Phyre^2

Email	l.a.kelley@imperial.ac.uk
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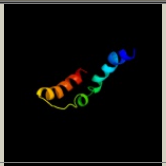
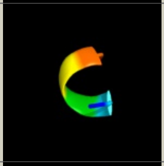
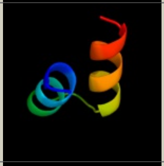
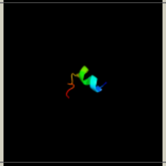
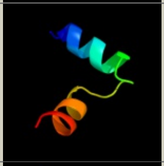
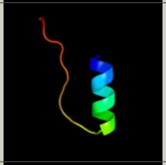
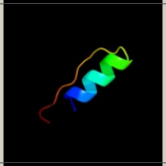
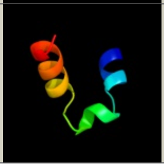
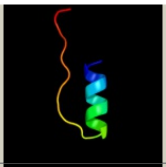
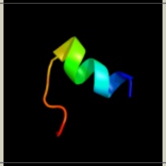
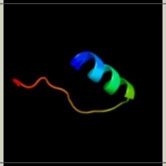
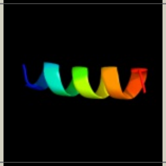
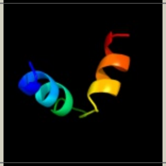
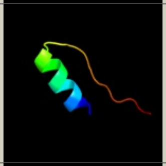
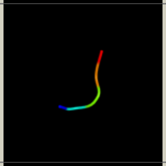
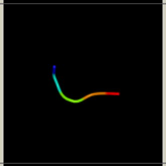
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1z9ha1	Alignment		56.9	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
2	d1nkua_	Alignment		40.1	26	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
3	c2jg6A_	Alignment		32.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
4	c2xf5C_	Alignment		20.1	100	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**gp23.1; **PDBTitle:** crystal structure of bacillus subtilis spp1 phage gp23.1, a2 putative chaperone.
5	d2ntka1	Alignment		17.6	17	**Fold:**Ntn hydrolase-like **Superfamily:**Archaeal IMP cyclohydrolase PurO **Family:**Archaeal IMP cyclohydrolase PurO
6	c1wypA_	Alignment		14.5	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**calponin 1; **PDBTitle:** solution structure of the ch domain of human calponin 1
7	d2csha2	Alignment		13.3	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
8	c1ei5A_	Alignment		13.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-aminopeptidase; **PDBTitle:** crystal structure of a d-aminopeptidase from ochrobactrum2 anthropi
9	c3br8A_	Alignment		12.7	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
10	d2acya_	Alignment		11.9	22	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
11	d1e7la2	Alignment		11.8	30	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Recombination endonuclease VII, N-terminal domain

12	c2bjeA_	Alignment		11.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylphosphatase; **PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
13	c2d86A_	Alignment		10.9	24	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**vav-3 protein; **PDBTitle:** solution structure of the ch domain from human vav-3 protein
14	d1w2ia_	Alignment		10.1	43	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
15	c1bmxA_	Alignment		9.9	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**human immunodeficiency virus type 1 capsid; **PDBTitle:** hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
16	c3o3vB_	Alignment		9.9	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of clbp peptidase domain
17	d1ulra_	Alignment		9.6	35	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
18	c1i8yA_	Alignment		9.5	60	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin-1; **PDBTitle:** semi-automatic structure determination of the cg1 3-302 peptide based on aria
19	d1i8ya_	Alignment		9.5	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Granulin repeat **Family:**Granulin repeat
20	d1gxua_	Alignment		8.8	22	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
21	d1urra_	Alignment	not modelled	8.7	26	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
22	d1h67a_	Alignment	not modelled	8.7	25	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
23	d2hkua2	Alignment	not modelled	8.6	23	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
24	c3o59X_	Alignment	not modelled	8.0	31	**PDB header:**transferase **Chain:** X: **PDB Molecule:**dna polymerase ii large subunit; **PDBTitle:** dna polymerase d large subunit dp2(1-300) from pyrococcus horikoshii
25	c3a7kD_	Alignment	not modelled	7.9	19	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**halorhodopsin; **PDBTitle:** crystal structure of halorhodopsin from natronomonas2 pharaonis
26	c3tg9A_	Alignment	not modelled	7.7	16	**PDB header:**penicillin binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein; **PDBTitle:** the crystal structure of penicillin binding protein from bacillus2 halodurans
27	d1ujoa_	Alignment	not modelled	7.2	21	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
28	d1ui5a2	Alignment	not modelled	6.0	9	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
29	c1zbhA	Alignment	not modelled	5.9	18	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**3'-5' exonuclease eri1;

29	c1zbhA_	Alignment	not modelled	5.9	18	**PDBTitle:** 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease
30	c1wymA_	Alignment	not modelled	5.6	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**transgelin-2; **PDBTitle:** solution structure of the ch domain of human transgelin-2
31	c2wnmA_	Alignment	not modelled	5.6	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gene 2; **PDBTitle:** solution structure of gp2
32	c3i6xC_	Alignment	not modelled	5.4	6	**PDB header:**calmodulin-binding, membrane protein **Chain:** C: **PDB Molecule:**ras gtpase-activating-like protein iqgap1; **PDBTitle:** crystal structure of the calponin homology domain of iqgap1