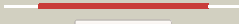



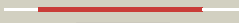



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2890c_(rpsB)_3199129_3199992
Date	Thu Aug 8 16:20:04 BST 2019
Unique Job ID	1431e3aafc81de08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4toiA_	 Alignment		100.0	44	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s2,ribosomal protein s1; PDBTitle: crystal structure of e.coli ribosomal protein s2 in complex with n-2 terminal domain of s1
2	c5o5jV_	 Alignment		100.0	96	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein s2; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
3	d2uubb1	 Alignment		100.0	52	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
4	c3bbnB_	 Alignment		100.0	39	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein s2; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
5	d2gy9b1	 Alignment		100.0	53	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
6	c3j6vB_	 Alignment		100.0	30	PDB header: ribosome Chain: B: PDB Molecule: 28s ribosomal protein s2, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
7	c3iz6A_	 Alignment		100.0	22	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
8	c3bchA_	 Alignment		100.0	26	PDB header: cell adhesion, ribosomal protein Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: crystal structure of the human laminin receptor precursor
9	c3izbA_	 Alignment		100.0	22	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein rps0 (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
10	c3j20B_	 Alignment		100.0	27	PDB header: ribosome Chain: B: PDB Molecule: 30s ribosomal protein s2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
11	c3zeyC_	 Alignment		100.0	27	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein sa, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

12	c2xznB_	Alignment		100.0	28	PDB header: ribosome Chain: B: PDB Molecule: rps0e; 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
13	d1vi6a_	Alignment		100.0	28	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
14	c2zkqb_	Alignment		100.0	24	PDB header: ribosomal protein/rna Chain: B: PDB Molecule: rna expansion segment es3; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
15	c1s1hB_	Alignment		100.0	24	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
16	c5xyiA_	Alignment		100.0	27	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: small subunit of trichomonas vaginalis ribosome
17	d1x94a_	Alignment		97.6	18	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
18	d1tk9a_	Alignment		97.2	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
19	c2x3yA_	Alignment		97.1	16	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
20	c5i01B_	Alignment		96.2	15	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
21	d1x92a_	Alignment	not modelled	95.9	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
22	c1nriA_	Alignment	not modelled	95.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
23	d1nria_	Alignment	not modelled	95.3	14	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
24	c2yvaB_	Alignment	not modelled	94.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
25	c3shoA_	Alignment	not modelled	94.3	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
26	d1m3sa_	Alignment	not modelled	93.8	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
27	c5by2A_	Alignment	not modelled	93.7	13	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
28	c3trjC_	Alignment	not modelled	93.0	18	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
29	c4ivnB_	Alignment	not modelled	92.4	21	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the vibrio vulnificus nanr protein complexed with mannac-

					6p
30	c4s12C_	Alignment	not modelled	91.6	15 PDB header: lyase Chain: C: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
31	c4lzd_	Alignment	not modelled	91.1	15 PDB header: lyase/lyase inhibitor Chain: D: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: crystal structure of murq from h.influenzae with bound inhibitor
32	c3knzA_	Alignment	not modelled	90.0	22 PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of a putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
33	c2am1B_	Alignment	not modelled	89.8	12 PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
34	c3fxaA_	Alignment	not modelled	88.0	16 PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
35	c2a3nA_	Alignment	not modelled	85.9	22 PDB header: sugar binding protein Chain: A: PDB Molecule: putative glucosamine-fructose-6-phosphate aminotransferase; PDBTitle: crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
36	d1vima_	Alignment	not modelled	85.2	12 Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
37	c5uqiA_	Alignment	not modelled	84.8	13 PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
38	c3cvjB_	Alignment	not modelled	83.9	18 PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
39	c6dspB_	Alignment	not modelled	83.8	20 PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
40	c3c65A_	Alignment	not modelled	82.2	12 PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvr5' endonuclease2 domain
41	c4hwgA_	Alignment	not modelled	79.9	18 PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: structure of udp-n-acetylglucosamine 2-epimerase from rickettsia2 bellii
42	d1kzyc2	Alignment	not modelled	77.9	23 Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
43	c2nrrA_	Alignment	not modelled	71.3	18 PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnahe endonuclease domain of uvr5
44	d1jeoa_	Alignment	not modelled	68.6	15 Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
45	d1l7ba_	Alignment	not modelled	66.1	23 Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
46	c3etnD_	Alignment	not modelled	65.1	19 PDB header: isomerase Chain: D: PDB Molecule: putative phosphosugar isomerase involved in capsule PDBTitle: crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
47	d1pjqa1	Alignment	not modelled	64.7	13 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
48	c4nspA_	Alignment	not modelled	64.0	17 PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of human endov
49	c4ys6A_	Alignment	not modelled	63.5	18 PDB header: solute-binding protein Chain: A: PDB Molecule: putative solute-binding component of abc transporter; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_1585, target efi-3 511156) with bound beta-d-glucose
50	c4wzzA_	Alignment	not modelled	63.1	22 PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_0583, target efi-3 511148) with bound l-rhamnose
51	c3ga2A_	Alignment	not modelled	60.0	20 PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease_v (bsu36170) from bacillus2 subtilis, northeast structural genomics consortium target sr624
52	c5ghrA_	Alignment	not modelled	59.8	22 PDB header: dna binding protein/replication Chain: A: PDB Molecule: ssdna-specific exonuclease; PDBTitle: dna replication protein

53	d2f9ya1	Alignment	not modelled	59.7	28	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
54	c2f9iC	Alignment	not modelled	58.9	28	PDB header: transferase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
55	c1ir6A	Alignment	not modelled	58.5	19	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease recj; PDBTitle: crystal structure of exonuclease recj bound to manganese
56	d1lr6a	Alignment	not modelled	58.5	19	Fold: DHH phosphoesterases Superfamily: DHH phosphoesterases Family: Exonuclease RecJ
57	c3hgtA	Alignment	not modelled	57.7	11	PDB header: transcription Chain: A: PDB Molecule: hda1 complex subunit 3; PDBTitle: structural and functional studies of the yeast class ii hda12 hdac complex
58	c2r7aC	Alignment	not modelled	57.3	11	PDB header: transport protein Chain: C: PDB Molecule: bacterial heme binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein from shigella2 dysenteriae
59	c3gocB	Alignment	not modelled	55.5	20	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
60	c5f56A	Alignment	not modelled	54.7	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
61	d1j5xa	Alignment	not modelled	54.0	16	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
62	c4wwhA	Alignment	not modelled	54.0	22	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose
63	c3cf4A	Alignment	not modelled	52.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
64	c1xnwD	Alignment	not modelled	51.8	20	PDB header: ligase Chain: D: PDB Molecule: propionyl-coa carboxylase complex b subunit; PDBTitle: acyl-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i
65	c4rxuA	Alignment	not modelled	51.7	22	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
66	d1pixa3	Alignment	not modelled	51.0	26	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
67	c6epcN	Alignment	not modelled	50.8	19	PDB header: hydrolase Chain: N: PDB Molecule: 26s proteasome non-atpase regulatory subunit 1; PDBTitle: ground state 26s proteasome (gs2)
68	c1pixB	Alignment	not modelled	49.7	18	PDB header: lyase Chain: B: PDB Molecule: glutaconyl-coa decarboxylase a subunit; PDBTitle: crystal structure of the carboxyltransferase subunit of the2 bacterial ion pump glutaconyl-coenzyme a decarboxylase
69	c3n6rF	Alignment	not modelled	49.2	15	PDB header: ligase Chain: F: PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
70	d1f0ka	Alignment	not modelled	48.9	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
71	c4xpuA	Alignment	not modelled	48.9	16	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: the crystal structure of endov from e.coli
72	c2w36B	Alignment	not modelled	48.0	24	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
73	d1j6ua1	Alignment	not modelled	48.0	12	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
74	c4gudA	Alignment	not modelled	45.8	21	PDB header: transferase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit hish; PDBTitle: crystal structure of amidotransferase hish from vibrio cholerae
75	c3uuuB	Alignment	not modelled	45.7	20	PDB header: sugar binding protein Chain: B: PDB Molecule: multiple sugar-binding periplasmic receptor chve; PDBTitle: crystal structure of the periplasmic sugar binding protein chve
76	c6bwsA	Alignment	not modelled	45.5	36	PDB header: unknown function Chain: A: PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
77	c4zhtB	Alignment	not modelled	45.0	22	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-

