Phyre^2

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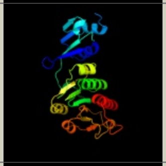
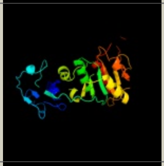
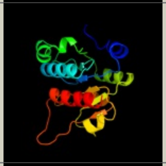
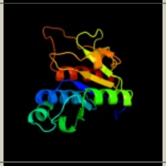
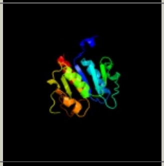
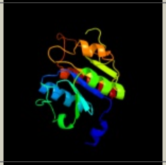
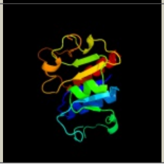
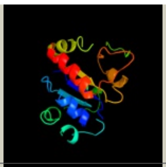
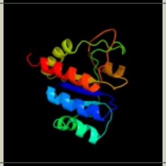
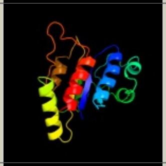
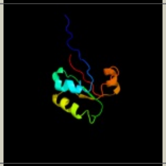
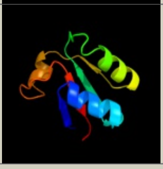
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gyqB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna (adenosine-2'-o-)-methyltransferase; **PDBTitle:** structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
2	c1ipaA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
3	c1x7pB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna methyltransferase; **PDBTitle:** crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
4	c2i6dA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna methyltransferase, trmh family; **PDBTitle:** the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
5	d1gz0a1	Alignment		100.0	30	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
6	c1gz0G_	Alignment		100.0	30	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
7	d1ipaa1	Alignment		100.0	26	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
8	c1zjrA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanosine-2'-o-)-methyltransferase; **PDBTitle:** crystal structure of a. aeolicus trmh/spou trna modifying enzyme
9	d1v2xa_	Alignment		100.0	25	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
10	c2ha8A_	Alignment		100.0	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**tar (hiv-1) rna loop binding protein; **PDBTitle:** methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
11	d1mxia_	Alignment		100.0	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase

12	c3onpA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna/rrna methyltransferase (spou); **PDBTitle:** crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
13	c3ic6A_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative methylase family protein; **PDBTitle:** crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
14	c3e5yB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trmh family rna methyltransferase; **PDBTitle:** crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
15	c3l8uA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
16	c3ktyA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable methyltransferase; **PDBTitle:** crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
17	c3ilkB_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized trna/rrna methyltransferase hi0380; **PDBTitle:** the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
18	c3dcmX_	Alignment		99.9	19	**PDB header:**transferase **Chain:** X: **PDB Molecule:**uncharacterized protein tm_1570; **PDBTitle:** crystal structure of the thermotoga maritima spout family2 rna-methyltransferase protein tm1570 in complex with s-3 adenosyl-l-methionine
19	d1gz0f2	Alignment		99.8	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
20	d1gz0a2	Alignment		99.7	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
21	d1ipaa2	Alignment	not modelled	98.6	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
22	c2yy8B_	Alignment	not modelled	97.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
23	d2o3aa1	Alignment	not modelled	96.5	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
24	d1vhka2	Alignment	not modelled	96.5	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
25	c4a1dG_	Alignment	not modelled	96.1	14	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**rpl30; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
26	c1vhyB_	Alignment	not modelled	95.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
27	d2bo1a1	Alignment	not modelled	95.5	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
28	d1t0kb_	Alignment	not modelled	95.3	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins

29	c3cpqB_	Alignment	not modelled	95.2	6	**PDB header:**ribosomal protein **Chain:** B: **PDB Molecule:**50s ribosomal protein l30e; **PDBTitle:** crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
30	d1w41a1	Alignment	not modelled	95.1	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
31	c3on1A_	Alignment	not modelled	95.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2414 protein; **PDBTitle:** the structure of a protein with unknown function from bacillus2 halodurans c
32	d1vqof1	Alignment	not modelled	94.8	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
33	c2zkr6_	Alignment	not modelled	94.6	14	**PDB header:**ribosomal protein/rna **Chain:** 6: **PDB Molecule:**60s ribosomal protein l30e; **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
34	d1jj2f_	Alignment	not modelled	94.4	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
35	d1nxza2	Alignment	not modelled	94.4	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
36	c2lbwA_	Alignment	not modelled	94.2	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 2; **PDBTitle:** solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
37	d1rlga_	Alignment	not modelled	94.1	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
38	d2fc3a1	Alignment	not modelled	94.1	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
39	c3ai9X_	Alignment	not modelled	93.8	8	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
40	d1xbia1	Alignment	not modelled	93.6	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
41	c3o85A_	Alignment	not modelled	93.5	11	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l7ae; **PDBTitle:** giardia lamblia 15.5kd rna binding protein
42	d2czwa1	Alignment	not modelled	93.4	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
43	c1vhkA_	Alignment	not modelled	93.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
44	d2aifa1	Alignment	not modelled	92.6	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
45	d2qwva1	Alignment	not modelled	91.9	9	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
46	d2ozba1	Alignment	not modelled	91.2	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
47	c3kw2A_	Alignment	not modelled	90.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
48	d2vgna3	Alignment	not modelled	90.2	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
49	d2qmma1	Alignment	not modelled	89.6	23	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
50	c2zkrf_	Alignment	not modelled	89.4	11	**PDB header:**ribosomal protein/rna **Chain:** F: **PDB Molecule:**rna expansion segment es7 part iii; **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
51	c3iz5H_	Alignment	not modelled	88.9	12	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l7a (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
52	d2alea1	Alignment	not modelled	88.8	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
53	d2qi2a3	Alignment	not modelled	87.9	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
54	c2vgmA_	Alignment	not modelled	87.7	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
						PDB header:ribosome

