

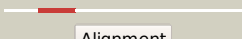

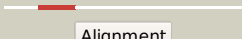
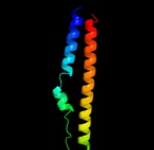
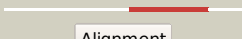





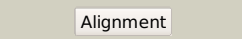













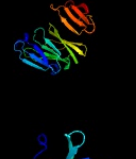



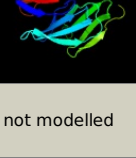


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0980c_(PE_PGRS18)_1095082_1096455
Date	Wed Jul 31 22:05:04 BST 2019
Unique Job ID	adc672a3754f3797

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfxA_	 Alignment		100.0	43	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38a1	 Alignment		100.0	28	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c1qniE_	 Alignment		99.9	19	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	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
6	c6gc1A_	 Alignment		99.9	26	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
7	d1qnia2	 Alignment		99.9	19	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
8	c3sbrF_	 Alignment		99.9	15	PDB header: oxidoreductase Chain: F: PDB Molecule: nitrous-oxide reductase; PDBTitle: pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
9	c5i5iA_	 Alignment		99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
10	c3hrpA_	 Alignment		99.9	18	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
11	c2iwbB_	 Alignment		99.9	18	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

12	c3u4yA	Alignment		99.9	19	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.
13	c3mbrX	Alignment		99.9	15	PDB header: transferase Chain: X; PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of the glutaminy cyclase from xanthomonas2 campestris
14	c3vh0C	Alignment		99.9	31	PDB header: protein binding/dna Chain: C; PDB Molecule: uncharacterized protein ynce; PDBTitle: crystal structure of e. coli ynce complexed with dna
15	c3tc9B	Alignment		99.9	17	PDB header: hydrolase Chain: B; PDB Molecule: hypothetical hydrolase; PDBTitle: crystal structure of an auxiliary nutrient binding protein (bt_3476)2 from bacteroides thetaiotaomicron vpi-5482 at 2.23 a resolution
16	c1gq1B	Alignment		99.9	16	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
17	c3bwsA	Alignment		99.9	22	PDB header: unknown function Chain: A; PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
18	c3s94A	Alignment		99.9	13	PDB header: signaling protein Chain: A; PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of lrp6-e1e2
19	c3s8vA	Alignment		99.9	14	PDB header: signaling protein Chain: A; PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of lrp6-dkk1 complex
20	d1pjax	Alignment		99.9	22	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
21	d1fwxa2	Alignment	not modelled	99.9	17	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
22	c3no1A	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A; PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutaminy cyclase (trigonal2 form)
23	c5f30B	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B; PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
24	c4hw6D	Alignment	not modelled	99.9	19	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
25	c2iwaA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A; PDB Molecule: glutamine cyclotransferase; PDBTitle: unbound glutaminy cyclotransferase from carica papaya.
26	c3kyaA	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: putative phosphatase; PDBTitle: crystal structure of putative phosphatase (np_812416.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.77 a resolution
27	c6rteB	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
28	d2p4oa1	Alignment	not modelled	99.8	16	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like

29	c1l0qC_	Alignment	not modelled	99.8	42	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
30	c1nnoA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
31	d1npea_	Alignment	not modelled	99.8	13	Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
32	d1jofa_	Alignment	not modelled	99.8	17	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-muocoante lactonizing enzyme Family: 3-carboxy-cis,cis-muocoante lactonizing enzyme
33	c2z2pA_	Alignment	not modelled	99.8	13	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
34	c6fb3A_	Alignment	not modelled	99.8	22	PDB header: cell adhesion Chain: A: PDB Molecule: teneurin-2; PDBTitle: teneurin 2 partial extracellular domain
35	c6fayA_	Alignment	not modelled	99.8	18	PDB header: cell adhesion Chain: A: PDB Molecule: od23 protein; PDBTitle: teneurin3 monomer
36	c6f0qB_	Alignment	not modelled	99.8	41	PDB header: de novo protein Chain: B: PDB Molecule: pizza6-ayw; PDBTitle: crystal structure of pizza6-ayw
37	d1qksa2	Alignment	not modelled	99.8	16	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
38	c2qc5A_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: A: PDB Molecule: streptogramin b lactonase; PDBTitle: streptogramin b lyase structure
39	d1jmx_b	Alignment	not modelled	99.8	25	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
40	c3hfbB_	Alignment	not modelled	99.8	25	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.
41	c3dsmA_	Alignment	not modelled	99.8	24	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.
42	c5c2vB_	Alignment	not modelled	99.8	39	PDB header: oxidoreductase Chain: B: PDB Molecule: hydrazine synthase beta subunit; PDBTitle: kueningenia stuttgartiensis hydrazine synthase
43	c1n7dA_	Alignment	not modelled	99.8	16	PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: extracellular domain of the ldl receptor
44	c6d69A_	Alignment	not modelled	99.8	32	PDB header: protein binding Chain: A: PDB Molecule: nhl repeat region of d. melanogaster thin; PDBTitle: crystal structure of the nhl repeat region of d. melanogaster thin
45	d1ijqa1	Alignment	not modelled	99.8	17	Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
46	c5d9bA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: luciferin regenerating enzyme; PDBTitle: luciferin-regenerating enzyme solved by siras using xfel (refined2 against native data)
47	c3soqA_	Alignment	not modelled	99.8	12	PDB header: protein binding/antagonist Chain: A: PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: the structure of the first ywtd beta propeller domain of lrp6 in2 complex with a dkk1 peptide
48	c2i0tB_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
49	c3fw0A_	Alignment	not modelled	99.8	19	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)
50	c2ghsA_	Alignment	not modelled	99.8	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
51	d2ghsa1	Alignment	not modelled	99.8	18	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
52	c2j57L_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: x-ray reduced paraccocus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
53	c3nokB_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: glutaminy cyclase; PDBTitle: crystal structure of myxococcus xanthus glutaminy cyclase

