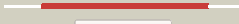



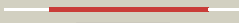




























Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2138_(lppL)_2397338_2398414
 Date Mon Aug 5 13:25:25 BST 2019
 Unique Job ID c4fe0092ffbbc92a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bwsA_	 Alignment		99.9	14	PDB header: unknown function Chain: A: PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
2	c6rteB_	 Alignment		99.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
3	c2j57j_	 Alignment		99.9	13	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: x-ray reduced paraccoccus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
4	c1qniE_	 Alignment		99.9	13	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrous-oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from pseudomonas nautica,2 at 2.4a resolution
5	c1fwxB_	 Alignment		99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
6	c3dm0A_	 Alignment		99.9	13	PDB header: sugar binding protein,signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein fused with rack1; PDBTitle: maltose binding protein fusion with rack1 from a. thaliana
7	c3u4yA_	 Alignment		99.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein (dtox_1751)2 from desulfotomaculum acetoxidans dsm 771.
8	d1qnia2	 Alignment		99.9	13	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
9	c5f30B_	 Alignment		99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
10	d2madh_	 Alignment		99.9	11	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
11	c1nnoA_	 Alignment		99.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa

12	c1gq1B_	Alignment		99.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
13	c4qrjA_	Alignment		99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of a putative 6-phosphogluconolactonase2 (bacuni_04672) from bacteroides uniformis atcc 8492 at 2.20 a3 resolution
14	c5tzsT_	Alignment		99.9	14	PDB header: translation Chain: T: PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome
15	c2iwaA_	Alignment		99.9	9	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: unbound glutaminyl cyclotransferase from carica papaya.
16	c3vh0C_	Alignment		99.9	14	PDB header: protein binding/dna Chain: C: PDB Molecule: uncharacterized protein ynce; PDBTitle: crystal structure of e. coli ynce complexed with dna
17	c6nd4T_	Alignment		99.9	14	PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
18	c3hfgB_	Alignment		99.9	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein lp_2219; PDBTitle: crystal structure of the lp_2219 protein from lactobacillus plantarum.2 northeast structural genomics consortium target lpr118.
19	d1pbyb_	Alignment		99.9	18	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
20	d2bbkh_	Alignment		99.8	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
21	c5juyB_	Alignment	not modelled	99.8	9	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
22	c5a1vK_	Alignment	not modelled	99.8	10	PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
23	c4yczA_	Alignment	not modelled	99.8	11	PDB header: structural protein Chain: A: PDB Molecule: fusion protein of sec13 and nup145c; PDBTitle: y-complex hub (nup85-nup120-nup145c-sec13 complex) from m. thermophila2 (a.k.a. t. heterothallica)
24	d1pjxa_	Alignment	not modelled	99.8	17	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
25	c3fgbB_	Alignment	not modelled	99.8	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein q89zh8_bactn; PDBTitle: crystal structure of the q89zh8_bactn protein from bacteroides2 thetaiotaomicron. northeast structural genomics consortium target3 btr289b.
26	c6igbB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic gluconolactonase, ppgl; PDBTitle: the structure of pseudomonas aeruginosa periplasmic gluconolactonase,2 ppgl
27	d1fwxa2	Alignment	not modelled	99.8	11	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
28	c3c75J_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin

