Phyre2

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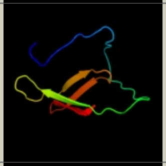
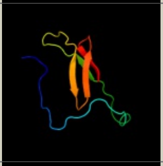
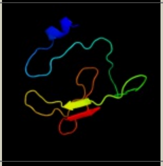
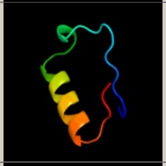
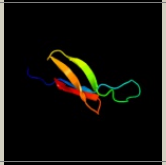
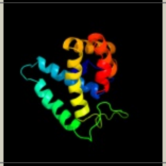
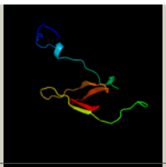
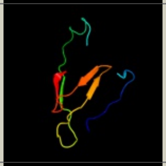
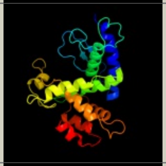
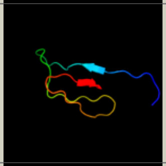
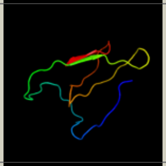
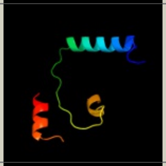
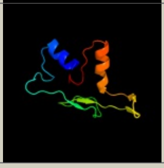
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b37A_	Alignment		88.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
2	c3ebhA_	Alignment		85.6	12	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**m1 family aminopeptidase; **PDBTitle:** structure of the m1 alanylaminopeptidase from malaria complexed with2 bestatin
3	c2boyC_	Alignment		84.8	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
4	c2xsuA_	Alignment		82.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2 dioxygenase; **PDBTitle:** crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
5	c2xdtA_	Alignment		82.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1
6	d1s9aa_	Alignment		81.1	24	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
7	c3rhtB_	Alignment		79.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**(gatase1)-like protein; **PDBTitle:** crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
8	c2gtqA_	Alignment		79.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
9	d3pccm_	Alignment		76.6	41	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
10	c1z5hB_	Alignment		75.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
11	c2azqA_	Alignment		74.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1

12	d2burb1	Alignment		74.3	25	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
13	c3n9tA_	Alignment		71.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
14	c1v06A_	Alignment		70.2	18	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** axh domain of the transcription factor hbp1 from m.musculus
15	c3hj8A_	Alignment		60.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
16	c3se6A_	Alignment		58.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 2; **PDBTitle:** crystal structure of the human endoplasmic reticulum aminopeptidase 2
17	d2bura1	Alignment		58.1	33	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
18	c1tmxA_	Alignment		56.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
19	d1yqea1	Alignment		55.5	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
20	d1bqba_	Alignment		51.7	21	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
21	c3nqzB_	Alignment	not modelled	51.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed vibriolysin mcp-02 with e369a2 mutation
22	d1npca_	Alignment	not modelled	51.0	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
23	c3mdjB_	Alignment	not modelled	50.5	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
24	c3nqxA_	Alignment	not modelled	48.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of vibriolysin mcp-02 mature enzyme, a zinc2 metalloprotease from m4 family
25	c3qnfA_	Alignment	not modelled	48.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
26	c1slmA_	Alignment	not modelled	45.8	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
27	d1cc5a_	Alignment	not modelled	44.4	6	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
28	c1w5cT_	Alignment	not modelled	43.4	35	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**cytochrome c-550; **PDBTitle:** photosystem ii from thermosynechococcus elongatus

29	d1kjpa_	Alignment	not modelled	43.2	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
30	c2vqxA_	Alignment	not modelled	42.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metalloproteinase; **PDBTitle:** precursor of protealysin, metalloproteinase from serratia2 proteamaculans.
31	d1kx7a_	Alignment	not modelled	41.5	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
32	d2gk3a1	Alignment	not modelled	41.2	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**STM3548-like
33	c2c1dB_	Alignment	not modelled	39.6	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
34	d2j44a2	Alignment	not modelled	39.2	24	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
35	c3sozC_	Alignment	not modelled	38.4	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**cytoplasmic protein stm1381; **PDBTitle:** cytoplasmic protein stm1381 from salmonella typhimurium lt2
36	c1w2lA_	Alignment	not modelled	36.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
37	d1g9ka2	Alignment	not modelled	35.3	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
38	d2iqha1	Alignment	not modelled	35.0	15	**Fold:**Flu NP-like **Superfamily:**flu NP-like **Family:**Flu NP-like
39	d1h32b_	Alignment	not modelled	35.0	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
40	d1a56a_	Alignment	not modelled	34.7	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
41	d1hroa_	Alignment	not modelled	34.3	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
42	d1qwta_	Alignment	not modelled	34.1	30	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**Interferon regulatory factor 3 (IRF3), transactivation domain
43	c1om8A_	Alignment	not modelled	32.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
44	c1r8oA_	Alignment	not modelled	32.3	50	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kunitz trypsin inhibitor; **PDBTitle:** crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifera langsdorffii seeds
45	d3pcca_	Alignment	not modelled	31.3	29	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
46	d2j43a1	Alignment	not modelled	31.2	32	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
47	d1kb0a1	Alignment	not modelled	31.0	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
48	d1t0ba_	Alignment	not modelled	30.8	6	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
49	c1xi4D_	Alignment	not modelled	30.8	22	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**clathrin heavy chain; **PDBTitle:** clathrin d6 coat
50	d1dmha_	Alignment	not modelled	30.5	22	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
51	d1h3ga2	Alignment	not modelled	30.4	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
52	c2kp6A_	Alignment	not modelled	30.0	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
53	c3e8vA_	Alignment	not modelled	29.2	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible transglutaminase-family protein; **PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
54	d1mz4a_	Alignment	not modelled	29.0	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
55	d1f1fa_	Alignment	not modelled	29.0	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c

