Phyre2

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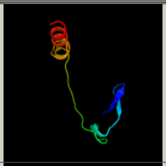
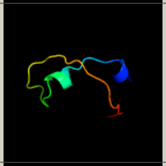
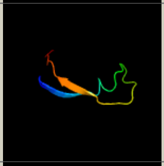
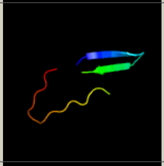
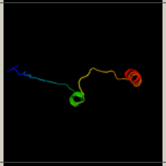
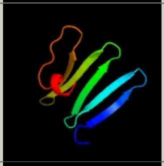
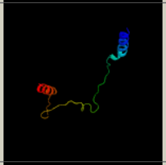
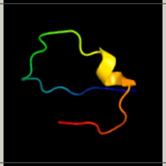
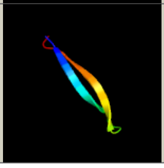
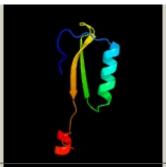
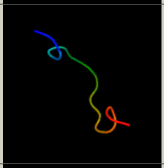
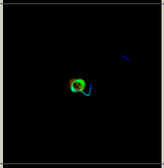
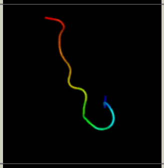
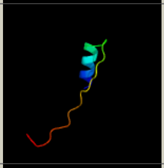
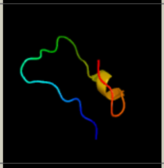
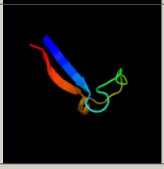
Description	RVBD1053c_(-)_1176016_1176291
Date	Wed Jul 31 22:05:12 BST 2019
Unique Job ID	ba42284defdf1977

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a69A_	Alignment		46.1	24	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar hook protein flge; **PDBTitle:** atomic model of the bacterial flagellar hook based on2 docking an x-ray derived structure and terminal two alpha-3 helices into an 7.1 angstrom resolution cryoem map
2	c5jxlA_	Alignment		33.8	32	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar hook protein flge; **PDBTitle:** cryo-em structure of the flagellar hook of campylobacter jejuni
3	c3m9pA_	Alignment		22.8	28	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**male-specific lethal 3 homolog; **PDBTitle:** human msl3 chromodomain bound to dna and h4k20me1 peptide
4	c3m9qA_	Alignment		20.6	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein male-specific lethal-3; **PDBTitle:** drosophila msl3 chromodomain
5	c3t9wA_	Alignment		17.4	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small laccase, multi-copper oxidase; **PDBTitle:** small laccase from amycolatopsis sp. atcc 39116
6	c4i2yB_	Alignment		16.9	22	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**rgeco1; **PDBTitle:** crystal structure of the genetically encoded calcium indicator rgeco1
7	c3e19D_	Alignment		15.9	21	**PDB header:**transcription regulator, metal binding p **Chain:** D: **PDB Molecule:**feoa; **PDBTitle:** crystal structure of iron uptake regulatory protein (feoa) solved by2 sulfur sad in a monoclinic space group
8	c5lhxA_	Alignment		13.3	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase plk4; **PDBTitle:** pb3 domain of drosophila melanogaster plk4 (sak)
9	c4ifdK_	Alignment		13.2	38	**PDB header:**hydrolase/rna **Chain:** K: **PDB Molecule:**exosome complex exonuclease rrp6; **PDBTitle:** crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
10	c1zctB_	Alignment		12.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-1; **PDBTitle:** structure of glycogenin truncated at residue 270 in a complex with udp
11	c4bkwA_	Alignment		11.7	36	**PDB header:**receptor **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 9; **PDBTitle:** crystal structure of the c-terminal region of human zfyve9

12	c3cxjB_	Alignment		10.8	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
13	c2lxwA_	Alignment		10.7	47	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**xiap-associated factor 1; **PDBTitle:** the solution structure of xiap(ring)-binding domain of human xaf1
14	c5wrhA_	Alignment		10.1	37	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar basal-body rod protein flgg; **PDBTitle:** flgg structure based on the cryoem map of the bacterial flagellar2 polyrod
15	c2qziA_	Alignment		10.1	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a conserved protein of unknown function from2 streptococcus thermophilus lmg 18311.
16	c4xvnC_	Alignment		9.8	64	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**small terminase; **PDBTitle:** crystal structure of the small terminase from thermophilic phage g20c
17	c2kgsA_	Alignment		9.7	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
18	d1ll2a_	Alignment		9.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
19	d1x6ma_	Alignment		9.3	20	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
20	c3hieA_	Alignment		8.5	34	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex
21	c3tztB_	Alignment	not modelled	8.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 8; **PDBTitle:** the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
22	c1zcyA_	Alignment	not modelled	7.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
23	c4uegB_	Alignment	not modelled	6.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-2; **PDBTitle:** crystal structure of human glycogenin-2 catalytic domain
24	d1kwia_	Alignment	not modelled	6.8	36	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cathelicidin motif
25	c3kzwD_	Alignment	not modelled	6.5	31	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
26	c3h8gC_	Alignment	not modelled	6.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
27	d1c3pa_	Alignment	not modelled	5.8	28	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
28	d1e3ha5	Alignment	not modelled	5.8	48	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
						PDB header:hydrolase

29	c1gytG_	Alignment	not modelled	5.6	43	**Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
30	c2wshC_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**endonuclease ii; **PDBTitle:** structure of bacteriophage t4 endoii e118a mutant
31	d1c55a_	Alignment	not modelled	5.2	63	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
32	c3jruB_	Alignment	not modelled	5.1	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
33	c5wxkB_	Alignment	not modelled	5.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**elongation factor p; **PDBTitle:** earp bound with domain i of ef-p
34	c4ksiA_	Alignment	not modelled	5.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1, chloroplastic; **PDBTitle:** crystal structure analysis of the acidic leucine aminopeptidase of2 tomato
35	c3u0kA_	Alignment	not modelled	5.0	20	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**rcamp; **PDBTitle:** crystal structure of the genetically encoded calcium indicator rcamp