29	c5a5uB_	Alignment	not modelled	99.8	9	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of mammalian eif3 in the context of the 43s preinitiation2 complex
30	c3sbrF_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: F: PDB Molecule: nitrous-oxide reductase; PDBTitle: pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
31	d2p4oa1	Alignment	not modelled	99.8	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like
32	c3mbrX_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: X: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of the glutamyl cyclase from xanthomonas2 campestris
33	c4nsxA_	Alignment	not modelled	99.8	12	PDB header: protein binding Chain: A: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: crystal structure of the utp21 tandem wd domain
34	c2h47F_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase/electron transport Chain: F: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
35	d1ri6a_	Alignment	not modelled	99.8	12	Fold: 7-bladed beta-propeller Superfamily: Putative isomerase YbhE Family: Putative isomerase YbhE
36	c3nolA_	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutamyl cyclase (trigonal2 form)
37	c2i0tB_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
38	c3g4hB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
39	c4e54B_	Alignment	not modelled	99.8	13	PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna damage-binding protein 2; PDBTitle: damaged dna induced uv-damaged dna-binding protein (uv-ddb)2 dimerization and its roles in chromatinized dna repair
40	c2oajA_	Alignment	not modelled	99.8	13	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: protein sni1; PDBTitle: crystal structure of sro7 from s. cerevisiae
41	d1jmxB_	Alignment	not modelled	99.8	13	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
42	d1jofa_	Alignment	not modelled	99.8	13	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-mucoante lactonizing enzyme Family: 3-carboxy-cis,cis-mucoante lactonizing enzyme
43	c5n1aB_	Alignment	not modelled	99.8	11	PDB header: translation Chain: B: PDB Molecule: utp4; PDBTitle: crystal structure of utp4 from chaetomium thermophilum
44	c6cmkB_	Alignment	not modelled	99.8	10	PDB header: metal binding protein Chain: B: PDB Molecule: aztd protein; PDBTitle: crystal structure of citrobacter koseri aztd
45	c6nd4H_	Alignment	not modelled	99.8	10	PDB header: ribosome Chain: H: PDB Molecule: utp17; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
46	c5dfzB_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
47	c5i5iA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
48	d1nira2	Alignment	not modelled	99.8	12	Fold: 8-bladed beta-propeller Superfamily: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase Family: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
49	c6gc1A_	Alignment	not modelled	99.8	14	PDB header: unknown function Chain: A: PDB Molecule: nhl repeat-containing protein 2; PDBTitle: crystal structure of trx-like and nhl repeat containing domains of2 human nhlrc2
50	c2w18A_	Alignment	not modelled	99.8	13	PDB header: nuclear protein Chain: A: PDB Molecule: partner and localizer of brca2; PDBTitle: crystal structure of the c-terminal wd40 domain of human2 palb2
51	c5n4aA_	Alignment	not modelled	99.8	12	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 80; PDBTitle: crystal structure of chlamydomonas ift80
52	c2aq5A_	Alignment	not modelled	99.8	12	PDB header: structural protein Chain: A: PDB Molecule: coronin-1a; PDBTitle: crystal structure of murine coronin-1
53	d1qksa2	Alignment	not modelled	99.8	10	Fold: 8-bladed beta-propeller Superfamily: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase Family: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
54	c5c2vB_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: hydrazine synthase beta subunit;

						PDBTitle: kuenenia stuttgartiensis hydrazine synthase
55	c6nd4W_	Alignment	not modelled	99.8	11	PDB header: ribosome Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
56	c3wj9A_	Alignment	not modelled	99.8	9	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2a; PDBTitle: crystal structure of the eukaryotic initiation factor
57	c4yhCA_	Alignment	not modelled	99.8	12	PDB header: structural protein Chain: A: PDB Molecule: sterol regulatory element-binding protein cleavage- PDBTitle: crystal structure of the wd40 domain of scap from fission yeast
58	c6ck1C_	Alignment	not modelled	99.7	11	PDB header: metal binding protein Chain: C: PDB Molecule: a1b2f4 protein; PDBTitle: crystal structure of paracoccus denitrificans aztd
59	c1l0qC_	Alignment	not modelled	99.7	19	PDB header: protein binding Chain: C: PDB Molecule: surface layer protein; PDBTitle: tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
60	c3nokB_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: glutaminy cyclase; PDBTitle: crystal structure of myxococcus xanthus glutaminy cyclase
61	c6nd4Q_	Alignment	not modelled	99.7	14	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
62	d1l0qa2	Alignment	not modelled	99.7	20	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
63	d2dg1a1	Alignment	not modelled	99.7	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
64	c6nd4O_	Alignment	not modelled	99.7	9	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
65	c4ozuA_	Alignment	not modelled	99.7	11	PDB header: structural protein Chain: A: PDB Molecule: coronin; PDBTitle: crystal structure of wd40 domain from toxoplasma gondii coronin
66	c5cvoD_	Alignment	not modelled	99.7	11	PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
67	c6em5m_	Alignment	not modelled	99.7	14	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l14-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
68	c6n8sA_	Alignment	not modelled	99.7	12	PDB header: lipid binding protein Chain: A: PDB Molecule: lethal(2) giant larvae protein homolog 2; PDBTitle: crystal structure of the human cell polarity protein lethal giant2 larvae 2 (lg2). apkc phosphorylated, crystal form 3.
69	c5cvoA_	Alignment	not modelled	99.7	11	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
70	c3lrVA_	Alignment	not modelled	99.7	9	PDB header: splicing Chain: A: PDB Molecule: pre-mrna-splicing factor 19; PDBTitle: the prp19 wd40 domain contains a conserved protein interaction region2 essential for its function.
71	c3jroA_	Alignment	not modelled	99.7	9	PDB header: transport protein, structural protein Chain: A: PDB Molecule: fusion protein of protein transport protein sec13 and PDBTitle: nup84-nup145c-sec13 edge element of the npc lattice
72	c6chgD_	Alignment	not modelled	99.7	6	PDB header: transferase Chain: D: PDB Molecule: klla0a08800p; PDBTitle: crystal structure of the yeast compass catalytic module
73	c5k1bB_	Alignment	not modelled	99.7	12	PDB header: protein binding/hydrolase Chain: B: PDB Molecule: wd repeat-containing protein 48; PDBTitle: crystal structure of the uaf1/usp12 complex in f222 space group
74	c4bzka_	Alignment	not modelled	99.7	10	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec31; PDBTitle: the structure of the copii coat assembled on membranes
75	c3ei4D_	Alignment	not modelled	99.7	14	PDB header: dna binding protein Chain: D: PDB Molecule: dna damage-binding protein 2; PDBTitle: structure of the hssdb1-hssdb2 complex
76	c3iytG_	Alignment	not modelled	99.7	11	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
77	d1gxra_	Alignment	not modelled	99.7	17	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
78	c3e5zA_	Alignment	not modelled	99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative gluconolactonase; PDBTitle: x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
79	c5cviA_	Alignment	not modelled	99.7	10	PDB header: protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48 (uaf-1), residues 2-580
80	c3dr2A_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: exported gluconolactonase; PDBTitle: structural and functional analyses of xc5397 from2

						xanthomonas campestris: a gluconolactonase important in3 glucose secondary metabolic pathways
81	c3qqzA_	Alignment	not modelled	99.7	11	PDB header: metal binding protein Chain: A: PDB Molecule: putative uncharacterized protein yjik; PDBTitle: crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
82	c2iwkB_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: inhibitor-bound form of nitrous oxide reductase from2 achromobacter cycloclastes at 1.7 angstrom resolution
83	c6nd4S_	Alignment	not modelled	99.7	12	PDB header: ribosome Chain: S: PDB Molecule: utp18; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
84	c4wjuB_	Alignment	not modelled	99.7	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: ribosome assembly protein 4; PDBTitle: crystal structure of rsa4 from saccharomyces cerevisiae
85	c6r5kA_	Alignment	not modelled	99.7	12	PDB header: rna binding protein Chain: A: PDB Molecule: pan2-pan3 deadenylation complex catalytic subunit pan2; PDBTitle: cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
86	c5i2tA_	Alignment	not modelled	99.7	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: periodic tryptophan protein 2; PDBTitle: domain characterization of the wd protein pwp2 and their relevance in2 ribosome biogenesis
87	c1nr0A_	Alignment	not modelled	99.7	10	PDB header: structural protein Chain: A: PDB Molecule: actin interacting protein 1; PDBTitle: two seven-bladed beta-propeller domains revealed by the2 structure of a c. elegans homologue of yeast actin3 interacting protein 1 (aip1).
88	c6cb1s_	Alignment	not modelled	99.7	14	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l20-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 3)
89	c4wjsA_	Alignment	not modelled	99.6	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: rsa4; PDBTitle: crystal structure of rsa4 from chaetomium thermophilum
90	c3hrpA_	Alignment	not modelled	99.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of structural genomics protein of unknown function2 (np_812590.1) from bacteroides thetaiotaomicron vpi-5482 at 1.70 a3 resolution
91	c6qk7A_	Alignment	not modelled	99.6	10	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 1; PDBTitle: elongator catalytic subcomplex elp123 lobe
92	c6nd4L_	Alignment	not modelled	99.6	13	PDB header: ribosome Chain: L: PDB Molecule: utp5; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
93	c4czvB_	Alignment	not modelled	99.6	10	PDB header: gene regulation Chain: B: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the neurospora crassa pan2 wd40 domain
94	c5a1vL_	Alignment	not modelled	99.6	10	PDB header: transport protein Chain: L: PDB Molecule: coatomer subunit beta; PDBTitle: the structure of the copi coat linkage i
95	c5wbiA_	Alignment	not modelled	99.6	16	PDB header: protein binding Chain: A: PDB Molecule: regulatory-associated protein of tor 1; PDBTitle: crystal structure of the arabidopsis thaliana raptor
96	c3dsmA_	Alignment	not modelled	99.6	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bacuni_02894; PDBTitle: crystal structure of the surface layer protein bacuni_02894 from2 bacteroides uniformis, northeast structural genomics consortium3 target btr193d.
97	c5a1uC_	Alignment	not modelled	99.6	7	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat triad
98	c6e29C_	Alignment	not modelled	99.6	12	PDB header: protein binding Chain: C: PDB Molecule: swd1-like protein; PDBTitle: crystal structure of myceliophtheria_thermophila cps50 (swd1) beta-2 propeller domain
99	c2j04B_	Alignment	not modelled	99.6	7	PDB header: transcription Chain: B: PDB Molecule: ydr362cp; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor iiic
100	c4i79B_	Alignment	not modelled	99.6	12	PDB header: cell cycle Chain: B: PDB Molecule: nucleoporin nup43; PDBTitle: crystal structure of human nup43
101	d1yfqA_	Alignment	not modelled	99.6	9	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: Cell cycle arrest protein BUB3
102	c2z2pA_	Alignment	not modelled	99.6	9	PDB header: lyase/antibiotic Chain: A: PDB Molecule: virginiamycin b lyase; PDBTitle: crystal structure of catalytically inactive h270a virginiamycin b2 lyase from staphylococcus aureus with quinupristin
103	c4ui9R_	Alignment	not modelled	99.6	8	PDB header: cell cycle Chain: R: PDB Molecule: fizzy-related protein homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
104	c4hw6D_	Alignment	not modelled	99.6	10	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein, ipt/tig domain protein; PDBTitle: crystal structure of an auxiliary nutrient binding protein2 (bacova_00264) from bacteroides ovatus atcc 8483 at 1.70 a resolution
105	c5d9hA_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: luciferin regenerating enzyme;

105	c3u9vA_	Alignment	not modelled	99.6	17	PDBTitle: luciferin-regenerating enzyme solved by siras using xfel (refined2 against native data)
106	c5nzcC_	Alignment	not modelled	99.6	11	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage iv
107	c2qe8B_	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (ava_4197) from anabaena2 variabilis atcc 29413 at 1.35 a resolution
108	c3fw0A_	Alignment	not modelled	99.6	12	PDB header: lyase Chain: A: PDB Molecule: peptidyl-glycine alpha-amidating monooxygenase; PDBTitle: structure of peptidyl-alpha-hydroxyglycine alpha-amidating2 lyase (pal) bound to alpha-hydroxyhippuric acid (non-3 peptidic substrate)
109	d1ospo_	Alignment	not modelled	99.6	12	Fold: open-sided beta-meander Superfamily: Outer surface protein Family: Outer surface protein
110	c2pm9A_	Alignment	not modelled	99.6	10	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec31; PDBTitle: crystal structure of yeast sec13/31 vertex element of the copii2 vesicular coat
111	c4o9dA_	Alignment	not modelled	99.6	13	PDB header: gene regulation Chain: A: PDB Molecule: rik1-associated factor 1; PDBTitle: structure of dos1 propeller
112	c4h5jB_	Alignment	not modelled	99.6	10	PDB header: protein transport Chain: B: PDB Molecule: guanine nucleotide-exchange factor sec12; PDBTitle: crystal structure of the guanine nucleotide exchange factor sec12 (p642 form)
113	c2vduB_	Alignment	not modelled	99.6	10	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(7)-)-methyltransferase- PDBTitle: structure of trm8-trm82, the yeast trna m7g methylation2 complex
114	c1nexD_	Alignment	not modelled	99.6	15	PDB header: ligase, cell cycle Chain: D: PDB Molecule: cdc4 protein; PDBTitle: crystal structure of scskp1-sccdc4-cpd peptide complex
115	c2ghsA_	Alignment	not modelled	99.6	18	PDB header: calcium-binding protein Chain: A: PDB Molecule: agr_c_1268p; PDBTitle: crystal structure of a calcium-binding protein, regucalcin2 (agr_c_1268) from agrobacterium tumefaciens str. c58 at 1.55 a3 resolution
116	d2ghsa1	Alignment	not modelled	99.6	18	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
117	c5a31R_	Alignment	not modelled	99.6	13	PDB header: cell cycle Chain: R: PDB Molecule: the anaphase-promoting complex chain r; PDBTitle: structure of the human apc-cdh1-hsl1-ubch10 complex.
118	c6fqIA_	Alignment	not modelled	99.6	13	PDB header: rna binding protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase trim71; PDBTitle: crystal structure of danio rerio lin41 filamin-nhl domains in complex2 with mab-10 3'utr 13mer rna
119	c6iczW_	Alignment	not modelled	99.6	11	PDB header: splicing Chain: W: PDB Molecule: pre-mrna-processing factor 17; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
120	c6mzcG_	Alignment	not modelled	99.6	11	PDB header: transcription Chain: G: PDB Molecule: transcription initiation factor tfiid subunit 5; PDBTitle: human tfiid bc core