Phyre2

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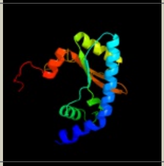
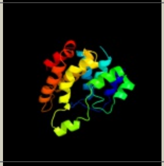
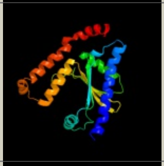
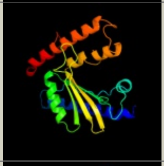
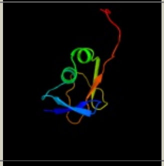
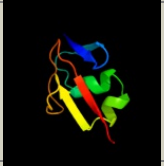
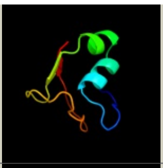
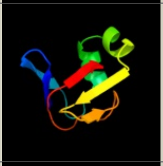
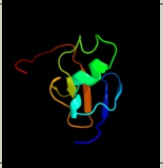
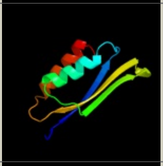
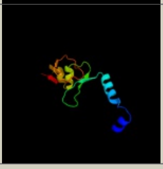
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vj7B_	Alignment		100.0	39	**PDB header:**hydrolase, transferase **Chain:** B: **PDB Molecule:**bifunctional rela/spot; **PDBTitle:** crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
2	d1vj7a1	Alignment		100.0	30	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
3	c3nr1A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain-containing protein 3; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
4	d1vj7a2	Alignment		100.0	49	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RelA/SpoT domain
5	c3nqwB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cg11900; **PDBTitle:** a metazoan ortholog of spot hydrolyzes ppgpp and plays a role in2 starvation responses
6	d2be3a1	Alignment		100.0	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RelA/SpoT domain
7	c3l9dA_	Alignment		99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative gtp pyrophosphokinase; **PDBTitle:** the crystal structure of smu.1046c from streptococcus mutans ua159
8	c2kmmA_	Alignment		99.9	49	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
9	c3hvzB_	Alignment		99.9	59	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
10	c2ekiA_	Alignment		99.8	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
11	d1tkea1	Alignment		99.7	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain

12	d1wxqa2	Alignment		99.7	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
13	d1nyra2	Alignment		99.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
14	c3ibwA_	Alignment		99.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
15	c1wwtA_	Alignment		99.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
16	d1u8sa2	Alignment		98.6	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
17	c1tkeA_	Alignment		98.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
18	c2dwqB_	Alignment		98.4	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gtp-binding protein; **PDBTitle:** thermus thermophilus ychf gtp-binding protein
19	d1sc6a3	Alignment		98.3	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
20	c2ohfA_	Alignment		98.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein 9; **PDBTitle:** crystal structure of human ola1 in complex with amppcp
21	c1wxqA_	Alignment	not modelled	98.2	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
22	d1ygya3	Alignment	not modelled	98.2	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
23	d2f1fa1	Alignment	not modelled	98.2	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
24	d2fgca2	Alignment	not modelled	98.1	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
25	d2pc6a2	Alignment	not modelled	98.1	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
26	c1jalA_	Alignment	not modelled	98.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ychf protein; **PDBTitle:** ychf protein (hi0393)
27	c2pc6C_	Alignment	not modelled	98.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
28	c2fgcA_	Alignment	not modelled	97.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima

29	c1ni3A_	Alignment	not modelled	97.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ychf gtp-binding protein; **PDBTitle:** structure of the schizosaccharomyces pombe ychf gtpase
30	c2f1fA_	Alignment	not modelled	97.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
31	c1nyqA_	Alignment	not modelled	97.9	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
32	c1qf6A_	Alignment	not modelled	97.8	26	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
33	d1zpva1	Alignment	not modelled	97.6	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
34	c1u8sB_	Alignment	not modelled	97.5	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
35	c2nyiB_	Alignment		97.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
36	c3n0vD_	Alignment	not modelled	97.5	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
37	c1y7pB_	Alignment	not modelled	97.4	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
38	d1u8sa1	Alignment	not modelled	97.2	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
39	c3nrbD_	Alignment	not modelled	97.1	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
40	c1ygyA_	Alignment	not modelled	97.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
41	c1ybaC_	Alignment	not modelled	97.0	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
42	c3o1lB_	Alignment	not modelled	96.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
43	c3k5pA_	Alignment	not modelled	96.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
44	c3obiC_	Alignment	not modelled	96.6	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
45	c3louB_	Alignment	not modelled	96.6	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
46	d2f06a2	Alignment	not modelled	96.3	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
47	d1rwua_	Alignment	not modelled	96.1	9	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
48	c1rwuA_	Alignment	not modelled	96.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
49	d1phza1	Alignment	not modelled	96.0	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
50	d1zud21	Alignment	not modelled	95.7	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
51	c2qmxB_	Alignment	not modelled	95.6	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
52	c2f06B_	Alignment	not modelled	95.4	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides

						thetaiotaomicron
53	d2qmwa2	Alignment	not modelled	95.3	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
54	d2hj1a1	Alignment	not modelled	95.1	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
55	c2hj1A_	Alignment	not modelled	95.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
56	c2phmA_	Alignment	not modelled	95.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
57	c3mwbA_	Alignment	not modelled	95.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
58	c3mtjA_	Alignment	not modelled	94.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
59	d2f06a1	Alignment	not modelled	94.5	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
60	c3cwiA_	Alignment	not modelled	93.9	9	**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
61	c3luyA_	Alignment	not modelled	93.8	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
62	d1tygb_	Alignment	not modelled	93.8	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
63	c1tygG_	Alignment	not modelled	92.2	19	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
64	d1vjka_	Alignment	not modelled	91.8	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
65	c2kl0A_	Alignment	not modelled	91.8	20	**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
66	c2qieB_	Alignment	not modelled	91.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
67	c1tdjA_	Alignment	not modelled	91.6	16	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
68	d2cu3a1	Alignment	not modelled	91.4	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
69	c3po0A_	Alignment	not modelled	90.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
70	c2qmwA_	Alignment	not modelled	90.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
71	c2dqbB_	Alignment	not modelled	90.3	28	**PDB header:**hydrolase, dna binding protein **Chain:** B: **PDB Molecule:**deoxyguanosinetriphosphate triphosphohydrolase, putative; **PDBTitle:** crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
72	d1y7pa2	Alignment	not modelled	90.0	25	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**AF1403 N-terminal domain-like
73	c1dm9A_	Alignment	not modelled	88.6	4	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
74	d1dm9a_	Alignment	not modelled	88.6	4	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
75	d2qgsa1	Alignment	not modelled	88.5	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
76	c2ogiA_	Alignment	not modelled	87.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein sag1661; **PDBTitle:** crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
77	c2dtjA_	Alignment	not modelled	86.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
						Fold:beta-Grasp (ubiquitin-like)

78	d1jala2	Alignment	not modelled	86.2	31	**Superfamily:**TGS-like **Family:**G domain-linked domain
79	c2o08B_	Alignment	not modelled	86.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh1327 protein; **PDBTitle:** crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
80	c3ccgA_	Alignment	not modelled	85.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd superfamily hydrolase; **PDBTitle:** crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
81	c2k6pA_	Alignment	not modelled	84.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
82	d2piea1	Alignment	not modelled	84.5	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
83	d1fm0d_	Alignment	not modelled	83.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
84	c3gqsB_	Alignment	not modelled	82.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
85	d1ni3a2	Alignment	not modelled	81.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
86	d2cyya2	Alignment	not modelled	80.5	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
87	c3fm8A_	Alignment	not modelled	80.1	30	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
88	c3p96A_	Alignment	not modelled	79.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
89	d3djba1	Alignment	not modelled	79.1	18	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
90	d1rwsa_	Alignment	not modelled	79.0	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
91	d2joqa1	Alignment	not modelled	77.7	9	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**HP0495-like
92	d3b57a1	Alignment	not modelled	77.6	21	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
93	c3l76B_	Alignment	not modelled	77.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
94	c2g1eA_	Alignment	not modelled	76.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
95	c2eh0A_	Alignment	not modelled	76.2	26	**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
96	d1c06a_	Alignment	not modelled	75.1	23	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
97	d2g1la1	Alignment	not modelled	75.0	22	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
98	c2bs2E_	Alignment	not modelled	74.0	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
99	d2fug33	Alignment	not modelled	73.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
100	d1yjma1	Alignment	not modelled	72.9	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
101	c2re1A_	Alignment	not modelled	72.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
102	c3bbnD_	Alignment	not modelled	72.4	32	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
103	c2qjlA_	Alignment	not modelled	72.2	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
104	c3mzoA_	Alignment	not modelled	71.8	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lin2634 protein; **PDBTitle:** crystal structure of a hd-domain phosphohydrolase (lin2634) from2 listeria innocua at 1.98 a resolution

105	d1xo3a_	Alignment	not modelled	71.3	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
106	c2jqlA_	Alignment	not modelled	71.0	35	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
107	d1gxca_	Alignment	not modelled	70.7	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
108	c1gxcA_	Alignment	not modelled	70.7	17	**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
109	d2uubd1	Alignment	not modelled	70.5	32	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
110	d2heka1	Alignment	not modelled	70.5	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
111	d2pq7a1	Alignment	not modelled	69.4	15	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
112	d1p9ka_	Alignment	not modelled	69.2	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
113	c3dwmA_	Alignment	not modelled	68.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
114	d1g3ga_	Alignment	not modelled	68.2	30	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
115	d1dmza_	Alignment	not modelled	68.2	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
116	c3kt9A_	Alignment	not modelled	68.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
117	d3dtoa1	Alignment	not modelled	68.0	20	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
118	d1vioa2	Alignment	not modelled	67.5	36	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
119	d1wgka_	Alignment	not modelled	67.2	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
120	c3hx1B_	Alignment	not modelled	67.1	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a