Phyre^2

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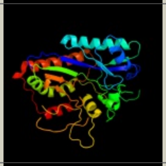
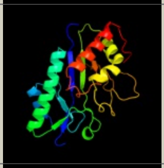
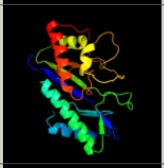
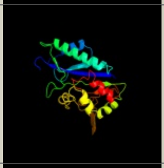
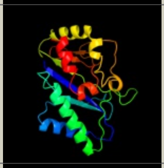
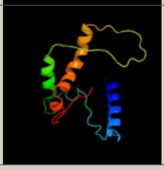
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r8ga_	Alignment		100.0	97	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase family 2 (GCS2)
2	d1tt4a_	Alignment		100.0	84	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase family 2 (GCS2)
3	c1tt4B_	Alignment		100.0	84	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
4	c2gwcE_	Alignment		100.0	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamate cysteine ligase; **PDBTitle:** crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
5	c3nztA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ftom francisella tularensis in complex with amp
6	d2d32a1	Alignment		100.0	17	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamate-cysteine ligase
7	c3ln7A_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
8	c3ln6A_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
9	c3lvwA_	Alignment		99.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** glutathione-inhibited scgcl
10	d1f52a2	Alignment		99.2	18	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain
11	d2bvca2	Alignment		99.1	18	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Glutamine synthetase catalytic domain

12	c1fpyE_	Alignment		99.1	19	**PDB header:**ligase **Chain:** E: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
13	c3ng0A_	Alignment		99.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
14	c1htoB_	Alignment		99.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
15	c2qc8J_	Alignment		98.8	14	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
16	c3o6xC_	Alignment		98.7	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
17	c2d3aJ_	Alignment		98.6	15	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
18	c3fkyD_	Alignment		98.5	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
19	c2j9iL_	Alignment		98.4	13	**PDB header:**ligase **Chain:** L: **PDB Molecule:**glutamate-ammonia ligase domain-containing **PDBTitle:** lengsin is a survivor of an ancient family of class i2 glutamine synthetases in eukaryotes that has undergone3 evolutionary re-engineering for a tissue-specific role4 in the vertebrate eye lens.
20	c3oqhB_	Alignment		44.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc; **PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic
21	d2qkwa1	Alignment	not modelled	13.1	11	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Avirulence protein AvrPto **Family:**Avirulence protein AvrPto
22	c2qkwA_	Alignment	not modelled	13.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** structural basis for activation of plant immunity by2 bacterial effector protein avrpto
23	d1dpsa_	Alignment	not modelled	12.1	5	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
24	c2chpC_	Alignment	not modelled	11.1	7	**PDB header:**dna-binding protein **Chain:** C: **PDB Molecule:**metalloregulation dna-binding stress protein; **PDBTitle:** crystal structure of the dodecameric ferritin mrga from2 b.subtilis 168
25	c3oqvA_	Alignment	not modelled	10.9	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**albc; **PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei
26	d1p94a_	Alignment	not modelled	10.8	19	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
27	c2xgwA_	Alignment	not modelled	10.5	5	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**peroxide resistance protein; **PDBTitle:** zinc-bound crystal structure of streptococcus pyogenes dpr
28	d2eg6a1	Alignment	not modelled	10.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Dihydroorotase

29	c2c6rA_	Alignment	not modelled	10.2	7	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**dna-binding stress response protein, dps family; **PDBTitle:** fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
30	c2vxxB_	Alignment	not modelled	9.0	15	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**starvation induced dna binding protein; **PDBTitle:** x-ray structure of dpsa from thermosynechococcus elongatus
31	c1g5jB_	Alignment	not modelled	9.0	55	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bad protein; **PDBTitle:** complex of bcl-xl with peptide from bad
32	c3iq1A_	Alignment	not modelled	8.4	7	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**dps family protein; **PDBTitle:** crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
33	d1tjoa_	Alignment	not modelled	8.2	7	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
34	d1ji4a_	Alignment	not modelled	8.2	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
35	d2d6fc3	Alignment	not modelled	7.5	19	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
36	c2yjkF_	Alignment	not modelled	7.4	7	**PDB header:**metal-binding protein **Chain:** F: **PDB Molecule:**afp; **PDBTitle:** structure of dps from microbacterium arborescens in the2 high iron form
37	c2krkA_	Alignment	not modelled	7.2	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**26s protease regulatory subunit 8; **PDBTitle:** solution nmr structure of 26s protease regulatory subunit 82 from h.sapiens, northeast structural genomics consortium3 target target hr3102a
38	c2wlaA_	Alignment	not modelled	6.9	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dps-like peroxide resistance protein; **PDBTitle:** streptococcus pyogenes dpr
39	c2f7nA_	Alignment	not modelled	6.9	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding stress response protein, dps family; **PDBTitle:** structure of d. radiodurans dps-1
40	d2yw6a1	Alignment	not modelled	6.6	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
41	c2c41K_	Alignment	not modelled	6.5	7	**PDB header:**iron-binding/oxidation protein **Chain:** K: **PDB Molecule:**dps family dna-binding stress response protein; **PDBTitle:** x-ray structure of dps from thermosynechococcus elongatus
42	c3rj1G_	Alignment	not modelled	6.5	38	**PDB header:**transcription **Chain:** G: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 6; **PDBTitle:** architecture of the mediator head module
43	d1n1qa_	Alignment	not modelled	6.3	7	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
44	c2d5kC_	Alignment	not modelled	6.3	12	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**dps family protein; **PDBTitle:** crystal structure of dps from staphylococcus aureus
45	d1o9ra_	Alignment	not modelled	6.2	5	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
46	c2bzwB_	Alignment	not modelled	6.0	56	**PDB header:**transcription **Chain:** B: **PDB Molecule:**bcl2-antagonist of cell death; **PDBTitle:** the crystal structure of bcl-xl in complex with full-length2 bad
47	c2z90D_	Alignment	not modelled	5.9	5	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**starvation-inducible dna-binding protein or fine **PDBTitle:** crystal structure of the second dps from mycobacterium2 smegmatis
48	d1umna_	Alignment	not modelled	5.9	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
49	d1jiga_	Alignment	not modelled	5.9	7	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
50	d2fjca1	Alignment	not modelled	5.9	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
51	c3hfhB_	Alignment	not modelled	5.9	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** crystal structure of tandem ff domains
52	d1ji5a_	Alignment	not modelled	5.8	10	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
53	c2q25C_	Alignment	not modelled	5.7	12	**PDB header:**virus,hydrolase/rna **Chain:** C: **PDB Molecule:**protein alpha; **PDBTitle:** flock house virus coat protein d75n mutant
54	d2bk6a1	Alignment	not modelled	5.7	7	**Fold:**Ferritin-like **Superfamily:**Ferritin-like

						Family: Ferritin
55	c3kwoA_	Alignment	not modelled	5.7	2	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative bacterioferritin; **PDBTitle:** crystal structure of putative bacterioferritin from2 campylobacter jejuni
56	d1vela_	Alignment	not modelled	5.5	12	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
57	d1j5ya2	Alignment	not modelled	5.3	12	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
58	d2eiaa1	Alignment	not modelled	5.1	17	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
59	c3jzeC_	Alignment	not modelled	5.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dihydroorotase; **PDBTitle:** 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2