Phyre^2

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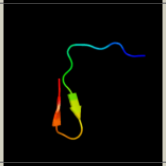
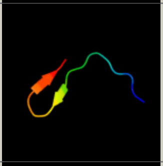
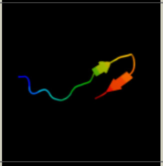
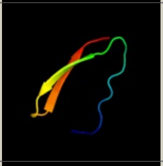
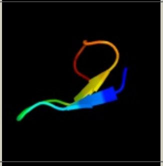
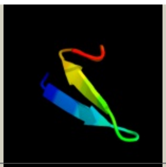
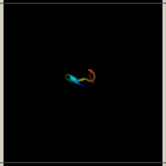
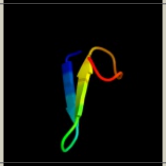
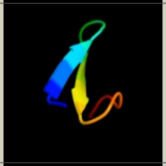
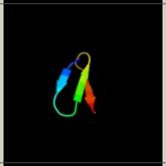
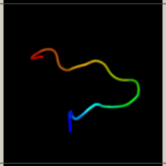
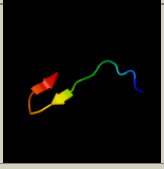
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j20a2	Alignment		38.9	21	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
2	c1nvpC_	Alignment		26.0	18	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia beta chain; **PDBTitle:** human tfiia/tbp/dna complex
3	d1nvpc_	Alignment		26.0	18	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
4	c1nh2C_	Alignment		25.4	18	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
5	d1nh2c_	Alignment		25.4	18	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
6	c3ipfA_	Alignment		24.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
7	c3obaA_	Alignment		23.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
8	c2pfuA_	Alignment		22.6	5	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
9	d1k92a2	Alignment		22.6	33	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
10	c1bhgB_	Alignment		21.5	19	**PDB header:**glycosidase **Chain:** B: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** human beta-glucuronidase at 2.6 a resolution
11	c3mv14_	Alignment		21.0	25	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium

12	c1jz6C_	Alignment		20.7	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
13	c3lpgA_	Alignment		20.4	6	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea
14	c1yq2C_	Alignment		19.4	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1)
15	d2g82a1	Alignment		19.1	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
16	c3bgaB_	Alignment		19.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
17	d1obfo1	Alignment		19.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	d1vc2a1	Alignment		18.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
19	d6paxa1	Alignment		18.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
20	d1ytfc_	Alignment		18.1	19	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
21	d1hdgo1	Alignment	not modelled	16.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
22	c1k97A_	Alignment	not modelled	16.4	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
23	d2b4ro1	Alignment	not modelled	16.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
24	d1gado1	Alignment	not modelled	14.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
25	d1k78a1	Alignment	not modelled	13.3	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
26	d1d6za4	Alignment	not modelled	12.7	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
27	c1rm1C_	Alignment	not modelled	12.3	19	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
28	c3mhaB_	Alignment	not modelled	11.9	83	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**lipoprotein lprg; **PDBTitle:** crystal structure of lprg from mycobacterium tuberculosis bound to pim
						Fold:NAD(P)-binding Rossmann-fold domains

29	d1u8fo1	Alignment	not modelled	11.6	28	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
30	d1dk7a_	Alignment	not modelled	11.2	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
31	d1zud21	Alignment	not modelled	10.6	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
32	d2caya1	Alignment	not modelled	10.3	21	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
33	d1oela2	Alignment	not modelled	10.2	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
34	c2w7vB_	Alignment	not modelled	10.1	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** periplasmic domain of epsl from vibrio parahaemolyticus
35	c3cmgA_	Alignment	not modelled	10.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
36	c1ifpA_	Alignment	not modelled	9.9	32	**PDB header:**virus **Chain:** A: **PDB Molecule:**major coat protein assembly; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
37	d1k8ba_	Alignment	not modelled	9.8	7	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
38	d3cmco1	Alignment	not modelled	9.3	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
39	d3gpdg1	Alignment	not modelled	8.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	d1yqea1	Alignment	not modelled	8.6	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
41	d2odgc1	Alignment	not modelled	8.4	50	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
42	d1dssg1	Alignment	not modelled	8.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	d1j0xo1	Alignment	not modelled	7.8	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	d1srva_	Alignment	not modelled	7.6	50	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
45	c1tygG_	Alignment	not modelled	7.5	17	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
46	c1kh2D_	Alignment	not modelled	7.4	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
47	c2jv8A_	Alignment	not modelled	7.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ne1242; **PDBTitle:** solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4
48	d1dm9a_	Alignment	not modelled	7.2	46	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
49	c1dm9A_	Alignment	not modelled	7.2	46	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
50	c3bbnI_	Alignment	not modelled	7.1	27	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein s9; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
51	d2vqei1	Alignment	not modelled	7.1	55	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
52	c3m6cA_	Alignment	not modelled	6.9	56	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**60 kda chaperonin 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis groel1 apical domain
53	c2gfqC_	Alignment	not modelled	6.8	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
54	c2kd2A_	Alignment	not modelled	6.7	26	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** nmr structure of faim-ctd
55	d1sjpa2	Alignment	not modelled	6.6	50	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like

						Family: GroEL-like chaperone, apical domain
56	d1x87a_	Alignment	not modelled	6.6	27	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
57	c2cqjA_	Alignment	not modelled	6.6	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein **PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
58	c3fn9B_	Alignment	not modelled	6.5	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
59	c2jtxA_	Alignment	not modelled	6.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor iie subunit **PDBTitle:** nmr structure of the tfiie-alpha carboxyl terminus
60	d2gy9i1	Alignment	not modelled	6.4	36	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
61	c3em0A_	Alignment	not modelled	6.4	9	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**ileal bile acid-binding protein; **PDBTitle:** crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b).
62	d1sjpa3	Alignment	not modelled	6.3	13	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
63	c2dw3A_	Alignment	not modelled	6.2	30	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**intrinsic membrane protein pufx; **PDBTitle:** solution structure of the rhodobacter sphaeroides pufx2 membrane protein
64	d1tygb_	Alignment	not modelled	6.1	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
65	d1ffva2	Alignment	not modelled	6.1	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
66	d1kh0a_	Alignment	not modelled	6.1	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
67	c2zkqi_	Alignment	not modelled	6.1	27	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
68	d1we3a2	Alignment	not modelled	6.1	50	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
69	d1v6ga2	Alignment	not modelled	6.0	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
70	d1gxqa_	Alignment	not modelled	5.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
71	d1vioa2	Alignment	not modelled	5.9	10	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
72	c2rnqA_	Alignment	not modelled	5.9	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor iie subunit **PDBTitle:** solution structure of the c-terminal acidic domain of tfiie2 alpha
73	d2cu3a1	Alignment	not modelled	5.9	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
74	c2jwlB_	Alignment	not modelled	5.9	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
75	c3ci0K_	Alignment	not modelled	5.8	11	**PDB header:**protein transport **Chain:** K: **PDB Molecule:**pseudopilin gspk; **PDBTitle:** the crystal structure of the gspk-gspi-gspj complex from2 enterotoxigenic escherichia coli type 2 secretion system
76	c2k6xA_	Alignment	not modelled	5.8	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
77	c2yglA_	Alignment	not modelled	5.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blood group a-and b-cleaving endo-beta-galactosidase; **PDBTitle:** the x-ray crystal structure of tandem cbm51 modules of sp3gh98, the2 family 98 glycoside hydrolase from streptococcus pneumoniae3 sp3-bs71
78	d1kida_	Alignment	not modelled	5.6	38	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
79	d1z45a1	Alignment	not modelled	5.6	19	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Aldose 1-epimerase (mutarotase)
80	d2pkqo1	Alignment	not modelled	5.6	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						PDB header:ligase

81	c3bmaC_	Alignment	not modelled	5.5	11	**Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase; **PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
82	d2gfqa1	Alignment	not modelled	5.5	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
83	c3sy6A_	Alignment	not modelled	5.4	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbrial protein bf1861; **PDBTitle:** crystal structure of a fimbrial protein bf1861 [bacteroides fragilis2 nctc 9343] (bf1861) from bacteroides fragilis nctc 9343 at 1.90 a3 resolution
84	d1dgja2	Alignment	not modelled	5.3	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
85	d1rm6c2	Alignment	not modelled	5.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
86	c2jzyA_	Alignment	not modelled	5.1	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
87	d2cfua1	Alignment	not modelled	5.1	14	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Alkylsulfatase C-terminal domain-like
88	c2wj7D_	Alignment	not modelled	5.0	32	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** human alphab crystallin