Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q2M7R5
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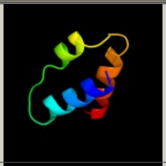
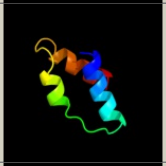
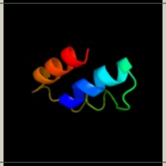
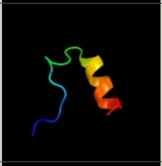
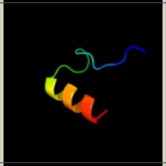
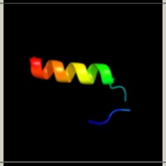
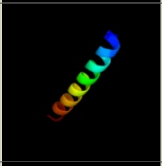
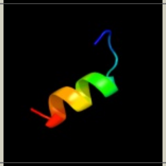
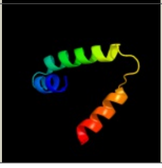
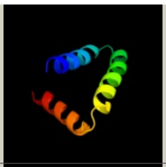
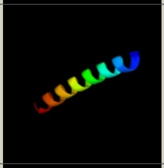
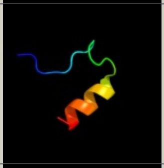
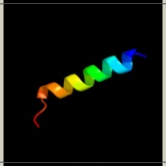
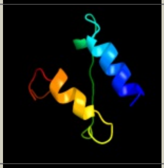
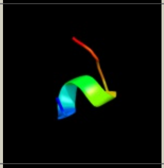
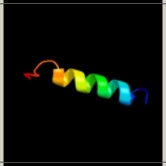
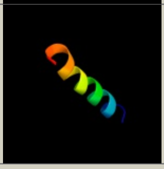
Unique Job ID	db2a286ae0244ecb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ae9a1	Alignment		82.0	26	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
2	d2idob1	Alignment		79.6	28	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
3	d1se7a_	Alignment		79.0	28	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
4	d2eyqa6	Alignment		52.5	39	**Fold:**TRCF domain-like **Superfamily:**TRCF domain-like **Family:**TRCF domain
5	c2qsrA_	Alignment		44.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of c-terminal domain of transcription-repair2 coupling factor
6	c1zxhA_	Alignment		18.3	44	**PDB header:**immune system/protein binding **Chain:** A: **PDB Molecule:**immunoglobulin g binding protein g; **PDBTitle:** g311 mutant protein
7	d1mvka_	Alignment		17.5	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
8	c1urqA_	Alignment		17.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m-tomosyn isoform; **PDBTitle:** crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn
9	d1em7a_	Alignment		17.3	44	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
10	c3gxqB_	Alignment		16.3	67	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**putative regulator of transfer genes arta; **PDBTitle:** structure of arta and dna complex
11	d1x9fc_	Alignment		16.0	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins

12	d1x9fa_	Alignment		15.2	9	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
13	c1gl2A_	Alignment		13.7	36	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**endobrevin; **PDBTitle:** crystal structure of an endosomal snare core complex
14	c2eyqA_	Alignment		13.5	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
15	c1k6mA_	Alignment		12.4	29	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
16	d2ieaa1	Alignment		12.2	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
17	d1q3ma_	Alignment		11.2	67	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
18	c2i1vB_	Alignment		11.2	24	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
19	c3qf7D_	Alignment		10.5	86	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
20	c1bifA_	Alignment		9.6	29	**PDB header:**bifunctional enzyme **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; **PDBTitle:** 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
21	d1p7ea_	Alignment	not modelled	9.5	39	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
22	d1pgaa_	Alignment	not modelled	9.4	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
23	d2es9a1	Alignment	not modelled	9.4	63	**Fold:**YoaC-like **Superfamily:**YoaC-like **Family:**YoaC-like
24	c1bm4A_	Alignment	not modelled	9.3	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
25	d3nlaa_	Alignment	not modelled	9.3	60	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
26	c3b5nE_	Alignment	not modelled	9.1	29	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**synaptobrevin homolog 1; **PDBTitle:** structure of the yeast plasma membrane snare complex
27	c2zs0A_	Alignment	not modelled	9.0	7	**PDB header:**oxygen storage, oxygen transport **Chain:** A: **PDB Molecule:**extracellular giant hemoglobin major globin subunit a1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
28	c1yhuW_	Alignment	not modelled	8.9	15	**PDB header:**oxygen storage/transport **Chain:** W: **PDB Molecule:**hemoglobin b1a chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.

