Phyre2

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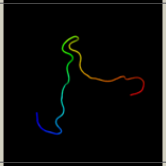
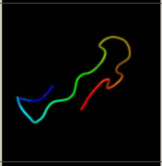
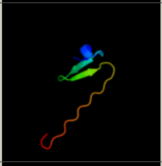
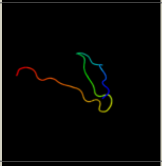
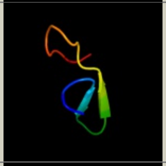
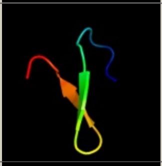
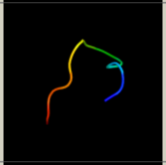
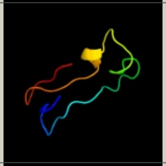
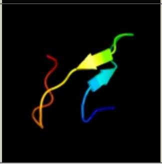
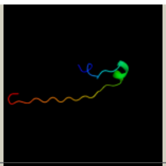
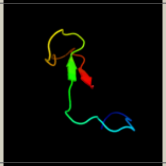
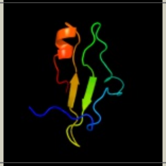
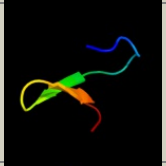
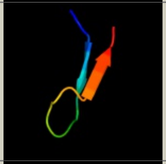
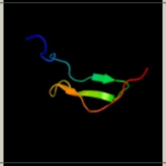
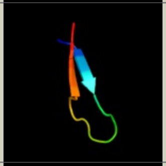
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l1sA_	Alignment		100.0	74	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yohn; **PDBTitle:** yp_001336205.1
2	c1rfoC_	Alignment		31.0	35	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**whisker antigen control protein; **PDBTitle:** trimeric foldon of the t4 phagehead fibritin
3	c3ilaG_	Alignment		29.6	20	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
4	d2fhzb1	Alignment		24.6	25	**Fold:**Colicin D/E5 nuclease domain **Superfamily:**Colicin D/E5 nuclease domain **Family:**Colicin E5 nuclease domain
5	d2hkja2	Alignment		24.5	16	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
6	c3phzA_	Alignment		23.7	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ricin b-related lectin; **PDBTitle:** crystal structure analysis of polyporus squamosus lectin bound to2 human-type influenza-binding epitope neu5aca2-6galb1-4glcnac
7	d1tf5a1	Alignment		21.6	13	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
8	c1avyA_	Alignment		17.9	35	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)
9	d1bf2a2	Alignment		17.0	54	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
10	c2otrA_	Alignment		16.9	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp0892; **PDBTitle:** solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
11	d1nkta1	Alignment		16.9	9	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA

12	c2zbkB_	Alignment		14.4	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
13	c2bpsA_	Alignment		12.9	25	**PDB header:**ubiquitin **Chain:** A: **PDB Molecule:**yukd protein; **PDBTitle:** ubiquitin-like protein yukd of bacillus subtilis
14	d1z8ma1	Alignment		11.8	11	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
15	c1ox3A_	Alignment		10.9	35	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** crystal structure of mini-fibritin
16	d2z1ca1	Alignment		10.6	31	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
17	d1m7ja2	Alignment		10.4	27	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
18	d2ot2a1	Alignment		9.7	25	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
19	d1ggpb1	Alignment		9.4	8	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
20	d2rbia_	Alignment		9.3	18	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Bacterial ribonucleases
21	c1mx0D_	Alignment	not modelled	9.3	9	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
22	c1v1hB_	Alignment	not modelled	9.0	29	**PDB header:**adenovirus **Chain:** B: **PDB Molecule:**fibritin, fiber protein; **PDBTitle:** adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibritin foldon trimerisation motif with3 a short linker
23	c2c4bB_	Alignment	not modelled	8.5	20	**PDB header:**fusion protein **Chain:** B: **PDB Molecule:**barnase mcoeeti fusion; **PDBTitle:** inhibitor cystine knot protein mcoeeti fused to the2 catalytically inactive barnase mutant h102a
24	d2jnaa1	Alignment	not modelled	8.0	22	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
25	d1m0da_	Alignment	not modelled	7.4	15	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
26	d2c4ba1	Alignment	not modelled	7.3	18	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Bacterial ribonucleases
27	c3f8mA_	Alignment	not modelled	6.9	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
28	d1goua_	Alignment	not modelled	6.9	18	**Fold:**Microbial ribonucleases **Superfamily:**Microbial ribonucleases **Family:**Bacterial ribonucleases

29	d2f2fa1	Alignment	not modelled	6.5	19	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
30	d1upsa2	Alignment	not modelled	6.4	19	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase, GngC, C-terminal domain
31	c1xk5A_	Alignment	not modelled	5.9	56	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide
32	c3gjxE_	Alignment	not modelled	5.6	56	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
33	c3tqnC_	Alignment	not modelled	5.3	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
34	c3bwgA_	Alignment	not modelled	5.2	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
35	d2noca1	Alignment	not modelled	5.2	41	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
36	c2q2eB_	Alignment	not modelled	5.2	31	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
37	c2ihoA_	Alignment	not modelled	5.1	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**lectin; **PDBTitle:** crystal structure of moa, a lectin from the mushroom marasmius oreades2 in complex with the trisaccharide gal(1,3)gal(1,4)glcnac
38	c3gb8B_	Alignment	not modelled	5.1	56	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of crm1/snurportin-1 complex