						Family:monodomain cytochrome c
56	d1lfma_	Alignment	not modelled	27.9	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
57	d1cxca_	Alignment	not modelled	27.7	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	d1yb3a1	Alignment	not modelled	27.4	35	**Fold:**YktB/PF0168-like **Superfamily:**YktB/PF0168-like **Family:**PF0168-like
59	d1ccra_	Alignment	not modelled	27.4	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
60	c2gfqC_	Alignment	not modelled	27.3	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
61	d1u4ga_	Alignment	not modelled	27.3	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Thermolysin-like
62	d1kapp2	Alignment	not modelled	26.8	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
63	c2rjqA_	Alignment	not modelled	26.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adamts-5; **PDBTitle:** crystal structure of adamts5 with inhibitor bound
64	d1rqpa1	Alignment	not modelled	26.6	15	**Fold:**Bacterial fluorinating enzyme, C-terminal domain **Superfamily:**Bacterial fluorinating enzyme, C-terminal domain **Family:**Bacterial fluorinating enzyme, C-terminal domain
65	d1cota_	Alignment	not modelled	26.5	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
66	d1h8la1	Alignment	not modelled	25.8	18	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
67	c2h5gA_	Alignment	not modelled	24.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta 1-pyrroline-5-carboxylate synthetase; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate synthetase
68	d1m70a2	Alignment	not modelled	24.8	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
69	c2zonG_	Alignment	not modelled	24.3	13	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
70	c2lb0A_	Alignment	not modelled	23.9	14	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
71	c2lazA_	Alignment	not modelled	23.7	14	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
72	d1nkga1	Alignment	not modelled	23.5	16	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Rhamnogalacturonase B, RhgB, middle domain
73	c2zzsW_	Alignment	not modelled	23.4	33	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
74	c2v4bB_	Alignment	not modelled	23.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adamts-1; **PDBTitle:** crystal structure of human adamts-1 catalytic domain and2 cysteine-rich domain (apo-form)
75	c2j83B_	Alignment	not modelled	23.1	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
76	c2zxyA_	Alignment	not modelled	22.9	13	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
77	d3c2ca_	Alignment	not modelled	22.8	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
78	d1jb7b_	Alignment	not modelled	22.8	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
79	d2j43a2	Alignment	not modelled	22.4	24	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
80	c1su3A_	Alignment	not modelled	22.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
81	d1i8oa_	Alignment	not modelled	22.0	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

82	d1m70a1	Alignment	not modelled	21.6	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
83	c1wgzC_	Alignment	not modelled	21.6	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**carboxypeptidase 1; **PDBTitle:** crystal structure of carboxypeptidase 1 from thermus thermophilus
84	c1uwyA_	Alignment	not modelled	21.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
85	c2o1wB_	Alignment	not modelled	21.2	23	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
86	d1c6sa_	Alignment	not modelled	21.1	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
87	d1j3sa_	Alignment	not modelled	20.7	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
88	c1cwvA_	Alignment	not modelled	20.6	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**invasin; **PDBTitle:** crystal structure of invasin: a bacterial integrin-binding protein
89	d1dy7b1	Alignment	not modelled	20.4	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
90	c1otcB_	Alignment	not modelled	20.4	23	**PDB header:**protein/dna **Chain:** B: **PDB Molecule:**protein (telomere-binding protein beta subunit); **PDBTitle:** the o. nova telomere end binding protein complexed with2 single strand dna
91	d1c52a_	Alignment	not modelled	20.3	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
92	c2i47A_	Alignment	not modelled	20.1	71	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
93	d2i47a1	Alignment	not modelled	20.1	71	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
94	d1fi3a_	Alignment	not modelled	20.0	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
95	c3evpA_	Alignment	not modelled	19.8	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**circular-permutated green fluorescent protein; **PDBTitle:** crystal structure of circular-permutated egfp
96	d1ql3a_	Alignment	not modelled	19.7	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
97	d1h9xa1	Alignment	not modelled	19.6	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
98	d1e29a_	Alignment	not modelled	19.5	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
99	c2d0sA_	Alignment	not modelled	19.5	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus