Phyre^2

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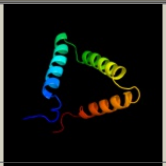
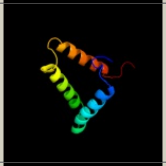
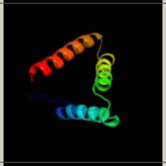
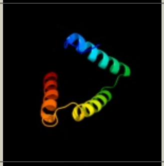
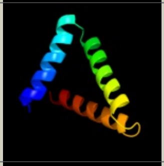
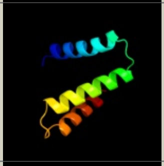
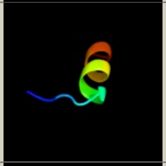
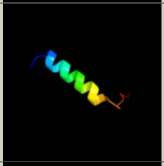
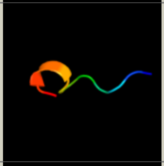
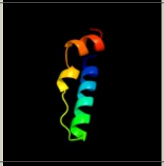
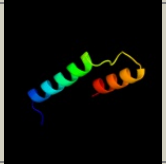
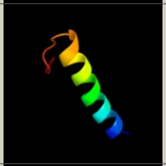
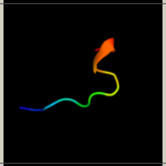
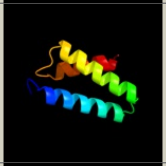
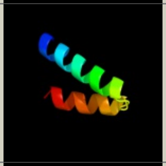
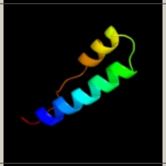
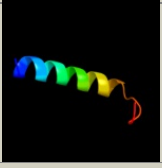
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jrxa1	Alignment		100.0	100	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
2	d2jpqa1	Alignment		100.0	52	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
3	d2juwa1	Alignment		100.0	56	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
4	d2juza1	Alignment		100.0	46	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
5	d2qtia1	Alignment		100.0	55	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
6	d2otaa1	Alignment		100.0	42	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
7	c2hjmB_	Alignment		31.4	47	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
8	d1gvnb_	Alignment		19.3	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Plasmid maintenance system epsilon/zeta, toxin zeta subunit
9	c2yiuE_	Alignment		18.4	45	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
10	d1s69a_	Alignment		16.5	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
11	c3kinB_	Alignment		16.2	38	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**kinesin heavy chain; **PDBTitle:** kinesin (dimeric) from rattus norvegicus

12	d1idra_	Alignment		16.1	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
13	c3fxeA_	Alignment		15.8	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein icmq; **PDBTitle:** crystal structure of interacting domains of icmr and icmq (seleno-2 derivative)
14	c2op8A_	Alignment		14.6	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
15	c3cwbQ_	Alignment		14.4	42	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
16	d1ls1a1	Alignment		13.2	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
17	c2b8kD_	Alignment		13.0	40	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase ii 32 kda **PDBTitle:** 12-subunit rna polymerase ii
18	d1dlwa_	Alignment		12.3	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
19	c2xykB_	Alignment		11.9	7	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**2-on-2 hemoglobin; **PDBTitle:** group ii 2-on-2 hemoglobin from the plant pathogen2 agrobacterium tumefaciens
20	c2bmmA_	Alignment		11.1	16	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca; **PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca
21	d1otfa_	Alignment	not modelled	10.5	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
22	c2qguA_	Alignment	not modelled	10.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
23	d1ppjd1	Alignment	not modelled	10.4	56	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
24	c2kjwA_	Alignment	not modelled	10.4	17	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
25	d1ooha_	Alignment	not modelled	10.3	25	**Fold:**EF Hand-like **Superfamily:**Insect pheromone/odorant-binding proteins **Family:**Insect pheromone/odorant-binding proteins
26	d1bjpa_	Alignment	not modelled	10.0	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
27	c2kinB_	Alignment	not modelled	9.8	38	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**kinesin; **PDBTitle:** kinesin (monomeric) from rattus norvegicus
28	d1jjcb4	Alignment	not modelled	9.6	24	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS

29	c3abfB_	Alignment	not modelled	9.6	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
30	d3cx5d1	Alignment	not modelled	9.4	67	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
31	d1sb0a_	Alignment	not modelled	9.4	11	**Fold:**Kix domain of CBP (creb binding protein) **Superfamily:**Kix domain of CBP (creb binding protein) **Family:**Kix domain of CBP (creb binding protein)
32	c3ry0A_	Alignment	not modelled	9.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
33	d1wgwa_	Alignment	not modelled	9.3	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
34	c3eujB_	Alignment	not modelled	9.3	15	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, symmetric dimer
35	d1j8yf1	Alignment	not modelled	9.3	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
36	c2f59B_	Alignment	not modelled	9.1	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
37	d1nqua_	Alignment	not modelled	8.8	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
38	c2x4kB_	Alignment	not modelled	8.7	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
39	c1dlyA_	Alignment	not modelled	8.7	14	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
40	d1dlya_	Alignment	not modelled	8.7	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
41	d1ux8a_	Alignment	not modelled	8.6	9	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
42	c3m20A_	Alignment	not modelled	8.3	4	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
43	c1p84D_	Alignment	not modelled	8.1	60	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
44	d1ul7a_	Alignment	not modelled	7.9	20	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1
45	d2vy4a1	Alignment	not modelled	7.9	46	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**CHHC finger
46	d1c41a_	Alignment	not modelled	7.8	21	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
47	d1ejba_	Alignment	not modelled	7.8	7	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
48	c3b64A_	Alignment	not modelled	7.7	11	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
49	c3h0gP_	Alignment	not modelled	7.3	22	**PDB header:**transcription **Chain:** P: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb4; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
50	c2erbA_	Alignment	not modelled	7.2	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant binding protein; **PDBTitle:** agamobp1, and odorant binding protein from anopheles2 gambiae complexed with peg
51	c3mb2G_	Alignment	not modelled	7.1	15	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
52	c3mlcC_	Alignment	not modelled	7.0	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
53	d1qzxa1	Alignment	not modelled	6.9	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins

						Family: Domain of the SRP/SRP receptor G-proteins
54	c3aq8A_	Alignment	not modelled	6.9	6	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
55	c2kscA_	Alignment	not modelled	6.9	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
56	d1y14a_	Alignment	not modelled	6.8	40	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNA polymerase II subunit RBP4 (RpoF)
57	c3mk9A_	Alignment	not modelled	6.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ricin; **PDBTitle:** stabilized ricin immunogen 1-33/44-198
58	d2aala1	Alignment	not modelled	6.3	10	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
59	d1m47a_	Alignment	not modelled	6.2	27	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
60	d1di0a_	Alignment	not modelled	6.2	10	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
61	d2c35a1	Alignment	not modelled	6.1	28	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNA polymerase II subunit RBP4 (RpoF)
62	c2p5tD_	Alignment	not modelled	6.1	27	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**pezt; **PDBTitle:** molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
63	d1gyxa_	Alignment	not modelled	5.9	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
64	d1rvv1_	Alignment	not modelled	5.5	24	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
65	c3n4dF_	Alignment	not modelled	5.3	4	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
66	c2vxgB_	Alignment	not modelled	5.2	33	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cg6181-pa, isoform a; **PDBTitle:** crystal structure of the conserved c-terminal region of ge-2 1
67	c2j37W_	Alignment	not modelled	5.2	13	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
68	d1c2ya_	Alignment	not modelled	5.2	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase