Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P0AC28
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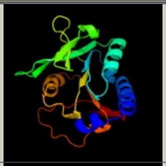
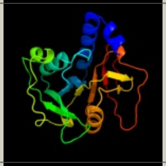
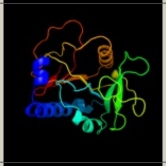
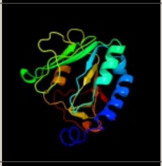
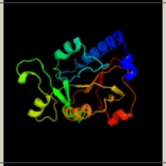
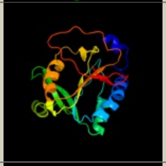
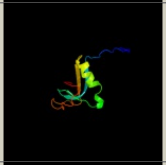
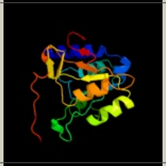
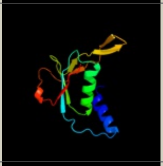
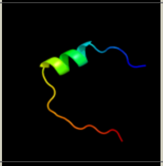
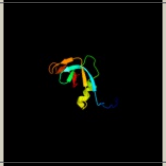
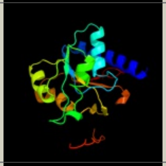
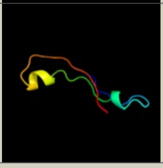
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jcbA_	Alignment		100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase family protein; **PDBTitle:** the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)
2	c1ydmC_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein yqgn; **PDBTitle:** x-ray structure of northeast structural genomics target sr44
3	d1soua_	Alignment		100.0	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
4	c3hy4A_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase; **PDBTitle:** structure of human mthfs with n5-iminium phosphate
5	d1sbqa_	Alignment		100.0	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
6	c1u3fA_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydrofolate synthetase; **PDBTitle:** structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
7	d1wkca_	Alignment		100.0	26	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
8	d1t9ka_	Alignment		78.9	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
9	d1k6da_	Alignment		70.4	8	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
10	c2yvkA_	Alignment		66.0	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
11	c1w2wJ_	Alignment		61.1	17	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits

12	c3ecsD_	Alignment		50.7	21	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
13	c3uk7B_	Alignment		48.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
14	d1e1oa2	Alignment		36.1	4	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
15	c3rrlC_	Alignment		35.2	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
16	d1wu7a2	Alignment		35.0	29	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
17	d1bbua2	Alignment		27.2	8	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
18	d1t5oa_	Alignment		24.9	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
19	d1qe0a2	Alignment		23.6	29	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
20	d1h4vb2	Alignment		20.7	33	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
21	c1sy7B_	Alignment	not modelled	19.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
22	d1oi4a1	Alignment	not modelled	18.7	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
23	c2ywdA_	Alignment	not modelled	17.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
24	d1z7ma1	Alignment	not modelled	17.5	28	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
25	d1kmma2	Alignment	not modelled	16.1	33	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
26	d1p80a1	Alignment	not modelled	15.7	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
27	d1m0da_	Alignment	not modelled	14.5	11	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
28	d1gpma2	Alignment	not modelled	13.4	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
						Fold: Phosphoglucomutase, first 3 domains

29	d1kfia2	Alignment	not modelled	13.3	10	**Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
30	d2gfqa1	Alignment	not modelled	13.3	29	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
31	c2gfqC_	Alignment	not modelled	12.5	29	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
32	c3cdkA_	Alignment	not modelled	12.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
33	d3pmga2	Alignment	not modelled	12.3	42	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
34	d1yqea1	Alignment	not modelled	11.2	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
35	d1ooya1	Alignment	not modelled	11.2	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
36	c2eg5C_	Alignment	not modelled	10.7	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**xanthosine methyltransferase; **PDBTitle:** the structure of xanthosine methyltransferase
37	c3racA_	Alignment	not modelled	10.5	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidine-trna ligase; **PDBTitle:** crystal strucutre of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
38	d1p5dx2	Alignment	not modelled	10.3	50	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
39	c1hyoB_	Alignment	not modelled	10.0	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fumarylacetoacetate hydrolase; **PDBTitle:** crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
40	d1q7ra_	Alignment	not modelled	9.8	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
41	c2bldD_	Alignment	not modelled	9.6	26	**PDB header:**virus **Chain:** D: **PDB Molecule:**penton protein; **PDBTitle:** the quasi-atomic model of human adenovirus type 52 capsid (part 1)
42	d1vb5a_	Alignment	not modelled	9.5	8	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
43	d1fvia1	Alignment	not modelled	9.0	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
44	d1sdoa_	Alignment	not modelled	8.9	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BstyI
45	c3l7nA_	Alignment	not modelled	8.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
46	d1w7ab4	Alignment	not modelled	8.7	22	**Fold:**MutS N-terminal domain-like **Superfamily:**DNA repair protein MutS, domain I **Family:**DNA repair protein MutS, domain I
47	c3bboO_	Alignment	not modelled	8.6	19	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**ribosomal protein l16; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
48	c2rnmC_	Alignment	not modelled	8.4	55	**PDB header:**protein fibril **Chain:** C: **PDB Molecule:**small s protein; **PDBTitle:** structure of the het-s(218-289) prion in its amyloid form2 obtained by solid-state nmr
49	c2kkuA_	Alignment	not modelled	8.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
50	d2nv0a1	Alignment	not modelled	8.2	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
51	c3nkgA_	Alignment	not modelled	8.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein geba250068378; **PDBTitle:** crystal structure of geba250068378 from sulfurospirillum deleyianum
52	c3ot1B_	Alignment	not modelled	7.9	18	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
53	c2ftcI_	Alignment	not modelled	7.9	29	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**mitochondrial ribosomal protein l16; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
54	d3hdha1	Alignment	not modelled	7.8	57	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
						Fold: RuBisCO, small subunit

55	d1gk8i_	Alignment	not modelled	7.6	24	**Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
56	d1utca2	Alignment	not modelled	7.6	45	**Fold:**7-bladed beta-propeller **Superfamily:**Clathrin heavy-chain terminal domain **Family:**Clathrin heavy-chain terminal domain
57	d1wdka1	Alignment	not modelled	7.6	67	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
58	d2g39a2	Alignment	not modelled	7.5	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
59	c1jqoA_	Alignment	not modelled	7.5	39	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
60	d1jqoa_	Alignment	not modelled	7.5	39	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
61	d2gyck1	Alignment	not modelled	7.4	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
62	c1c9lA_	Alignment	not modelled	7.4	45	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin; **PDBTitle:** peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin
63	d1lbqa_	Alignment	not modelled	7.4	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
64	d1sy7a1	Alignment	not modelled	7.3	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
65	c3b5iB_	Alignment	not modelled	7.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine:salicylic acid carboxyl **PDBTitle:** crystal structure of indole-3-acetic acid methyltransferase
66	d2abwa1	Alignment	not modelled	7.2	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
67	c3a11D_	Alignment	not modelled	7.0	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
68	d2j01q1	Alignment	not modelled	6.9	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
69	d1jqna_	Alignment	not modelled	6.9	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
70	d1vcoa1	Alignment	not modelled	6.7	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
71	c3c1nA_	Alignment	not modelled	6.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
72	d1hyoa2	Alignment	not modelled	6.4	32	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
73	c3d3uA_	Alignment	not modelled	6.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
74	d1f0ya1	Alignment	not modelled	6.2	67	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
75	c2zakB_	Alignment	not modelled	6.1	45	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
76	d1gsaa1	Alignment	not modelled	6.0	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
77	d2zjrj1	Alignment	not modelled	6.0	21	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L16p
78	c3kvhA_	Alignment	not modelled	6.0	58	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
79	d2a9va1	Alignment	not modelled	6.0	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
80	c1zejA_	Alignment	not modelled	5.8	50	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution

81	d1i1qb_	Alignment	not modelled	5.7	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
82	d1xr4a2	Alignment	not modelled	5.6	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
83	d1b8ta4	Alignment	not modelled	5.6	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
84	c1bpoA_	Alignment	not modelled	5.5	45	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (clathrin); **PDBTitle:** clathrin heavy-chain terminal domain and linker
85	d1s6la1	Alignment	not modelled	5.4	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
86	c2bs5A_	Alignment	not modelled	5.3	50	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**fucose-binding lectin protein; **PDBTitle:** lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose
87	c2ywjA_	Alignment	not modelled	5.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
88	d1wl8a1	Alignment	not modelled	5.1	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
89	d1t3ta2	Alignment	not modelled	5.1	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)