Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8J4
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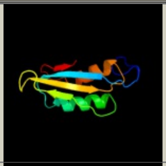
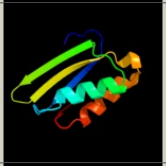
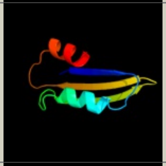
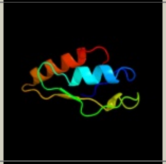
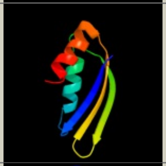
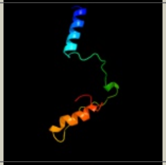
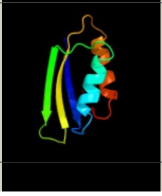
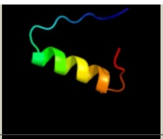
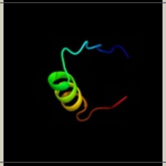
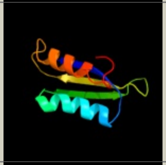
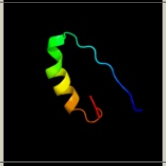
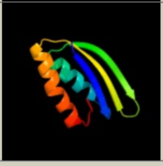
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rwua_	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
2	c1rwuA_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
3	d2joqa1	Alignment		99.9	12	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**HP0495-like
4	c3ibwA_	Alignment		96.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
5	d1sc6a3	Alignment		82.0	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
6	d1zpva1	Alignment		68.0	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
7	c2jsxA_	Alignment		67.5	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
8	d1u8sa1	Alignment		64.5	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
9	c2cg4B_	Alignment		64.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
10	d2fgca2	Alignment		57.6	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
11	d2f1fa1	Alignment		56.6	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like

12	d1u69a_	Alignment		55.4	7	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
13	d1tsja_	Alignment		48.8	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
14	d2pc6a2	Alignment		46.6	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
15	c2f1fA_	Alignment		43.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
16	c3n0vD_	Alignment		41.7	6	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
17	c3k5pA_	Alignment		40.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
18	d2qmwa2	Alignment		38.7	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
19	d2cg4a2	Alignment		38.2	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
20	c1u8sB_	Alignment		37.8	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
21	c3omsA_	Alignment	not modelled	29.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phnb protein; **PDBTitle:** putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
22	c2kxoA_	Alignment	not modelled	28.6	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
23	c2fgcA_	Alignment	not modelled	28.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
24	d1u8sa2	Alignment	not modelled	26.9	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
25	d2gz1a2	Alignment	not modelled	21.3	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
26	c2e1cA_	Alignment	not modelled	19.6	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
27	c2pc6C_	Alignment	not modelled	17.0	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
28	d1ygya3	Alignment	not modelled	16.6	3	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal)

						domain
29	c2vbzA_	Alignment	not modelled	15.5	18	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
30	d1u7ia_	Alignment	not modelled	14.0	22	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
31	d1phza1	Alignment	not modelled	13.1	7	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
32	d1ev0a_	Alignment	not modelled	12.5	20	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
33	c2nyiB_	Alignment	not modelled	12.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
34	d2aala1	Alignment	not modelled	12.2	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
35	d1o8ba2	Alignment	not modelled	12.2	16	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
36	d1m0sa2	Alignment	not modelled	11.1	19	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
37	d1uj4a2	Alignment	not modelled	10.2	19	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
38	c2yx5A_	Alignment	not modelled	9.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
39	c1cf2Q_	Alignment	not modelled	9.8	10	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**protein (glyceraldehyde-3-phosphate **PDBTitle:** three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus
40	c3hjaB_	Alignment	not modelled	9.7	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
41	d1lk5a2	Alignment	not modelled	9.6	26	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
42	c2e1aD_	Alignment	not modelled	9.5	7	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
43	d1lp1b_	Alignment	not modelled	9.4	19	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
44	d1fc2c_	Alignment	not modelled	9.4	19	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
45	d2cyya2	Alignment	not modelled	9.4	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
46	c1i1gA_	Alignment	not modelled	9.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
47	d2drpa2	Alignment	not modelled	8.1	22	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
48	c3mgjA_	Alignment	not modelled	7.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
49	c3ptyA_	Alignment	not modelled	7.7	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arabinosyltransferase c; **PDBTitle:** crystal structure of the c-terminal extracellular domain of2 mycobacterium tuberculosis embc
50	c3i4pA_	Alignment	not modelled	7.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
51	c3nrbD_	Alignment	not modelled	7.3	6	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
52	d1deeg_	Alignment	not modelled	7.1	13	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
53	d2hjsa2	Alignment	not modelled	7.0	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain

						Family:GAPDH-like
54	c1vdxA_	Alignment	not modelled	6.9	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**hypothetical protein ph0099; **PDBTitle:** crystal structure of a pyrococcus horikoshii protein with2 similarities to 2'5' rna-ligase
55	c1zyiA_	Alignment	not modelled	6.9	5	**PDB header:**translation **Chain:** A: **PDB Molecule:**methylosome subunit picln; **PDBTitle:** solution structure of icln, a multifunctional protein2 involved in regulatory mechanisms as different as cell3 volume regulation and rna splicing
56	c2zw2B_	Alignment	not modelled	6.5	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
57	c2cfxD_	Alignment	not modelled	6.5	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
58	d2jwda1	Alignment	not modelled	6.5	19	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
59	d1iuha_	Alignment	not modelled	6.3	16	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**2'-5' RNA ligase LigT
60	d1udma_	Alignment	not modelled	6.1	15	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
61	c2e7xA_	Alignment	not modelled	6.1	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
62	d2nzca1	Alignment	not modelled	6.1	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
63	d1j7ma_	Alignment	not modelled	5.9	25	**Fold:**Kringle-like **Superfamily:**Kringle-like **Family:**Fibronectin type II module
64	c2k49A_	Alignment	not modelled	5.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
65	c1qo6A_	Alignment	not modelled	5.5	13	**PDB header:**cell adhesion protein **Chain:** A: **PDB Molecule:**fibronectin; **PDBTitle:** solution structure of a pair of modules from the2 gelatin-binding domain of fibronectin
66	c1fllA_	Alignment	not modelled	5.5	22	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** molecular basis for cd40 signaling mediated by traf3
67	d1mb4a2	Alignment	not modelled	5.5	19	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
68	d1ks0a_	Alignment	not modelled	5.4	13	**Fold:**Kringle-like **Superfamily:**Kringle-like **Family:**Fibronectin type II module
69	c3lr4A_	Alignment	not modelled	5.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
70	d1eaka5	Alignment	not modelled	5.3	27	**Fold:**Kringle-like **Superfamily:**Kringle-like **Family:**Fibronectin type II module
71	d1f08a_	Alignment	not modelled	5.3	15	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Replication initiation protein E1
72	c3l20A_	Alignment	not modelled	5.2	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from staphylococcus aureus
73	c2yyyB_	Alignment	not modelled	5.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
74	d1l6ja5	Alignment	not modelled	5.1	13	**Fold:**Kringle-like **Superfamily:**Kringle-like **Family:**Fibronectin type II module