Phyre^2

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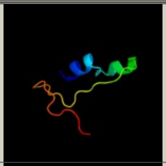
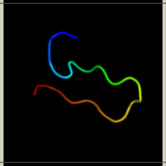
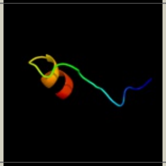
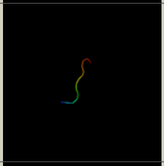
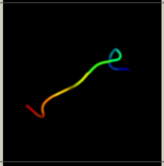
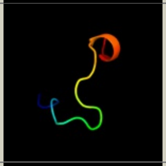
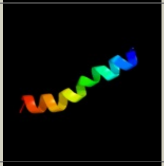
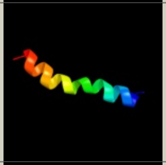
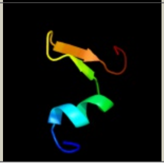
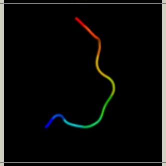
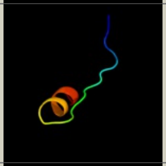
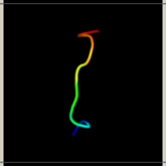
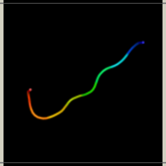
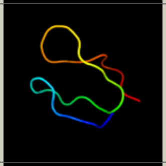
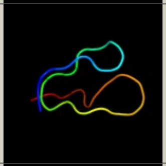
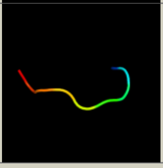
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ig4a_	Alignment		50.9	32	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
2	c2a2bA_	Alignment		49.6	41	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bacteriocin curvacin a; **PDBTitle:** curvacin a
3	c2q3eH_	Alignment		16.6	29	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
4	d1flca1	Alignment		11.7	45	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Hemagglutinin domain of haemagglutinin-esterase-fusion glycoprotein HEF1
5	d1ua7a1	Alignment		11.0	10	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
6	c3ebkA_	Alignment		9.9	22	**PDB header:**allergen **Chain:** A: **PDB Molecule:**allergen bla g 4; **PDBTitle:** crystal structure of major allergens, bla g 4 from2 cockroaches
7	c2yqpA_	Alignment		8.5	44	**PDB header:**gene regulation, hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx59; **PDBTitle:** solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
8	d1q90r_	Alignment		8.5	33	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
9	c1q90R_	Alignment		8.5	33	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
10	c3plnA_	Alignment		8.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
11	d1qkia2	Alignment		7.6	45	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like

12	c3ggpA_	Alignment		7.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
13	d1hx0a1	Alignment		7.1	40	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
14	c3prjB_	Alignment		7.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
15	d1g94a1	Alignment		6.6	40	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
16	d1jaea1	Alignment		6.6	40	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
17	c2bhlB_	Alignment		6.6	45	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
18	c1e0fI_	Alignment		6.5	37	**PDB header:**coagulation/crystal structure/heparin-b **Chain:** I: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
19	d1e0fi_	Alignment		6.5	37	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
20	d3dhpa1	Alignment		6.3	40	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
21	d1t27a_	Alignment	not modelled	6.2	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Phoshatidylinositol transfer protein, PITP
22	d1r0va3	Alignment	not modelled	6.1	29	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
23	d1rmka_	Alignment	not modelled	6.0	45	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
24	d1h9aa1	Alignment	not modelled	6.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
25	c2l3bA_	Alignment	not modelled	5.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376
26	d2a1la1	Alignment	not modelled	5.9	20	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Phoshatidylinositol transfer protein, PITP
27	c2l7qA_	Alignment	not modelled	5.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein found in conjugate transposon; **PDBTitle:** solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
						PDB header:coagulation/crystal structure/heparin-b

28	c1e0fJ_	Alignment	not modelled	5.8	37	**Chain:** J: **PDB Molecule:**haemadin; **PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor
29	c1qkiE_	Alignment	not modelled	5.5	45	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+