Phyre2

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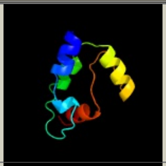
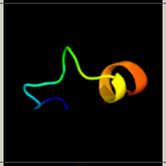
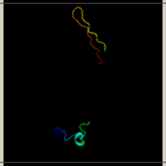
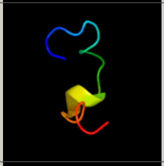
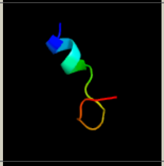
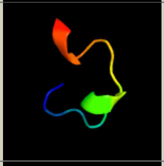
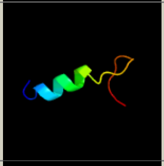
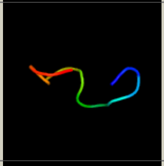
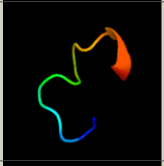
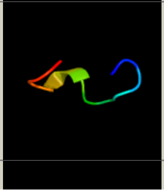
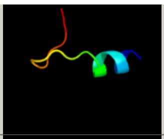
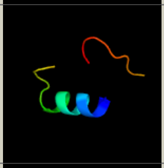
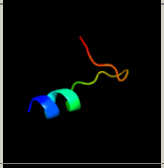
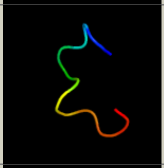
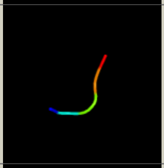
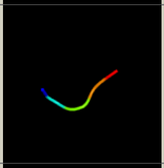
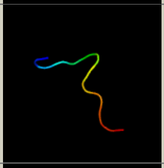
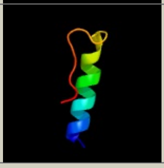
Description	RVBD3197A_(whiB7)_3568398_3568676
Date	Thu Aug 8 16:20:39 BST 2019
Unique Job ID	b144ad6a17050319

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oayA_	Alignment		99.9	31	**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	c4unfA_	Alignment		46.3	39	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endonuclease iii-1; **PDBTitle:** crystal structure of deinococcus radiodurans endonuclease iii-1
3	c1rrqA_	Alignment		42.2	27	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
4	d2f62a1	Alignment		22.7	14	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
5	d1rrqa1	Alignment		21.9	38	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
6	c3saeA_	Alignment		19.8	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-bisabolene synthase; **PDBTitle:** structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
7	c4uobA_	Alignment		18.8	38	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endonuclease iii-3; **PDBTitle:** crystal structure of deinococcus radiodurans endonuclease iii-3
8	c3pybB_	Alignment		18.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ent-copalyl diphosphate synthase, chloroplastic; **PDBTitle:** crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate
9	d1orna_	Alignment		18.1	38	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
10	d1kg2a_	Alignment		17.0	50	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
11	d1keaa_	Alignment		16.3	23	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase

12	c3p5rB_	Alignment		15.5	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**taxadiene synthase; **PDBTitle:** crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
13	c6dx2A_	Alignment		14.7	21	**PDB header:**hydrolase, protein binding **Chain:** A: **PDB Molecule:**rna-dependent rna polymerase; **PDBTitle:** crystal structure of the viral otu domain protease from dera ghazi2 khan virus
14	c3s9vD_	Alignment		14.0	28	**PDB header:**lyase, isomerase **Chain:** D: **PDB Molecule:**abietadiene synthase, chloroplastic; **PDBTitle:** abietadiene synthase from abies grandis
15	c3n5nX_	Alignment		11.2	38	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
16	c4fdxB_	Alignment		10.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonase tautomerase isozyme; **PDBTitle:** kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylibium petroleiphilum
17	d1i8ya_	Alignment		10.2	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Granulin repeat **Family:**Granulin repeat
18	c1i8yA_	Alignment		10.2	80	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin-1; **PDBTitle:** semi-automatic structure determination of the cg1 3-302 peptide based on aria
19	c5fj9P_	Alignment		9.7	0	**PDB header:**transcription **Chain:** P: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc6; **PDBTitle:** cryo-em structure of yeast apo rna polymerase iii at 4.6 a
20	c3gycB_	Alignment		9.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
21	c6f40P_	Alignment	not modelled	9.6	0	**PDB header:**transcription **Chain:** P: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc6; **PDBTitle:** rna polymerase iii open complex
22	d1fltx_	Alignment	not modelled	9.5	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
23	c4bozA_	Alignment	not modelled	9.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** structure of otud2 otu domain in complex with k11-linked di ubiquitin
24	c3c0rC_	Alignment	not modelled	8.2	29	**PDB header:**cell cycle, hydrolase **Chain:** C: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** structure of ovarian tumor (otu) domain in complex with ubiquitin
25	d2abka_	Alignment	not modelled	8.1	50	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
26	c2ru1A_	Alignment	not modelled	6.6	67	**PDB header:**hormone **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of esf3
27	c3m20A_	Alignment	not modelled	6.2	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
28	c3ry0A_	Alignment	not modelled	6.0	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
29	c5cw6A_	Alignment	not modelled	5.5	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**drbrcc36;

						PDBTitle: structure of metal dependent enzyme drbrcc36
30	c2mvmA_	Alignment	not modelled	5.5	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-delta; **PDBTitle:** solution structure of eef1bdelta car domain
31	c2mvnA_	Alignment	not modelled	5.5	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-delta; **PDBTitle:** solution structure of eef1bdelta car domain in tctp-bound state
32	c6dx1A_	Alignment	not modelled	5.4	25	**PDB header:**hydrolase, protein binding **Chain:** A: **PDB Molecule:**rna-dependent rna polymerase; **PDBTitle:** crystal structure of the viral otu domain protease from qalyub virus