4	28	PDB header: ligase Chain: A; PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: solution structure of ruh-076, a human cue domain
35	c2ekfA_	Alignment	not modelled	5.3	28	PDB header: ligase Chain: A; PDB Molecule: ancient ubiquitous protein 1; PDBTitle: solution structure of ruh-075, a human cue domain
36	c6mr1A_	Alignment	not modelled	5.2	63	PDB header: protein binding Chain: A; PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: rbcS-like subdomain of ccmm
37	c6k1hF_	Alignment	not modelled	5.1	20	PDB header: protein transport Chain: F; PDB Molecule: pts system mannose-specific eiid component; PDBTitle: structure of membrane protein
38	c2prxB_	Alignment	not modelled	5.0	10	PDB header: hydrolase Chain: B; PDB Molecule: thioesterase superfamily protein; PDBTitle: crystal structure of thioesterase superfamily protein (zp_00837258.1)2 from shewanella loihica pv-4 at 1.65 a resolution