Phyre^2

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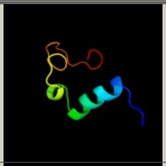
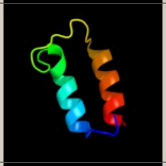
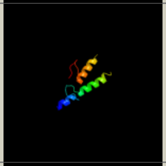
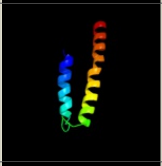
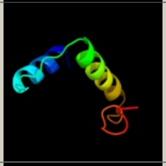
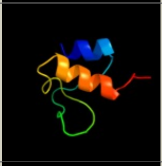
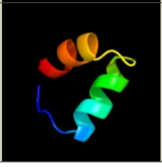
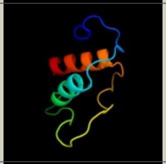
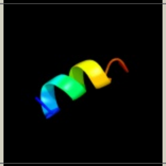
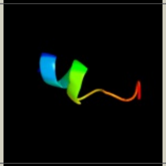
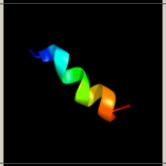
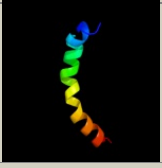
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jvwA_	Alignment		66.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
2	c2fwtA_	Alignment		47.4	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
3	d1zeea1	Alignment		40.5	33	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
4	c1vngA_	Alignment		22.1	13	**PDB header:**haloperoxidase **Chain:** A: **PDB Molecule:**vanadium chloroperoxidase; **PDBTitle:** chloroperoxidase from the fungus curvularia inaequalis:2 mutant h404a
5	c1wr1B_	Alignment		20.4	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
6	c2hl7A_	Alignment		19.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
7	c1yx3A_	Alignment		18.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
8	c2dnwA_	Alignment		18.1	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
9	c3g2bA_	Alignment		17.1	23	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
10	c2kw0A_	Alignment		16.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
11	d1wj7a1	Alignment		16.1	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain

12	c3hieA_	Alignment		15.9	44	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**exocyst complex component sec3; **PDBTitle:** structure of the membrane-binding domain of the sec3 subunit2 of the exocyst complex
13	c2bh7A_	Alignment		15.5	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
14	d1veja1	Alignment		11.7	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
15	c1ziiB_	Alignment		10.9	46	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
16	c1ziiA_	Alignment		10.9	46	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the dimeric2 state
17	c1zijA_	Alignment		10.4	46	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
18	c1zijC_	Alignment		10.4	46	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
19	c1zijB_	Alignment		10.4	46	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant asn16aba in the trimeric2 state
20	c2pjwH_	Alignment		10.2	21	**PDB header:**endocytosis/exocytosis **Chain:** H: **PDB Molecule:**uncharacterized protein yhl002w; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
21	c2l3gA_	Alignment	not modelled	10.2	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** solution nmr structure of ch domain of rho guanine nucleotide exchange2 factor 7 from homo sapiens, northeast structural genomics consortium3 target hr4495e
22	d1sr9a1	Alignment	not modelled	10.1	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
23	d1whra_	Alignment	not modelled	9.9	13	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
24	d1nq4a_	Alignment	not modelled	9.5	20	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
25	d1t8ka_	Alignment	not modelled	8.9	13	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
26	c2cnrA_	Alignment	not modelled	8.8	3	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structural studies on the interaction of scfas acp with2 acps
27	c2fq2A_	Alignment	not modelled	8.2	16	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
28	c2d86A_	Alignment	not modelled	8.0	28	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**vav-3 protein; **PDBTitle:** solution structure of the ch domain from human vav-3 protein

29	c2yfvC_	Alignment	not modelled	7.4	28	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**scm3; **PDBTitle:** the heterotrimeric complex of kluyveromyces lactis scm3, cse4 and h4
30	c2kwlA_	Alignment	not modelled	7.4	10	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
31	c2lafA_	Alignment	not modelled	7.3	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein 34; **PDBTitle:** nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
32	c2ae8C_	Alignment	not modelled	7.3	25	**PDB header:**lyase **Chain:** C: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase; **PDBTitle:** crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
33	c2g2qB_	Alignment	not modelled	7.2	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the crystal structure of g4, the poxviral disulfide oxidoreductase2 essential for cytoplasmic disulfide bond formation
34	d1gjja2	Alignment	not modelled	7.1	18	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
35	c2kebA_	Alignment	not modelled	7.0	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
36	d1q9ja1	Alignment	not modelled	7.0	28	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
37	c3ce7A_	Alignment	not modelled	6.9	8	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
38	d1whca_	Alignment	not modelled	6.8	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
39	c3pcqX_	Alignment	not modelled	6.7	58	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
40	d1jb0x_	Alignment	not modelled	6.6	58	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
41	c1jb0X_	Alignment	not modelled	6.6	58	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
42	d1rkta2	Alignment	not modelled	6.5	19	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
43	d2hlya1	Alignment	not modelled	6.4	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Atu2299-like
44	d1zcba1	Alignment	not modelled	6.2	36	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
45	c2fvfA_	Alignment	not modelled	6.2	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** structure of 10:0-acp (protein with docked fatty acid)
46	d1n7va_	Alignment	not modelled	6.2	60	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
47	c2dakA_	Alignment	not modelled	6.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
48	d1cipa1	Alignment	not modelled	5.8	38	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
49	d1tada1	Alignment	not modelled	5.8	38	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
50	c3ejbC_	Alignment	not modelled	5.5	13	**PDB header:**oxidoreductase/lipid transport **Chain:** C: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of p450bioi in complex with tetradecanoic2 acid ligated acyl carrier protein
51	d2af8a_	Alignment	not modelled	5.3	13	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
52	d1vkua_	Alignment	not modelled	5.3	19	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
53	d1zcaa1	Alignment	not modelled	5.2	36	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
54	d2bcjq1	Alignment	not modelled	5.1	38	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
						PDB header:cytokine

55	c3d87A_	Alignment	not modelled	5.1	44	**Chain:** A: **PDB Molecule:**interleukin-23 subunit p19; **PDBTitle:** crystal structure of interleukin-23