77	c4z1tB	Alignment	not modelled	43.0	22	epimerase/n- PDBTitle: crystal structure of udp-glcna2-2-epimerase
78	d2jfga1	Alignment	not modelled	44.7	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
79	c3g68A	Alignment	not modelled	44.2	18	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
80	c5xvnL	Alignment	not modelled	43.8	15	PDB header: immune system Chain: L: PDB Molecule: crisp-associated endonuclease cas1; PDBTitle: e. far cas1-cas2/prespacer binary complex
81	c3glmD	Alignment	not modelled	43.0	32	PDB header: lyase Chain: D: PDB Molecule: glutaconyl-coa decarboxylase subunit a; PDBTitle: glutaconyl-coa decarboxylase a subunit from clostridium symbiosum co-2 crystallized with crotonyl-coa
82	c2xhzC	Alignment	not modelled	42.4	16	PDB header: isomerase Chain: C: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
83	c5ingC	Alignment	not modelled	42.2	15	PDB header: transferase Chain: C: PDB Molecule: putative carboxyl transferase; PDBTitle: a crotonyl-coa reductase-carboxylase independent pathway for assembly2 of unusual alkylmalonyl-coa polyketide synthase extender unit
84	d1o6ca	Alignment	not modelled	41.7	23	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
85	c5nmwA	Alignment	not modelled	41.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
86	d1tjya	Alignment	not modelled	41.2	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
87	c4pz0A	Alignment	not modelled	40.7	18	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
88	c1vrgE	Alignment	not modelled	40.1	18	PDB header: ligase Chain: E: PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of propionyl-coa carboxylase, beta subunit (tm0716)2 from thermotoga maritima at 2.30 a resolution
89	c3qk7C	Alignment	not modelled	39.7	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulators; PDBTitle: crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
90	c5vj1M	Alignment	not modelled	39.6	24	PDB header: transferase Chain: M: PDB Molecule: mdce; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with coenzyme a
91	d1p3da1	Alignment	not modelled	39.5	25	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
92	c5braA	Alignment	not modelled	39.2	19	PDB header: solute-binding protein Chain: A: PDB Molecule: putative periplasmic binding protein with substrate ribose; PDBTitle: crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085)
93	c4yleA	Alignment	not modelled	39.1	12	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of an abc transpoter solute binding protein2 (ipr025997) from burkholderia multivorans (bmul_1631, target efi-3 511115) with an unknown ligand modelled as alpha-d-erythrofuranoose
94	c5ikID	Alignment	not modelled	38.5	11	PDB header: ligase Chain: D: PDB Molecule: geranyl-coa carboxylase, beta-subunit; PDBTitle: crystal structure of p. aeruginosa geranyl-coa carboxylase (gcc), beta2 subunit
95	c3fpvC	Alignment	not modelled	38.4	36	PDB header: heme binding protein Chain: C: PDB Molecule: extracellular haem-binding protein; PDBTitle: crystal structure of hbps
96	d2gv8a2	Alignment	not modelled	38.2	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
97	c3s2uA	Alignment	not modelled	37.8	22	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
98	d1euca1	Alignment	not modelled	37.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
99	c2nrzB	Alignment	not modelled	37.6	20	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrC bound to its2 catalytic divalent cation
100	c4q0gC	Alignment	not modelled	37.2	16	PDB header: ligase Chain: C: PDB Molecule: probable acetyl-/propionyl-coa carboxylase (beta subunit) PDBTitle: crystal structure of beta subunit of acyl-coa carboxylase accd1 from2 mycobacterium tuberculosis

101	c4l6wB_	Alignment	not modelled	36.6	26	PDB header: ligase Chain: B: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
102	d1xnaya1	Alignment	not modelled	36.5	39	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
103	d1on3a1	Alignment	not modelled	36.5	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
104	c1s3mA_	Alignment	not modelled	36.2	16	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
105	d1s3la_	Alignment	not modelled	36.2	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
106	d2a7sa2	Alignment	not modelled	36.1	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
107	d1a9xa4	Alignment	not modelled	36.0	27	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
108	c1x0uB_	Alignment	not modelled	35.8	25	PDB header: lyase Chain: B: PDB Molecule: hypothetical methylmalonyl-coa decarboxylase alpha subunit; PDBTitle: crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfobolus tokodaii
109	c5qj3A_	Alignment	not modelled	35.7	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: periplasmic heme-binding protein rhut from roseiflexus sp. rs-1 in2 two-heme bound form (holo-2)
110	c2a7sD_	Alignment	not modelled	35.5	18	PDB header: ligase Chain: D: PDB Molecule: probable propionyl-coa carboxylase beta chain 5; PDBTitle: crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis
111	c1on3E_	Alignment	not modelled	35.3	15	PDB header: transferase Chain: E: PDB Molecule: methylmalonyl-coa carboxyltransferase 12s PDBTitle: transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
112	c5e9tA_	Alignment	not modelled	35.0	30	PDB header: transferase/chaperone Chain: A: PDB Molecule: glycosyltransferase gtf1; PDBTitle: crystal structure of gtfa/b complex
113	c3u9rB_	Alignment	not modelled	34.9	21	PDB header: ligase Chain: B: PDB Molecule: methylcrotonyl-coa carboxylase, beta-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc), beta subunit
114	d1xnaya2	Alignment	not modelled	34.3	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
115	c3bbIA_	Alignment	not modelled	33.8	8	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of lacI family; PDBTitle: crystal structure of a regulatory protein of lacI family from2 chloroflexus aggregans
116	c1keeH_	Alignment	not modelled	33.7	27	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
117	d1vrqa1	Alignment	not modelled	33.5	50	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
118	c4kzkA_	Alignment	not modelled	33.2	17	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
119	d1vrqa2	Alignment	not modelled	33.2	22	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
120	d2a7sa1	Alignment	not modelled	33.0	39	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain