Phyre^2

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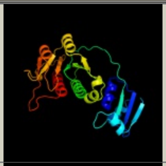
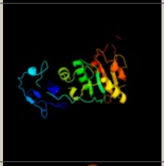
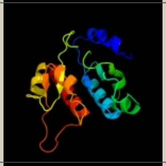
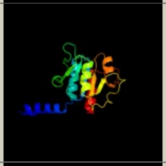
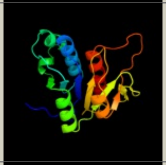
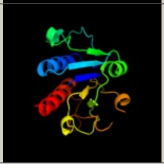
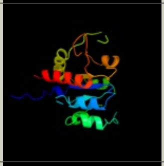
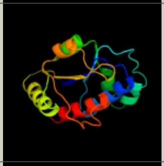
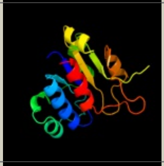
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ipaA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
2	c3gyqB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna (adenosine-2'-o-)-methyltransferase; **PDBTitle:** structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
3	c1x7pB_	Alignment		100.0	27	**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	24	**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	96	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
6	c1gz0G_	Alignment		100.0	96	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
7	d1v2xa_	Alignment		100.0	31	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
8	c1zjrA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanosine-2'-o-)-methyltransferase; **PDBTitle:** crystal structure of a. aeolicus trmh/spou trna modifying enzyme
9	d1ipaa1	Alignment		100.0	31	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
10	c2ha8A_	Alignment		100.0	23	**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	18	**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	18	**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	18	**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	21	**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	18	**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	17	**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	d1gz0a2	Alignment		99.6	99	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
20	d1gz0f2	Alignment		99.6	99	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
21	d1ipaa2	Alignment	not modelled	98.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
22	c2yy8B_	Alignment	not modelled	97.2	16	**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	c4a1dG_	Alignment	not modelled	96.6	11	**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.
24	d2o3aa1	Alignment	not modelled	96.5	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
25	c2zkr6_	Alignment	not modelled	96.5	11	**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
26	d2bo1a1	Alignment	not modelled	96.5	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
27	c3cpqB_	Alignment	not modelled	96.4	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)
						Fold: Bacillus chorismate mutase-like

28	d1t0kb_	Alignment	not modelled	96.3	11	**Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
29	d1vhka2	Alignment	not modelled	96.3	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
30	d1w41a1	Alignment	not modelled	96.3	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
31	d1vqof1	Alignment	not modelled	95.5	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
32	c3kw2A_	Alignment	not modelled	95.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
33	c1vhkA_	Alignment	not modelled	95.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
34	d1xbia1	Alignment	not modelled	95.4	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
35	c3on1A_	Alignment	not modelled	95.2	14	**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
36	d2fc3a1	Alignment	not modelled	95.2	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
37	d1rlga_	Alignment	not modelled	95.2	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
38	d2aifa1	Alignment	not modelled	95.1	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
39	d2vgna3	Alignment	not modelled	95.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
40	c3ai9X_	Alignment	not modelled	94.8	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
41	d1jj2f_	Alignment	not modelled	94.7	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
42	c2lbwA_	Alignment	not modelled	94.7	13	**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
43	d2qi2a3	Alignment	not modelled	94.6	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
44	c3o85A_	Alignment	not modelled	94.5	18	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l7ae; **PDBTitle:** giardia lamblia 15.5kd rna binding protein
45	d1x52a1	Alignment	not modelled	94.3	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
46	d2ozba1	Alignment	not modelled	94.3	12	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
47	d2czwa1	Alignment	not modelled	94.2	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
48	c3agjD_	Alignment	not modelled	93.9	16	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
49	d2qwva1	Alignment	not modelled	93.7	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
50	c3agjB_	Alignment	not modelled	93.6	16	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
51	c2qi2A_	Alignment	not modelled	93.1	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein pelota related protein; **PDBTitle:** crystal structure of the thermoplasma acidophilum pelota2 protein
52	c3obwA_	Alignment	not modelled	93.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
53	c2vgmA_	Alignment	not modelled	93.0	19	**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.
54	c1vhyB_	Alignment	not modelled	92.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein

						hi0303, pfam2 duf558
55	c3obyB_	Alignment	not modelled	92.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
56	c2ktvA_	Alignment	not modelled	92.4	11	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
57	d2alea1	Alignment	not modelled	91.7	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
58	c3agkA_	Alignment	not modelled	90.9	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** crystal structure of archaeal translation termination factor, arf1
59	c3mcaB_	Alignment	not modelled	90.2	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
60	c2xznU_	Alignment	not modelled	90.2	14	**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
61	c3e20C_	Alignment	not modelled	88.2	14	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
62	c3ir9A_	Alignment	not modelled	88.2	16	**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.
63	d1dt9a2	Alignment	not modelled	87.0	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
64	d2qmma1	Alignment	not modelled	86.3	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
65	c2egwB_	Alignment	not modelled	85.4	13	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
66	c1dt9A_	Alignment	not modelled	82.3	12	**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
67	c3cg6A_	Alignment	not modelled	82.2	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible 45 gamma; **PDBTitle:** crystal structure of gadd45 gamma
68	d1v6za2	Alignment	not modelled	78.2	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
69	c2zkrf_	Alignment	not modelled	78.0	16	**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
70	c1z85B_	Alignment	not modelled	77.9	20	**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
71	d1nxza2	Alignment	not modelled	76.7	12	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
72	d1k3ra2	Alignment	not modelled	68.2	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
73	c2cx8B_	Alignment	not modelled	66.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
74	c4a1eF_	Alignment	not modelled	64.7	13	**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
75	c2kg4A_	Alignment	not modelled	64.7	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
76	c3ib6B_	Alignment	not modelled	64.6	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
77	c3u5cM_	Alignment	not modelled	63.9	17	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
78	c3iz5H_	Alignment	not modelled	62.0	16	**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
						PDB header:ribosome

79	c3izcH_	Alignment	not modelled	59.0	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
80	c1k3rA_	Alignment	not modelled	54.3	21	**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
81	d1cl1a_	Alignment	not modelled	49.5	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
82	d1u7pa_	Alignment	not modelled	48.9	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
83	d1a53a_	Alignment	not modelled	41.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
84	c1t9hA_	Alignment	not modelled	35.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
85	c1r0lD_	Alignment	not modelled	34.6	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
86	d1jvna2	Alignment	not modelled	34.3	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
87	c2y0fD_	Alignment	not modelled	33.8	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
88	c1s1iG_	Alignment	not modelled	33.6	16	**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.
89	c2gqnB_	Alignment	not modelled	32.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
90	c2c3zA_	Alignment	not modelled	31.2	17	**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
91	c3a14B_	Alignment	not modelled	30.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
92	c2cb1A_	Alignment	not modelled	26.4	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
93	c2eghA_	Alignment	not modelled	25.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
94	c3q4gA_	Alignment	not modelled	22.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
95	c2kboA_	Alignment	not modelled	20.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g; **PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
96	c2x3yA_	Alignment	not modelled	19.6	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
97	d3by5a1	Alignment	not modelled	18.8	15	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
98	c3by5A_	Alignment	not modelled	18.8	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
99	d1cs1a_	Alignment	not modelled	18.3	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like