54	d2madh_	Alignment	not modelled	99.7	14	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
55	d2dgl1a1	Alignment	not modelled	99.7	19	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
56	c3fgbB_	Alignment	not modelled	99.7	21	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.
57	c3c75j_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
58	c2p9wA_	Alignment	not modelled	99.7	17	PDB header: allergen Chain: A: PDB Molecule: mal s 1 allergenic protein; PDBTitle: crystal structure of the major malassezia sympodialis allergen mala s2 1
59	d1q7fa_	Alignment	not modelled	99.7	24	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
60	c2h47F_	Alignment	not modelled	99.7	19	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)
61	d1pbyb_	Alignment	not modelled	99.7	23	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
62	c2qe8B_	Alignment	not modelled	99.7	18	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
63	c5tztT_	Alignment	not modelled	99.7	16	PDB header: translation Chain: T: PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome
64	d1rwiA_	Alignment	not modelled	99.7	30	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
65	c1jqA_	Alignment	not modelled	99.7	19	PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: crystal structure of the ldl receptor ywtd-egf domain pair
66	c4qriA_	Alignment	not modelled	99.7	14	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
67	d1l0qa2	Alignment	not modelled	99.7	43	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
68	c3dr2A_	Alignment	not modelled	99.7	13	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
69	c3g4hB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
70	c6cmkB_	Alignment	not modelled	99.7	12	PDB header: metal binding protein Chain: B: PDB Molecule: aztd protein; PDBTitle: crystal structure of citrobacter koseri aztd
71	d1v04a_	Alignment	not modelled	99.7	15	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: Serum paraoxonase/arylesterase 1, PON1
72	c6nd4T_	Alignment	not modelled	99.7	17	PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
73	c3e5zA_	Alignment	not modelled	99.7	13	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.
74	c6ck1C_	Alignment	not modelled	99.7	13	PDB header: metal binding protein Chain: C: PDB Molecule: a1b2f4 protein; PDBTitle: crystal structure of paracoccus denitrificans aztd
75	c5a1vK_	Alignment	not modelled	99.6	16	PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
76	c5a1uC_	Alignment	not modelled	99.6	16	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat triad
77	d2bbkh_	Alignment	not modelled	99.6	23	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
78	c6igbB_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic gluconolactonase, ppgl; PDBTitle: the structure of pseudomonas aeruginosa periplasmic gluconolactonase,2 ppgl
79	c6nd4O_	Alignment	not modelled	99.6	11	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the

						eukaryotic2 small ribosomal subunit
80	c5nzc_	Alignment	not modelled	99.6	15	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage iv
81	d1ri6a_	Alignment	not modelled	99.6	13	Fold: 7-bladed beta-propeller Superfamily: Putative isomerase YbhE Family: Putative isomerase YbhE
82	c5a1vl_	Alignment	not modelled	99.6	16	PDB header: transport protein Chain: L: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage i
83	c2fp8A_	Alignment	not modelled	99.6	15	PDB header: lyase Chain: A: PDB Molecule: strictosidine synthase; PDBTitle: structure of strictosidine synthase, the biosynthetic entry to the2 monoterpenoid indole alkaloid family
84	d1nira2	Alignment	not modelled	99.6	13	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
85	c4nxsA_	Alignment	not modelled	99.6	16	PDB header: protein binding Chain: A: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: crystal structure of the utp21 tandem wd domain
86	c3qqzA_	Alignment	not modelled	99.6	12	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
87	c3dm0A_	Alignment	not modelled	99.6	15	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
88	c3mkqA_	Alignment	not modelled	99.6	17	PDB header: transport protein Chain: A: PDB Molecule: coatomer beta'-subunit; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
89	c5juyB_	Alignment	not modelled	99.5	5	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
90	c3iytG_	Alignment	not modelled	99.5	11	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
91	c5a5uB_	Alignment	not modelled	99.5	11	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
92	c2oajA_	Alignment	not modelled	99.5	12	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: protein sni1; PDBTitle: crystal structure of sro7 from s. cerevisiae
93	c6nd4W_	Alignment	not modelled	99.5	12	PDB header: ribosome Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
94	d1crua_	Alignment	not modelled	99.5	19	Fold: 6-bladed beta-propeller Superfamily: Soluble quinoprotein glucose dehydrogenase Family: Soluble quinoprotein glucose dehydrogenase
95	c6nd4O_	Alignment	not modelled	99.5	16	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
96	c6fqIA_	Alignment	not modelled	99.5	23	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
97	c5dfzB_	Alignment	not modelled	99.4	11	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
98	c3a9gA_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pqq-dependent sugar dehydrogenase apo-form
99	c1nr0A_	Alignment	not modelled	99.4	14	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).
100	c5cvoD_	Alignment	not modelled	99.4	14	PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
101	c4uerb_	Alignment	not modelled	99.4	11	PDB header: translation Chain: B: PDB Molecule: us2; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
102	c3lrva_	Alignment	not modelled	99.3	11	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.
103	c2w18A_	Alignment	not modelled	99.3	16	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
104	c5i2tA_	Alignment	not modelled	99.3	11	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
						PDB header: transport protein

105	c5n4aA_	Alignment	not modelled	99.3	8	Chain: A; PDB Molecule: intraflagellar transport protein 80; PDBTitle: crystal structure of chlamydomonas ift80
106	c5cv0A_	Alignment	not modelled	99.3	14	PDB header: hydrolase/protein binding Chain: A; PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
107	d1ospo_	Alignment	not modelled	99.3	8	Fold: open-sided beta-meander Superfamily: Outer surface protein Family: Outer surface protein
108	c4noxA_	Alignment	not modelled	99.3	11	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of the nine-bladed beta-propeller of eif3b
109	c6n8sA_	Alignment	not modelled	99.3	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.
110	c3dasA_	Alignment	not modelled	99.3	29	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: structure of the pqq-bound form of aldose sugar2 dehydrogenase (adh) from streptomyces coelicolor
111	c4yczA_	Alignment	not modelled	99.3	16	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)
112	c6nd4L_	Alignment	not modelled	99.3	12	PDB header: ribosome Chain: L; PDB Molecule: utp5; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
113	c5wbiA_	Alignment	not modelled	99.3	12	PDB header: protein binding Chain: A; PDB Molecule: regulatory-associated protein of tor 1; PDBTitle: crystal structure of the arabidopsis thaliana raptor
114	c5ch2A_	Alignment	not modelled	99.3	12	PDB header: transferase Chain: A; PDB Molecule: putative polycomb protein eed; PDBTitle: crystal structure of an active polycomb repressive complex 2 in the2 basal state
115	c5mzhB_	Alignment	not modelled	99.2	29	PDB header: motor protein Chain: B; PDB Molecule: dynein assembly factor with wdr repeat domains 1; PDBTitle: crystal structure of oda16 from chlamydomonas reinhardtii
116	c4yh0A_	Alignment	not modelled	99.2	11	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
117	c3wj9A_	Alignment	not modelled	99.2	10	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 2a; PDBTitle: crystal structure of the eukaryotic initiation factor
118	c5ov3B_	Alignment	not modelled	99.2	23	PDB header: structural protein Chain: B; PDB Molecule: retinoblastoma-binding protein 5; PDBTitle: structure of the rbbp5 beta-propeller domain
119	c2ismA_	Alignment	not modelled	99.2	20	PDB header: sugar binding protein Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of the putative oxidoreductase (glucose2 dehydrogenase) (ttha0570) from thermus thermophilus hb8
120	c2ymuA_	Alignment	not modelled	99.2	18	PDB header: unknown function Chain: A; PDB Molecule: wd-40 repeat protein; PDBTitle: structure of a highly repetitive propeller structure