Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P36553
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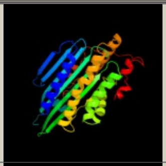
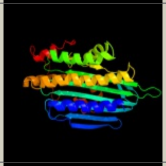
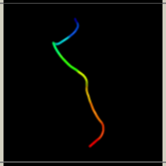
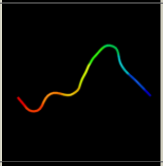
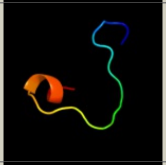
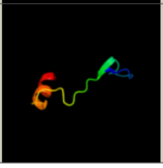
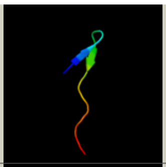
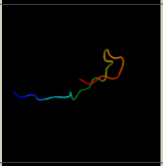
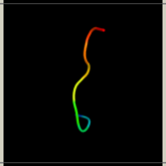
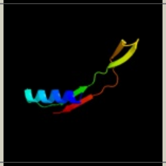
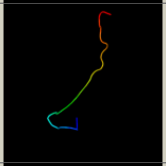
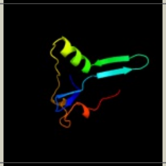
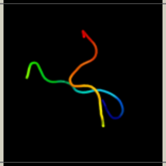
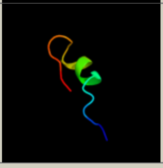
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2aexA_	Alignment		100.0	48	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen iii oxidase, mitochondrial; **PDBTitle:** the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyria
2	d1tkla_	Alignment		100.0	47	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
3	d1vjua_	Alignment		100.0	66	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
4	d1txna_	Alignment		100.0	44	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
5	c3lm3A_	Alignment		47.3	42	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase/deacetylase2 (bdi_3119) from parabacteroides distasonis at 1.44 a resolution
6	d1ci4a_	Alignment		35.3	18	**Fold:**SAM domain-like **Superfamily:**Barrier-to-autointegration factor, BAF **Family:**Barrier-to-autointegration factor, BAF
7	d1kkoa2	Alignment		28.7	40	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
8	d1kcza2	Alignment		28.3	50	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
9	c3fubA_	Alignment		27.9	27	**PDB header:**hormone **Chain:** A: **PDB Molecule:**gdnf family receptor alpha-1; **PDBTitle:** crystal structure of gdnf-gfralpha1 complex
10	c2v5eA_	Alignment		27.3	27	**PDB header:**receptor/glycoprotein complex **Chain:** A: **PDB Molecule:**gdnf family receptor alpha-1; **PDBTitle:** the structure of the gdnf\:coreceptor complex\: insights2 into ret signalling and heparin binding.
11	d1y7pa2	Alignment		26.9	26	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**AF1403 N-terminal domain-like

12	c2r7tA_	Alignment		21.7	38	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**rna-dependent rna polymerase; **PDBTitle:** crystal structure of rotavirus sa11 vp1/rna (ugugaacc)2 complex
13	c2r39A_	Alignment		21.1	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fixg-related protein; **PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus
14	c1kkoB_	Alignment		18.5	40	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-methylaspartate ammonia-lyase; **PDBTitle:** crystal structure of citrobacter amalonaticus2 methylaspartate ammonia lyase
15	d1j2ga1	Alignment		16.7	15	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
16	d1bdfa1	Alignment		16.1	33	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
17	d1t9ka_	Alignment		16.0	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
18	d1gg4a1	Alignment		15.7	21	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
19	c2pbyB_	Alignment		14.9	71	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
20	d1yuaa1	Alignment		13.1	47	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
21	c3ccjU_	Alignment	not modelled	13.0	29	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**50s ribosomal protein l24e; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
22	d1vb5a_	Alignment	not modelled	12.8	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
23	c2yvkA_	Alignment	not modelled	12.7	16	**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
24	c3llxA_	Alignment	not modelled	12.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**predicted amino acid aldolase or racemase; **PDBTitle:** crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
25	d1vqou1	Alignment	not modelled	12.3	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein L24e
26	d1auna_	Alignment	not modelled	12.0	38	**Fold:**Osmotin, thaumatin-like protein **Superfamily:**Osmotin, thaumatin-like protein **Family:**Osmotin, thaumatin-like protein
27	d2yzca1	Alignment	not modelled	11.7	26	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
28	c2zkru_	Alignment	not modelled	11.6	43	**PDB header:**ribosomal protein/rna **Chain:** U: **PDB Molecule:**rna expansion segment es41; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map

29	d1wmxb_	Alignment	not modelled	11.6	35	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat)
30	c1w2wJ_	Alignment	not modelled	11.5	22	**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
31	c3uo9B_	Alignment	not modelled	11.3	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
32	c2d35A_	Alignment	not modelled	11.1	60	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division activator ceda; **PDBTitle:** solution structure of cell division reactivation factor,2 ceda
33	c1yuaA_	Alignment	not modelled	10.9	47	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**topoisomerase i; **PDBTitle:** c-terminal domain of escherichia coli topoisomerase i
34	c2bn8A_	Alignment	not modelled	10.9	60	**PDB header:**cell cycle protein **Chain:** A: **PDB Molecule:**cell division activator ceda; **PDBTitle:** solution structure and interactions of the e.coli cell2 division activator protein ceda
35	c2yk5A_	Alignment	not modelled	10.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cmp-n-acetylneuraminate-beta-galactosamide-alpha-2,3- **PDBTitle:** structure of neisseria los-specific sialyltransferase (nst),2 in complex with cmp.
36	c3n2bD_	Alignment	not modelled	10.5	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
37	d2fkla1	Alignment	not modelled	10.0	33	**Fold:**Dodecin subunit-like **Superfamily:**Amyloid beta a4 protein copper binding domain (domain 2) **Family:**Amyloid beta a4 protein copper binding domain (domain 2)
38	c3ecsD_	Alignment	not modelled	9.9	24	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
39	c4a1eT_	Alignment	not modelled	9.6	29	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rpl24; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
40	d1ccwb_	Alignment	not modelled	9.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Glutamate mutase, large subunit
41	c1u2zC_	Alignment	not modelled	9.4	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-79 **PDBTitle:** crystal structure of histone k79 methyltransferase dot1p2 from yeast
42	c2ebsB_	Alignment	not modelled	9.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**oligoxyloglucan reducing end-specific **PDBTitle:** crystal structure anaalysis of oligoxyloglucan reducing-end-2 specific cellobiohydrolase (oxg-rcbh) d465n mutant3 complexed with a xyloglucan heptasaccharide
43	c3f42A_	Alignment	not modelled	9.2	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hp0035; **PDBTitle:** crystal structure of uncharacterized protein hp0035 from helicobacter2 pylori
44	c3izcZ_	Alignment	not modelled	9.1	29	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein rpl24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
45	d1e88a3	Alignment	not modelled	9.1	38	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
46	d2piaa2	Alignment	not modelled	9.1	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
47	d1uc8a1	Alignment	not modelled	8.8	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
48	d1tvca2	Alignment	not modelled	8.8	22	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
49	d1u5la_	Alignment	not modelled	8.6	10	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
50	d1tz9a_	Alignment	not modelled	8.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
51	d1tzpa_	Alignment	not modelled	8.2	35	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**MepA-like
52	d2a0ua1	Alignment	not modelled	8.1	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
53	d1gff1_	Alignment	not modelled	7.9	67	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses

						Family: Microviridae-like VP
54	d1qfja2	Alignment	not modelled	7.9	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
55	c3iz5Z_	Alignment	not modelled	7.7	29	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
56	d1pzra_	Alignment	not modelled	7.7	86	**Fold:**HLH-like **Superfamily:**Docking domain B of the erythromycin polyketide synthase (DEBS) **Family:**Docking domain B of the erythromycin polyketide synthase (DEBS)
57	d1ulva3	Alignment	not modelled	7.7	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**CBD9-like **Family:**Glucodextranase, domain C
58	d2ibaa1	Alignment	not modelled	7.5	16	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
59	d3be7a1	Alignment	not modelled	7.4	27	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Zn-dependent arginine carboxypeptidase-like
60	c3cxjB_	Alignment	not modelled	7.4	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
61	c2jv4A_	Alignment	not modelled	7.4	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis/trans isomerase; **PDBTitle:** structure characterisation of pina ww domain and comparison2 with other group iv ww domains, pin1 and ess1
62	c2xdyA_	Alignment	not modelled	7.4	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**post-transcriptional gene silencing protein qde-2; **PDBTitle:** crystal structure of the n. crassa qde-2 ago mid domain
63	d2d6fc2	Alignment	not modelled	7.4	44	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
64	d2bi0a1	Alignment	not modelled	7.3	46	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
65	d1edta_	Alignment	not modelled	7.3	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
66	d1ny722	Alignment	not modelled	7.3	27	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
67	d1pcva_	Alignment	not modelled	7.3	38	**Fold:**Osmotin, thaumatin-like protein **Superfamily:**Osmotin, thaumatin-like protein **Family:**Osmotin, thaumatin-like protein
68	d1ddga2	Alignment	not modelled	7.2	25	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
69	c2rhfA_	Alignment	not modelled	7.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
70	c3n8bB_	Alignment	not modelled	7.1	14	**PDB header:**nucleic acid binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
71	c1i7wB_	Alignment	not modelled	7.1	50	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**epithelial-cadherin; **PDBTitle:** beta-catenin/phosphorylated e-cadherin complex
72	d1e8ga1	Alignment	not modelled	7.0	10	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
73	c3nzpA_	Alignment	not modelled	7.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
74	c3nm7C_	Alignment	not modelled	7.0	14	**PDB header:**nucleic acid binding protein **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
75	d1pgl22	Alignment	not modelled	6.9	36	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
76	c2j3zA_	Alignment	not modelled	6.9	18	**PDB header:**toxin **Chain:** A: **PDB Molecule:**c2 toxin component i; **PDBTitle:** crystal structure of the enzymatic component c2-i of the2 c2-toxin from clostridium botulinum at ph 6.1
77	c3nzqB_	Alignment	not modelled	6.8	41	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
78	c3nm7D_	Alignment	not modelled	6.7	14	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
79	c3n8bA_	Alignment	not modelled	6.7	14	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha

80	d1ehsa_	Alignment	not modelled	6.6	19	**Fold:**Toxic hairpin **Superfamily:**Heat-stable enterotoxin B **Family:**Heat-stable enterotoxin B
81	c3ik2A_	Alignment	not modelled	6.5	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase a; **PDBTitle:** crystal structure of a glycoside hydrolase family 44 endoglucanase2 produced by clostridium acetobutylium atcc 824
82	c3aagA_	Alignment	not modelled	6.3	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**general glycosylation pathway protein; **PDBTitle:** crystal structure of c. jejuni pglb c-terminal domain
83	c1tvcA_	Alignment	not modelled	6.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
84	c2j10B_	Alignment	not modelled	6.2	58	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
85	c2ahnA_	Alignment	not modelled	6.2	38	**PDB header:**allergen **Chain:** A: **PDB Molecule:**thaumatin-like protein; **PDBTitle:** high resolution structure of a cherry allergen pru av 2
86	d1qt1a_	Alignment	not modelled	6.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
87	c2j10D_	Alignment	not modelled	6.1	58	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
88	c2j10A_	Alignment	not modelled	6.1	58	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
89	c3a11D_	Alignment	not modelled	6.1	20	**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
90	c3ic8D_	Alignment	not modelled	6.0	19	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
91	d1rqwa_	Alignment	not modelled	5.9	38	**Fold:**Osmotin, thaumatin-like protein **Superfamily:**Osmotin, thaumatin-like protein **Family:**Osmotin, thaumatin-like protein
92	c2k5dA_	Alignment	not modelled	5.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sag0934; **PDBTitle:** solution nmr structure of sag0934 from streptococcus2 agalactiae. northeast structural genomics target sar32[1-3 108].
93	d2aama1	Alignment	not modelled	5.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**TM1410-like
94	c2aamA_	Alignment	not modelled	5.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein tm1410; **PDBTitle:** crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
95	d1ry7a_	Alignment	not modelled	5.8	16	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
96	d1qqha_	Alignment	not modelled	5.8	8	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
97	c3mt1B_	Alignment	not modelled	5.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
98	c1s1iS_	Alignment	not modelled	5.6	29	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l24-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
99	d1t3la1	Alignment	not modelled	5.6	24	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain