Phyre2

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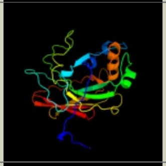
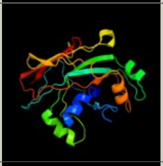
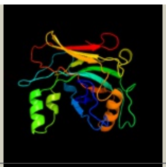
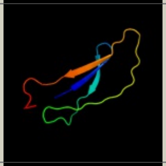
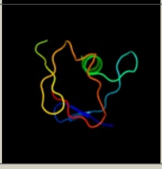
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nr9a_	Alignment		100.0	99	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
2	c1i7oC_	Alignment		100.0	39	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
3	c3l53F_	Alignment		100.0	46	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative fumarylacetoacetate isomerase/hydrolase; **PDBTitle:** crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
4	c3r6oA_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; **PDBTitle:** crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
5	d1gtta2	Alignment		100.0	39	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
6	c2dfuB_	Alignment		100.0	36	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
7	c1wzoC_	Alignment		100.0	35	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hpce; **PDBTitle:** crystal structure of the hpce from thermus thermophilus hb8
8	c3lzkC_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
9	c3qdfA_	Alignment		100.0	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
10	d1gtta1	Alignment		100.0	29	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
11	d1sawa_	Alignment		100.0	47	**Fold:**FAH **Superfamily:**FAH **Family:**FAH

12	d1nkqa_	Alignment		100.0	36	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
13	c2q1dX_	Alignment		100.0	22	**PDB header:**lyase **Chain:** X: **PDB Molecule:**2-keto-3-deoxy-d-arabinonate dehydratase; **PDBTitle:** 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
14	d1hyoa2	Alignment		100.0	24	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
15	c1hyoB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fumarylacetoacetate hydrolase; **PDBTitle:** crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
16	d1sv6a_	Alignment		100.0	18	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
17	c2eb5D_	Alignment		100.0	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2-oxo-hept-3-ene-1,7-dioate hydratase; **PDBTitle:** crystal structure of hpcg complexed with oxalate
18	d1c3ha_	Alignment		56.5	16	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
19	d2cu3a1	Alignment		51.5	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
20	c2kl0A_	Alignment		43.3	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
21	c3cwiA_	Alignment	not modelled	36.7	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
22	d1gr3a_	Alignment	not modelled	35.4	13	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
23	c1gr3A_	Alignment	not modelled	35.4	13	**PDB header:**collagen **Chain:** A: **PDB Molecule:**collagen x; **PDBTitle:** structure of the human collagen x nc1 trimer
24	d2evra2	Alignment	not modelled	34.9	37	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
25	d1zud21	Alignment	not modelled	30.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
26	d1pk6c_	Alignment	not modelled	29.4	21	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
27	d2vbua1	Alignment	not modelled	29.2	31	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
28	d1tygb_	Alignment	not modelled	28.9	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
						PDB header:structural protein

29	c2xivA_	Alignment	not modelled	25.6	29	**Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
30	c1tygG_	Alignment	not modelled	25.3	16	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
31	d2f4la1	Alignment	not modelled	22.1	35	**Fold:**CUB-like **Superfamily:**Acetamidase/Formamidase-like **Family:**Acetamidase/Formamidase-like
32	d2g1la1	Alignment	not modelled	19.3	35	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
33	d1t8sa_	Alignment	not modelled	19.2	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
34	d1o91a_	Alignment	not modelled	18.3	20	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
35	c1o91B_	Alignment	not modelled	18.3	20	**PDB header:**collagen **Chain:** B: **PDB Molecule:**collagen alpha 1(viii) chain; **PDBTitle:** crystal structure of a collagen viii nc1 domain trimer
36	d1pk6a_	Alignment	not modelled	17.0	21	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
37	c3gt2A_	Alignment	not modelled	15.2	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
38	c2ka3C_	Alignment	not modelled	13.9	32	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
39	c2fg0B_	Alignment	not modelled	13.1	39	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
40	d1pk6b_	Alignment	not modelled	12.6	20	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
41	d1mvfd_	Alignment	not modelled	12.1	20	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/Peml addiction antidote
42	c2pkpA_	Alignment	not modelled	10.9	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
43	d1dm9a_	Alignment	not modelled	10.9	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
44	c1dm9A_	Alignment	not modelled	10.9	18	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
45	d2qamc2	Alignment	not modelled	9.8	46	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	c3m9bK_	Alignment	not modelled	9.7	26	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
47	d1ds1a_	Alignment	not modelled	9.4	11	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
48	c3g8qA_	Alignment	not modelled	9.2	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump **PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
49	c2e6zA_	Alignment	not modelled	8.7	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
50	d1rl2a2	Alignment	not modelled	8.4	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	d1v7la_	Alignment	not modelled	8.1	49	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
52	c3pbiA_	Alignment	not modelled	7.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
53	d1x5na1	Alignment	not modelled	7.7	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
54	d1g7sa1	Alignment	not modelled	7.6	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
						PDB header:transcription

55	c2z8uQ_	Alignment	not modelled	6.9	25	**Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
56	c1gxcA_	Alignment	not modelled	6.9	21	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
57	d1gxca_	Alignment	not modelled	6.9	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
58	d2v4ja2	Alignment	not modelled	6.8	16	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
59	c3h1yA_	Alignment	not modelled	6.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
60	c3mjjD_	Alignment	not modelled	6.5	31	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted acetamidase/formamidase; **PDBTitle:** crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
61	d2i4sa1	Alignment	not modelled	6.5	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
62	d2ba0a2	Alignment	not modelled	6.5	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
63	c3eiwA_	Alignment	not modelled	6.2	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**htsa protein; **PDBTitle:** crystal structure of staphylococcus aureus lipoprotein, htsa
64	c1mp9B_	Alignment	not modelled	6.1	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
65	c3frnA_	Alignment	not modelled	6.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flga; **PDBTitle:** crystal structure of flagellar protein flga from thermotoga maritima2 msb8
66	d2q07a1	Alignment	not modelled	6.0	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
67	c2eh0A_	Alignment	not modelled	5.9	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b; **PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
68	c3nnkC_	Alignment	not modelled	5.7	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
69	d2q8oa1	Alignment	not modelled	5.7	38	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
70	c1d3uA_	Alignment	not modelled	5.6	16	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**tata-binding protein; **PDBTitle:** tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
71	d1hmja_	Alignment	not modelled	5.6	38	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
72	c1w9qB_	Alignment	not modelled	5.5	21	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the pdz tandem of human syntenin in2 complex with tnefaf peptide
73	c2r3yC_	Alignment	not modelled	5.4	18	**PDB header:**hydrolase/hydrolase activator **Chain:** C: **PDB Molecule:**protease degs; **PDBTitle:** crystal structure of the degs protease in complex with the2 ywf activating peptide
74	c3mb8A_	Alignment	not modelled	5.3	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
75	d1qe5a_	Alignment	not modelled	5.3	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
76	d1o6aa_	Alignment	not modelled	5.2	10	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)