












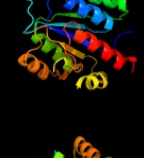


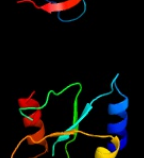


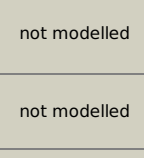


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2372c_(-)_2652047_2652835
Date	Mon Aug 5 13:25:52 BST 2019
Unique Job ID	74b47371acfee57

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4l69A_	 Alignment		100.0	96	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsme like methyltransferase
2	c5o96F_	 Alignment		100.0	26	PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: structure of the putative methyltransferase lpg2936 from legionella2 pneumophila in complex with the bound cofactor sam
3	c5vm8A_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of a ribosomal rna small subunit methyltransferase e2 from neisseria gonorrhoeae bound to s-adenosyl methionine
4	c4e8bA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
5	c1vhyB_	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
6	c4j3cB_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
7	c1vhkA_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
8	c3kw2A_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
9	c2cx8A_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
10	c2egwB_	 Alignment		100.0	23	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
11	c1z85B_	 Alignment		100.0	26	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

12	d1nxza2	Alignment		100.0	28	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
13	c2cx8B_	Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
14	d1vhka2	Alignment		100.0	38	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
15	d1v6za2	Alignment		100.0	36	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
16	d1nxza1	Alignment		99.5	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: YggJ N-terminal domain-like
17	d1vhka1	Alignment		99.4	16	Fold: PUA domain-like Superfamily: PUA domain-like Family: YggJ N-terminal domain-like
18	c3ai9X_	Alignment		96.1	21	PDB header: transferase Chain: X: PDB Molecule: upf0217 protein mj1640; PDBTitle: crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
19	d2qmma1	Alignment		95.7	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
20	d1v6za1	Alignment		95.6	25	Fold: PUA domain-like Superfamily: PUA domain-like Family: YggJ N-terminal domain-like
21	c1gz0G_	Alignment	not modelled	95.5	17	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase r1mb
22	d1gz0a1	Alignment	not modelled	95.4	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
23	c1x7pB_	Alignment	not modelled	95.3	15	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spoU methyltransferase avirb from <i>Streptomyces viridochromogenes</i> in complex with the cofactor adomet
24	c2ha8A_	Alignment	not modelled	94.2	11	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
25	c4x3mB_	Alignment	not modelled	93.4	19	PDB header: transferase Chain: B: PDB Molecule: rrna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from <i>Thermus thermophilus</i> (hb8) in2 complex with adenosine in space group p212121
26	c1zjrA_	Alignment	not modelled	93.2	13	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
27	d1ipaa1	Alignment	not modelled	93.2	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
28	c1ipaA_	Alignment	not modelled	92.9	19	PDB header: transferase Chain: A: PDB Molecule: rrna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase

29	c3onpA	Alignment	not modelled	92.6	14	PDB header: transferase Chain: A: PDB Molecule: trna/rrna methyltransferase (spou); PDBTitle: crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
30	c2i6dA	Alignment	not modelled	92.4	18	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.
31	c1gz0H	Alignment	not modelled	92.3	17	PDB header: transferase Chain: H: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase r1mb
32	c1k3rA	Alignment	not modelled	92.2	20	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
33	c5kzkA	Alignment	not modelled	91.3	17	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna methyltransferase, trmh family; PDBTitle: crystal structure of rrna methyltransferase from sinorhizobium2 melliloti
34	c2qiwa	Alignment	not modelled	90.8	16	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
35	c5co4A	Alignment	not modelled	90.3	17	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
36	d1v2xa	Alignment	not modelled	89.5	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
37	d1mxia	Alignment	not modelled	89.0	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
38	c3ktyA	Alignment	not modelled	88.0	12	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
39	c4e38A	Alignment	not modelled	86.8	19	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
40	c6bmaA	Alignment	not modelled	86.1	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
41	c4cngB	Alignment	not modelled	84.6	13	PDB header: transferase Chain: B: PDB Molecule: spou rrna methylase; PDBTitle: crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
42	c4rg1A	Alignment	not modelled	84.4	15	PDB header: transferase Chain: A: PDB Molecule: c9orf114; PDBTitle: methyltransferase domain of c9orf114
43	d1a53a	Alignment	not modelled	83.9	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	c5gm8A	Alignment	not modelled	83.7	18	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: methylation at position 32 of trna catalyzed by trmj alters oxidative2 stress response in pseudomonas aeruginosa
45	d1to0a	Alignment	not modelled	82.8	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
46	c3l8uA	Alignment	not modelled	82.0	10	PDB header: transferase Chain: A: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
47	c3qjaA	Alignment	not modelled	80.9	19	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
48	c2v82A	Alignment	not modelled	79.0	17	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
49	d1wbha1	Alignment	not modelled	78.2	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
50	d1vh0a	Alignment	not modelled	77.2	18	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
51	c2c3zA	Alignment	not modelled	74.9	19	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
52	c4pzka	Alignment	not modelled	74.8	16	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: crystal structure of putative rna methyltransferase from bacillus2 anthracis.
53	c6oviA	Alignment	not modelled	73.9	18	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent

						carbinolamine intermediate PDB header: transferase
54	c3e5yB_	Alignment	not modelled	73.5	21	Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
55	c4xb0A_	Alignment	not modelled	71.4	19	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: crystal structure of full length e.coli trmj in complex with sah
56	c5graA_	Alignment	not modelled	70.8	20	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: crystal structure of trmj from z. mobilis zm4
57	c3ilkB_	Alignment	not modelled	70.4	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
58	d1rpxa_	Alignment	not modelled	68.5	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
59	d1s2wa_	Alignment	not modelled	65.9	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
60	c3tsmB_	Alignment	not modelled	65.9	16	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
61	c2ze3A_	Alignment	not modelled	64.3	21	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
62	d1o6da_	Alignment	not modelled	64.2	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
63	d1piia2	Alignment	not modelled	63.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
64	d1i4na_	Alignment	not modelled	62.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
65	d1mxsa_	Alignment	not modelled	62.1	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
66	c5fmsA_	Alignment	not modelled	62.0	23	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 52 homolog; PDBTitle: mmift52 n-terminal domain
67	c2h6rG_	Alignment	not modelled	60.8	21	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
68	c3j21U_	Alignment	not modelled	60.4	15	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
69	d1vhca_	Alignment	not modelled	59.5	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
70	c3gyqB_	Alignment	not modelled	58.3	15	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o-)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
71	c5uncB_	Alignment	not modelled	58.1	22	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
72	c4qccA_	Alignment	not modelled	57.8	17	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
73	c5fmrC_	Alignment	not modelled	56.9	18	PDB header: transport protein Chain: C: PDB Molecule: intraflagellar transport protein component ift52; PDBTitle: crift52 n-terminal domain
74	d1ns5a_	Alignment	not modelled	55.8	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
75	c6humN_	Alignment	not modelled	55.1	31	PDB header: proton transport Chain: N: PDB Molecule: nad(p)h-quinone oxidoreductase subunit n; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
76	c4cndB_	Alignment	not modelled	54.5	14	PDB header: transferase Chain: B: PDB Molecule: trna (cytidine/uridine-2'-o-)-methyltransferase trmj; PDBTitle: crystal structure of e.coli trmj
77	c3f4wA_	Alignment	not modelled	53.6	18	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
78	d1k3ra2	Alignment	not modelled	52.2	26	Fold: alpha/beta knot Superfamily: alpha/beta knot

						Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
79	c4bk9B	Alignment	not modelled	51.8	19	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from <i>Zymomonas mobilis</i> atcc 29191
80	c1znnF	Alignment	not modelled	48.0	24	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
81	d1zna1	Alignment	not modelled	48.0	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
82	c2e6zA	Alignment	not modelled	47.5	8	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
83	c6ghcA	Alignment	not modelled	47.3	15	PDB header: hydrolase Chain: A: PDB Molecule: 5-methylcytosine-specific restriction enzyme a; PDBTitle: modification dependent <i>ecokmcra</i> restriction endonuclease
84	c3ic6A	Alignment	not modelled	47.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from <i>neisseria2 gonorrhoeae</i>
85	d1wa3a1	Alignment	not modelled	45.7	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
86	c4a1cS	Alignment	not modelled	45.3	15	PDB header: ribosome Chain: S: PDB Molecule: rpl26; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
87	c3zf7Z	Alignment	not modelled	42.8	9	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l26, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the <i>trypanosoma2 brucei</i> ribosome
88	c3igsB	Alignment	not modelled	42.6	15	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
89	c3ajxA	Alignment	not modelled	41.1	22	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
90	c3iz5Y	Alignment	not modelled	39.8	15	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l26 (l24p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of <i>triticum aestivum</i> translating 80s ribosome
91	c4nu7C	Alignment	not modelled	39.7	14	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from <i>Toxoplasma gondii</i> .
92	d1geqa	Alignment	not modelled	39.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
93	d1y71a1	Alignment	not modelled	38.0	18	Fold: SH3-like barrel Superfamily: Kinase-associated protein B-like Family: Kinase-associated protein B-like
94	c3exsB	Alignment	not modelled	38.0	11	PDB header: lyase Chain: B: PDB Molecule: rmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of <i>kgpdc</i> from <i>streptococcus mutans</i> in2 complex with d-r5p
95	c1yadD	Alignment	not modelled	37.4	24	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from <i>Bacillus subtilis</i>
96	d1te7a	Alignment	not modelled	36.5	18	Fold: PUA domain-like Superfamily: PUA domain-like Family: yqfB-like
97	d1vr4a1	Alignment	not modelled	36.2	23	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
98	d1qopa	Alignment	not modelled	35.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
99	d1vqot1	Alignment	not modelled	35.1	16	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
100	c5n2pA	Alignment	not modelled	35.0	10	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: <i>Sulfolobus solfataricus</i> tryptophan synthase a
101	c4n6eA	Alignment	not modelled	34.5	17	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis <i>bexx/cyso</i> complex
102	c3qkbB	Alignment	not modelled	32.5	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from <i>Pediococcus pentosaceus</i> atcc 257453 at 2.73 a resolution
103	c1y2iC	Alignment	not modelled	31.7	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein s0862; PDBTitle: crystal structure of <i>mcsG</i> target <i>apc27401</i> from <i>Shigella flexneri</i>

104	d1y2ia_	Alignment	not modelled	31.7	20	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
105	c2m0oA_	Alignment	not modelled	31.3	14	PDB header: peptide binding protein Chain: A; PDB Molecule: phd finger protein 1; PDBTitle: the solution structure of human phf1 in complex with h3k36me3
106	d2fia1_	Alignment	not modelled	31.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
107	c4mg4G_	Alignment	not modelled	30.9	21	PDB header: unknown function Chain: G; PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
108	c2e5pA_	Alignment	not modelled	30.2	15	PDB header: transcription Chain: A; PDB Molecule: phd finger protein 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
109	d1sf8a_	Alignment	not modelled	30.2	13	Fold: HSP90 C-terminal domain Superfamily: HSP90 C-terminal domain Family: HSP90 C-terminal domain
110	d1vc4a_	Alignment	not modelled	28.4	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
111	c2zpaB_	Alignment	not modelled	28.0	26	PDB header: transferase Chain: B; PDB Molecule: uncharacterized protein ypfi; PDBTitle: crystal structure of trna(met) cytidine acetyltransferase
112	c5exkG_	Alignment	not modelled	27.9	24	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
113	c1zlpA_	Alignment	not modelled	27.9	11	PDB header: lyase Chain: A; PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
114	c3ih1A_	Alignment	not modelled	27.7	16	PDB header: lyase Chain: A; PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
115	c1piiA_	Alignment	not modelled	27.3	19	PDB header: bifunctional(isomerase and synthase) Chain: A; PDB Molecule: n-(5'phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
116	c2eqmA_	Alignment	not modelled	26.8	15	PDB header: transcription Chain: A; PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
117	d1q6oa_	Alignment	not modelled	26.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
118	d1xi3a_	Alignment	not modelled	26.1	14	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
119	c3inpA_	Alignment	not modelled	25.9	14	PDB header: isomerase Chain: A; PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
120	c3ff4A_	Alignment	not modelled	25.7	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412