29	c1f02T_	Alignment	not modelled	8.5	100	**PDB header:**cell adhesion **Chain:** T: **PDB Molecule:**translocated intimin receptor; **PDBTitle:** crystal structure of c-terminal 282-residue fragment of2 intimin in complex with translocated intimin receptor3 (tir) intimin-binding domain
30	c3hg9B_	Alignment	not modelled	8.3	45	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**pilm; **PDBTitle:** crystal structure of putative pilm protein from pseudomonas aeruginosa2 2192
31	d1opsa_	Alignment	not modelled	8.3	40	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
32	c3kyqA_	Alignment	not modelled	8.3	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**synaptobrevin homolog ykt6; **PDBTitle:** lipid-induced conformational switch controls fusion activity of longin2 domain snare ykt6
33	c2bn5A_	Alignment	not modelled	8.2	35	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**psi; **PDBTitle:** p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
34	d1pgxa_	Alignment	not modelled	8.0	39	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
35	d1c8aa2	Alignment	not modelled	8.0	50	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
36	d2dy1a3	Alignment	not modelled	7.8	31	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
37	c2d2mC_	Alignment	not modelled	7.7	13	**PDB header:**oxygen storage/transport **Chain:** C: **PDB Molecule:**giant hemoglobin, b2(c) globin chain; **PDBTitle:** structure of an extracellular giant hemoglobin of the2 gutless beard worm oligobrachia mashikoi
38	c1n7sA_	Alignment	not modelled	7.6	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** high resolution structure of a truncated neuronal snare2 complex
39	c1wvoA_	Alignment	not modelled	7.5	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sialic acid synthase; **PDBTitle:** solution structure of rsgi ruh-029, an antifreeze protein2 like domain in human n-acetylneuraminic acid phosphate3 synthase gene.
40	d1fcla_	Alignment	not modelled	7.4	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
41	c2ckcA_	Alignment	not modelled	7.2	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
42	d2ckca1	Alignment	not modelled	7.2	29	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
43	d1qkza_	Alignment	not modelled	7.0	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
44	c3hd7A_	Alignment	not modelled	7.0	25	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
45	d1irqa_	Alignment	not modelled	6.8	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Omega transcriptional repressor
46	d1fd6a_	Alignment	not modelled	6.8	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
47	c3e0dA_	Alignment	not modelled	6.7	13	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
48	c1irqB_	Alignment	not modelled	6.5	50	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**omega transcriptional repressor; **PDBTitle:** crystal structure of omega transcriptional repressor at2 1.5a resolution
49	d1gb4a_	Alignment	not modelled	6.3	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
50	d2qfka1	Alignment	not modelled	6.1	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
51	d1mi0a_	Alignment	not modelled	5.9	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
52	d1urva_	Alignment	not modelled	5.9	6	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
53	c1ut0A_	Alignment	not modelled	5.9	6	**PDB header:**oxygen transport **Chain:** A: **PDB Molecule:**cytoglobin; **PDBTitle:** crystal structure of cytoglobin: the fourth globin type2 discovered in man displays heme hexa-coordination
54	c2ebzA	Alignment	not modelled	5.8	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 12;

54	c2ebzA_	Alignment	not modelled	5.8	22	**PDBTitle:** solution structure of the rgs domain from human regulator2 of g-protein signaling 12 (rgs12)
55	d1mhxa_	Alignment	not modelled	5.8	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
56	c1c8aA_	Alignment	not modelled	5.8	60	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**protein (antifreeze protein type iii); **PDBTitle:** nmr structure of intramolecular dimer antifreeze protein2 rd3, 40 sa structures
57	c3ideD_	Alignment	not modelled	5.7	33	**PDB header:**virus like particle **Chain:** D: **PDB Molecule:**capsid protein vp2; **PDBTitle:** structure of ipnv subviral particle
58	c3h9pB_	Alignment	not modelled	5.5	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative triphosphoribosyl-dephospho-coa synthase; **PDBTitle:** crystal structure of putative triphosphoribosyl-dephospho-coa synthase2 from archaeoglobus fulgidus
59	c2okrF_	Alignment	not modelled	5.4	47	**PDB header:**transferase **Chain:** F: **PDB Molecule:**map kinase-activated protein kinase 2; **PDBTitle:** crystal structure of the p38a-mapkap kinase 2 heterodimer
60	c2zs1D_	Alignment	not modelled	5.4	15	**PDB header:**oxygen storage, oxygen transport **Chain:** D: **PDB Molecule:**extracellular giant hemoglobin major globin subunit b1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
61	c1pznG_	Alignment	not modelled	5.4	41	**PDB header:**recombination **Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
62	d1hg7a_	Alignment	not modelled	5.3	60	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
63	d1bifa1	Alignment	not modelled	5.3	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
64	d2bv3a3	Alignment	not modelled	5.2	38	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
65	d2e50a1	Alignment	not modelled	5.2	23	**Fold:**NAP-like **Superfamily:**NAP-like **Family:**NAP-like
66	d1ucsa_	Alignment	not modelled	5.1	60	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain