Phyre2

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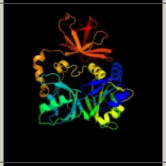
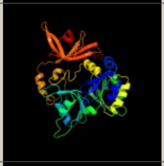
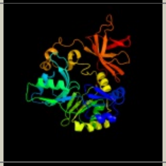
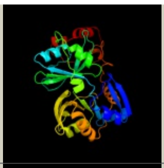
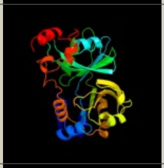
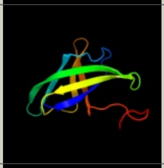
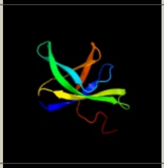
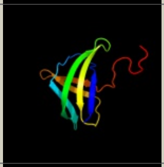
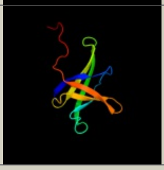
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vloA_	Alignment		100.0	96	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution
2	c1pj6A_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
3	c1x31A_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
4	c1v5vA_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
5	c1worA_	Alignment		100.0	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of t-protein of the glycine cleavage2 system
6	c1wsrA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of human t-protein of glycine cleavage2 system
7	c3girA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae
8	c1yx2B_	Alignment		100.0	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of the probable aminomethyltransferase2 from bacillus subtilis
9	c3tfhB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gcvt-like aminomethyltransferase protein; **PDBTitle:** dmsp-dependent demethylase from p. ubique - apo
10	d1vloa2	Alignment		100.0	96	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
11	d1pj5a4	Alignment		100.0	27	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain

12	d1v5va2	Alignment		100.0	37	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
13	d1wosa2	Alignment		100.0	42	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
14	c1vlyA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**unknown protein from 2d-page; **PDBTitle:** crystal structure of a putative aminomethyltransferase (ygfz) from2 escherichia coli at 1.30 a resolution
15	d1vlya2	Alignment		100.0	16	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
16	c2gagC_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**heterotetrameric sarcosine oxidase gamma-subunit; **PDBTitle:** heteroteterameric sarcosine: structure of a diflavin metaloenzyme at2 1.85 a resolution
17	d1vloa1	Alignment		99.9	98	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
18	d1v5va1	Alignment		99.8	35	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
19	d1pj5a1	Alignment		99.7	20	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
20	d1wosa1	Alignment		99.7	38	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
21	d1vlya1	Alignment	not modelled	97.0	8	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
22	c3gehA_	Alignment	not modelled	96.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
23	c1xzqB_	Alignment	not modelled	93.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
24	c1xzqA_	Alignment	not modelled	93.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
25	d1xzpa3	Alignment	not modelled	93.0	15	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**TrmE formyl-THF-binding domain
26	c3geiB_	Alignment	not modelled	91.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
27	d3bzka5	Alignment	not modelled	37.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
28	c2ysrA_	Alignment	not modelled	26.5	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dep domain-containing protein 1; **PDBTitle:** solution structure of the dep domain from human dep domain-2 containing protein 1
						PDB header:transcription

29	c2pn0D_	Alignment	not modelled	15.9	10	**Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
30	d2f23a2	Alignment	not modelled	14.7	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
31	c2nyiB_	Alignment	not modelled	12.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
32	c1m98A_	Alignment	not modelled	11.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
33	c2p4vA_	Alignment	not modelled	11.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
34	c2etnA_	Alignment	not modelled	10.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
35	c3ny7A_	Alignment	not modelled	9.7	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sulfate transporter; **PDBTitle:** stas domain of ychm bound to acp
36	d2etna2	Alignment	not modelled	9.4	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
37	c3brcA_	Alignment	not modelled	8.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein of unknown function; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
38	d1w4ma_	Alignment	not modelled	8.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
39	c1wylA_	Alignment	not modelled	7.1	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** solution structure of the ch domain of human nedd92 interacting protein with calponin homology and lim domains
40	c1v1hB_	Alignment	not modelled	6.8	30	**PDB header:**adenovirus **Chain:** B: **PDB Molecule:**fibritin, fiber protein; **PDBTitle:** adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibritin foldon trimerisation motif with3 a short linker
41	d1fsha_	Alignment	not modelled	6.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
42	c3i31A_	Alignment	not modelled	6.1	21	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** hera helicase rna binding domain is an rrm fold