Phyre^2

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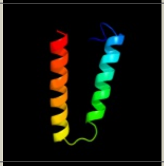
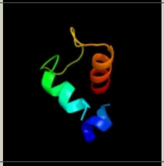
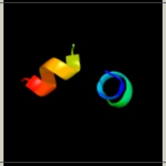
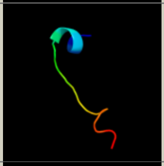
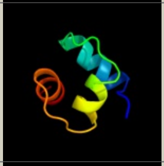
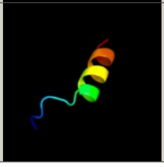
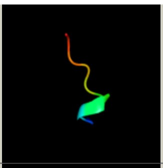
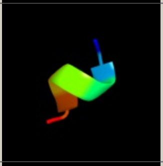
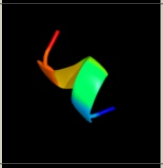
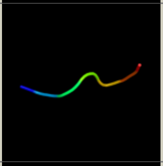
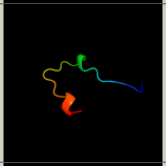
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2csfa1	Alignment		65.6	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
2	d1wiza_	Alignment		41.7	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
3	d2o4aa1	Alignment		32.6	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
4	c2w9yA_	Alignment		32.4	18	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**fatty acid/retinol binding protein protein 7, **PDBTitle:** the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
5	c1yseA_	Alignment		26.7	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein satb1; **PDBTitle:** solution structure of the mar-binding domain of satb1
6	d1x2la1	Alignment		22.6	47	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
7	d1wh8a_	Alignment		17.5	53	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
8	d1s7ea2	Alignment		15.1	53	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
9	c2eo2A_	Alignment		13.7	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**adult male hypothalamus cdna, riken full-length **PDBTitle:** solution structure of the insertion region (510-573) of2 fthfs domain from mouse methylenetetrahydrofolate3 dehydrogenase (nadp+ dependent) 1-like protein
10	d1wh6a_	Alignment		12.4	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
11	c1yqyA_	Alignment		11.2	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lethal factor; **PDBTitle:** structure of b. anthrax lethal factor in complex with a2 hydroxamate inhibitor

12	c1sp7A_	Alignment		11.0	60	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mini-collagen; **PDBTitle:** structure of the cys-rich c-terminal domain of hydra2 minicollagen
13	c3si5X_	Alignment		10.6	71	**PDB header:**cell cycle **Chain:** X: **PDB Molecule:**protein casc5; **PDBTitle:** kinetochore-bubr1 kinase complex
14	c3si5Y_	Alignment		10.4	71	**PDB header:**cell cycle **Chain:** Y: **PDB Molecule:**protein casc5; **PDBTitle:** kinetochore-bubr1 kinase complex
15	d1j7na3	Alignment		10.1	69	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
16	d1axib1	Alignment		9.3	57	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
17	c2dt7A_	Alignment		8.7	54	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
18	c2wj8N_	Alignment		7.4	36	**PDB header:**rna binding protein/rna **Chain:** N: **PDB Molecule:**nucleoprotein; **PDBTitle:** respiratory syncitial virus ribonucleoprotein
19	c1u2uB_	Alignment		7.3	55	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
20	c2w1oA_	Alignment		6.8	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p2; **PDBTitle:** nmr structure of dimerization domain of human ribosomal2 protein p2
21	d1xb4a1	Alignment	not modelled	6.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
22	c2d9sA_	Alignment	not modelled	6.0	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
23	c2zmeD_	Alignment	not modelled	5.7	31	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
24	c3cuqD_	Alignment	not modelled	5.7	31	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
25	c2hbpA_	Alignment	not modelled	5.7	17	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
26	c2fphX_	Alignment	not modelled	5.7	27	**PDB header:**dna binding protein **Chain:** X: **PDB Molecule:**ylmh; **PDBTitle:** cell division protein ylmh from streptococcus pneumoniae
27	c1xb4C_	Alignment	not modelled	5.5	8	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**hypothetical 23.6 kda protein in yuh1-ura8 **PDBTitle:** crystal structure of subunit vps25 of the endosomal2 trafficking complex escrt-ii
						PDB header:ribosome

28	c3iz5w_	Alignment	not modelled	5.5	27	**Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
29	c3izcw_	Alignment	not modelled	5.2	24	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein rpl22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
30	c3eq5G_	Alignment	not modelled	5.2	23	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ski-like protein; **PDBTitle:** crystal structure of fragment 137 to 238 of the human ski-like protein