55	c3izcH_	Alignment	not modelled	87.6	14	**Chain:** H: **PDB Molecule:**60s ribosomal protein rpl8 (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
56	c2xznU_	Alignment	not modelled	86.1	15	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein l7ae containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
57	c2egwB_	Alignment	not modelled	85.7	16	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
58	c3agkA_	Alignment	not modelled	83.9	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** crystal structure of archaeal translation termination factor, arf1
59	d1dt9a2	Alignment	not modelled	83.9	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
60	c4a1eF_	Alignment	not modelled	81.0	14	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl7a; **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
61	c3obwA_	Alignment	not modelled	80.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
62	c3agjD_	Alignment	not modelled	79.9	20	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
63	c2ktvA_	Alignment	not modelled	79.8	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
64	c3agjB_	Alignment	not modelled	79.1	20	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
65	c1ibjC_	Alignment	not modelled	78.6	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** crystal structure of cystathionine beta-lyase from arabidopsis2 thaliana
66	d1ibja_	Alignment	not modelled	78.6	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
67	d1x52a1	Alignment	not modelled	77.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
68	c1dt9A_	Alignment	not modelled	77.2	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein (eukaryotic peptide chain release factor **PDBTitle:** the crystal structure of human eukaryotic release factor2 erf1-mechanism of stop codon recognition and peptidyl-trna3 hydrolysis
69	c2qi2A_	Alignment	not modelled	76.0	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein pelota related protein; **PDBTitle:** crystal structure of the thermoplasma acidophilum pelota2 protein
70	c3cg6A_	Alignment	not modelled	74.5	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible 45 gamma; **PDBTitle:** crystal structure of gadd45 gamma
71	c2cx8B_	Alignment	not modelled	71.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
72	d1cs1a_	Alignment	not modelled	68.7	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
73	c1t9hA_	Alignment	not modelled	65.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
74	c3mcaB_	Alignment	not modelled	64.7	20	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
75	d1k3ra2	Alignment	not modelled	62.9	23	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
76	c3navB_	Alignment	not modelled	62.8	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
77	c3obyB_	Alignment	not modelled	61.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
78	d1o6da_	Alignment	not modelled	58.1	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
79	c4a2iV_	Alignment	not modelled	55.8	20	**PDB header:**ribosome/hydrolase **Chain:** V: **PDB Molecule:**putative ribosome biogenesis gtpase rsga;

						PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
80	c1z85B_	Alignment	not modelled	53.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein tm1380; **PDBTitle:** crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
81	c3ir9A_	Alignment	not modelled	53.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
82	d2ctza1	Alignment	not modelled	50.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
83	c2w8wA_	Alignment	not modelled	50.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser
84	c2rcnA_	Alignment	not modelled	48.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
85	c3u5cM_	Alignment	not modelled	47.4	14	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
86	c2yv5A_	Alignment	not modelled	46.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
87	d3eeqa1	Alignment	not modelled	46.7	15	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
88	c1k3rA_	Alignment	not modelled	46.1	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
89	d2w6ka1	Alignment	not modelled	45.8	10	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
90	c2kg4A_	Alignment	not modelled	44.3	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible protein **PDBTitle:** three-dimensional structure of human gadd45alpha in2 solution by nmr
91	c3ib6B_	Alignment	not modelled	43.1	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
92	c3a2bA_	Alignment	not modelled	42.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** crystal structure of serine palmitoyltransferase from sphingobacterium2 multivorum with substrate l-serine
93	c3qjaA_	Alignment	not modelled	40.2	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
94	c2cb1A_	Alignment	not modelled	39.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
95	c1s1iG_	Alignment	not modelled	38.9	14	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein l8-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.
96	d1piia2	Alignment	not modelled	38.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
97	c2fq1A_	Alignment	not modelled	38.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
98	c3e20C_	Alignment	not modelled	38.8	13	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
99	d1to0a_	Alignment	not modelled	38.2	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
100	d1u7pa_	Alignment	not modelled	36.4	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
101	d1y4ia1	Alignment	not modelled	34.5	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
102	c2nmpC_	Alignment	not modelled	33.9	8	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
103	c3qi6B_	Alignment	not modelled	33.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine gamma-synthase metb (cgs); **PDBTitle:** crystal structure of cystathionine gamma-synthase metb (cgs) from2 mycobacterium ulcerans agy99
104	c3nvtA	Alignment	not modelled	33.3	10	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase;

104	c3nvtA_	Alignment	not modelled	[illegible]	10	**PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
105	c2ekcA_	Alignment	not modelled	30.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
106	d1j2ra_	Alignment	not modelled	28.3	15	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
107	c3hqtB_	Alignment	not modelled	27.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
108	c3gndC_	Alignment	not modelled	27.2	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
109	d1qgna_	Alignment	not modelled	25.8	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
110	d2q02a1	Alignment	not modelled	24.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
111	c3ndnC_	Alignment	not modelled	24.9	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
112	d1bs0a_	Alignment	not modelled	24.8	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
113	d1ns5a_	Alignment	not modelled	24.5	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
114	d1vh0a_	Alignment	not modelled	24.4	22	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
115	c3j09A_	Alignment	not modelled	24.3	9	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
116	c2c3zA_	Alignment	not modelled	24.2	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
117	d1ka9h_	Alignment	not modelled	24.0	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
118	c2b34C_	Alignment	not modelled	23.1	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
119	d1ujpa_	Alignment	not modelled	22.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
120	c3j08A_	Alignment	not modelled	22.6	9	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa