Phyre^2

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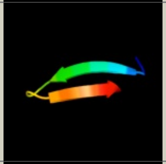
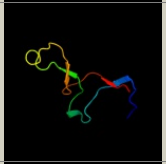
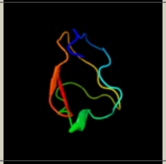
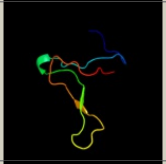
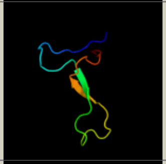
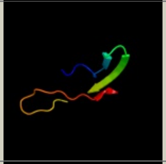
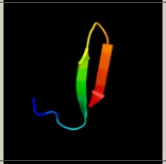
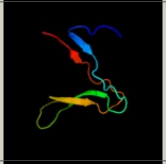
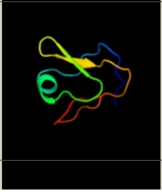
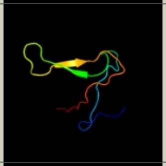
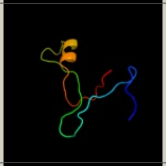
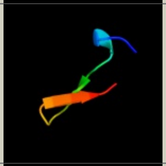
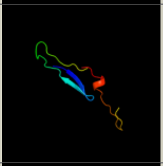
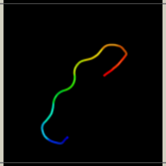
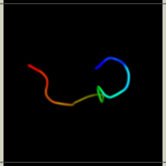
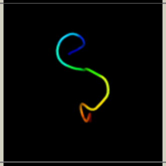
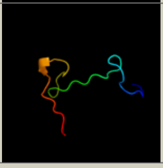
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d49A_	Alignment		46.5	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase c; **PDBTitle:** solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
2	d1goia1	Alignment		36.2	20	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
3	d1tiea_	Alignment		32.9	24	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
4	d2je6i2	Alignment		30.1	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
5	d3bx1c1	Alignment		21.0	20	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
6	c1r8oA_	Alignment		20.4	21	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kunitz trypsin inhibitor; **PDBTitle:** crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifera langsdorffii seeds
7	c2kcaA_	Alignment		19.7	11	**PDB header:**virus **Chain:** A: **PDB Molecule:**bacteriophage spp1 complete nucleotide sequence; **PDBTitle:** gp16
8	d1aiwa_	Alignment		16.9	31	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
9	d1ed7a_	Alignment		16.8	33	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
10	d1eyla_	Alignment		15.3	13	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
11	d2ba0a2	Alignment		15.1	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like

12	c2eifA_	Alignment		14.1	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (eukaryotic translation initiation factor 5a); **PDBTitle:** eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
13	c3iirA_	Alignment		13.9	13	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**trypsin inhibitor; **PDBTitle:** crystal structure of miraculin like protein from seeds of murraya2 koenigii
14	c2qn4B_	Alignment		11.5	24	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**alpha-amylase/subtilisin inhibitor; **PDBTitle:** structure and function study of rice bifunctional alpha-2 amylase/subtilisin inhibitor from oryza sativa
15	d1j83a_	Alignment		11.5	31	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 17 carbohydrate binding module, CBM17
16	c3floG_	Alignment		10.9	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase alpha subunit b; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
17	d1tdha3	Alignment		10.5	42	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
18	c2jufA_	Alignment		10.4	33	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**p53-associated parkin-like cytoplasmic protein; **PDBTitle:** nmr solution structure of parc cph domain. nesg target2 hr3443b/sgc-toronto
19	d2jnga1	Alignment		9.9	33	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**CPH domain
20	d1lkta_	Alignment		9.3	33	**Fold:**Head-binding domain of phage P22 tailspike protein **Superfamily:**Head-binding domain of phage P22 tailspike protein **Family:**Head-binding domain of phage P22 tailspike protein
21	c1fmeA_	Alignment	not modelled	7.9	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**fsd-ey peptide; **PDBTitle:** solution structure of fsd-ey, a novel peptide assuming a2 beta-beta-alpha fold
22	c3s9xA_	Alignment	not modelled	7.3	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asch domain; **PDBTitle:** high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
23	d1t62a_	Alignment	not modelled	7.2	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein EF3133
24	c1bkbA_	Alignment	not modelled	7.1	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
25	c3hksB_	Alignment	not modelled	7.1	13	**PDB header:**translation, rna binding protein **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
26	c2l23A_	Alignment	not modelled	7.0	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25; **PDBTitle:** nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
27	d2nn6h2	Alignment	not modelled	6.9	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
28	d1a1xa_	Alignment	not modelled	6.6	20	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products

29	d1wbaa_	Alignment	not modelled	5.3	9	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors