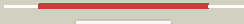



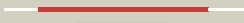



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3524 (-) _3960934_3961965
Date	Fri Aug 9 18:20:20 BST 2019
Unique Job ID	98f5b968d6c881d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fb3A_	 Alignment		100.0	21	PDB header: cell adhesion Chain: A: PDB Molecule: teneurin-2; PDBTitle: teneurin 2 partial extracellular domain
2	c3hrpA_	 Alignment		100.0	16	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
3	c6gc1A_	 Alignment		100.0	23	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
4	c6fayA_	 Alignment		100.0	20	PDB header: cell adhesion Chain: A: PDB Molecule: odz3 protein; PDBTitle: teneurin3 monomer
5	c2z2pA_	 Alignment		100.0	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
6	c6f0qB_	 Alignment		100.0	51	PDB header: de novo protein Chain: B: PDB Molecule: pizza6-ayw; PDBTitle: crystal structure of pizza6-ayw
7	c3fw0A_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: peptidyl-glycine alpha-amidating monoxygenase; PDBTitle: structure of peptidyl-alpha-hydroxyglycine alpha-amidating2 lyase (pal) bound to alpha-hydroxyhippuric acid (non-3 peptidic substrate)
8	c2qc5A_	 Alignment		100.0	12	PDB header: lyase Chain: A: PDB Molecule: streptogramin b lactonase; PDBTitle: streptogramin b lyase structure
9	c6d69A_	 Alignment		100.0	25	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
10	c4hw6D_	 Alignment		100.0	16	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
11	d1rwia_	 Alignment		100.0	43	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat

12	c3tc9B_	Alignment		100.0	11	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
13	c3kyaA_	Alignment		100.0	14	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
14	c6fqIA_	Alignment		100.0	21	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
15	c3bwsA_	Alignment		100.0	11	PDB header: unknown function Chain: A: PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
16	d2p4oa1	Alignment		100.0	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like
17	c3dr2A_	Alignment		100.0	16	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
18	d1pjxa_	Alignment		100.0	12	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
19	c3s8vA_	Alignment		99.9	15	PDB header: signaling protein Chain: A: PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of lrp6-dkk1 complex
20	d1q7fa_	Alignment		99.9	19	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
21	d2dg1a1	Alignment	not modelled	99.9	14	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
22	c3s94A_	Alignment	not modelled	99.9	15	PDB header: signaling protein Chain: A: PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of lrp6-e1e2
23	c2qe8B_	Alignment	not modelled	99.9	17	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
24	c3e5zA_	Alignment	not modelled	99.9	12	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.
25	c3soqA_	Alignment	not modelled	99.9	17	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
26	c5d9bA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: luciferin regenerating enzyme; PDBTitle: luciferin-regenerating enzyme solved by siras using xfel (refined2 against native data)
27	d2ghsa1	Alignment	not modelled	99.9	14	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
28	c2ghsa_	Alignment	not modelled	99.9	14	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
29	d1npea_	Alignment	not modelled	99.9	17 Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
30	c5a5uB_	Alignment	not modelled	99.9	10 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
31	c3u4yA_	Alignment	not modelled	99.9	15 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.
32	c1n7dA_	Alignment	not modelled	99.9	17 PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: extracellular domain of the ldl receptor
33	d1ijqa1	Alignment	not modelled	99.9	18 Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
34	c3g4hB_	Alignment	not modelled	99.9	14 PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
35	c3a9gA_	Alignment	not modelled	99.9	17 PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pqq-dependent sugar dehydrogenase apo-form
36	c5a1vK_	Alignment	not modelled	99.9	6 PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
37	c1ijqA_	Alignment	not modelled	99.9	17 PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: crystal structure of the ldl receptor ywtd-egf domain pair
38	c3dm0A_	Alignment	not modelled	99.9	11 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
39	c2p9wA_	Alignment	not modelled	99.9	13 PDB header: allergen Chain: A: PDB Molecule: mal s 1 allergenic protein; PDBTitle: crystal structure of the major malassezia sympodialis allergen mala s2 1
40	d1crua_	Alignment	not modelled	99.9	20 Fold: 6-bladed beta-propeller Superfamily: Soluble quinoprotein glucose dehydrogenase Family: Soluble quinoprotein glucose dehydrogenase
41	c3qqzA_	Alignment	not modelled	99.9	10 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
42	c5juyB_	Alignment	not modelled	99.9	8 PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
43	c5f30B_	Alignment	not modelled	99.9	9 PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
44	c2ismA_	Alignment	not modelled	99.9	19 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
45	c6nd4T_	Alignment	not modelled	99.9	10 PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
46	c2fp8A_	Alignment	not modelled	99.9	15 PDB header: lyase Chain: A: PDB Molecule: strictosidine synthase; PDBTitle: structure of strictosidine synthase, the biosynthetic entry to the2 monoterpenoid indole alkaloid family
47	c6nd4O_	Alignment	not modelled	99.9	16 PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
48	c4uerb_	Alignment	not modelled	99.8	11 PDB header: translation Chain: B: PDB Molecule: us2; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
49	c3wj9A_	Alignment	not modelled	99.8	8 PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2a; PDBTitle: crystal structure of the eukaryotic initiation factor
50	c5tztT_	Alignment	not modelled	99.8	10 PDB header: translation Chain: T: PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome
51	c5n1aB_	Alignment	not modelled	99.8	11 PDB header: translation Chain: B: PDB Molecule: utp4; PDBTitle: crystal structure of utp4 from chaetomium thermophilum
52	c3hfgB_	Alignment	not modelled	99.8	17 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.
53	c3dasA_	Alignment	not modelled	99.8	15 PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the pqq-bound form of aldose sugar2 dehydrogenase (adh) from streptomyces coelicolor
54	c5cvoD_	Alignment	not modelled	99.8	8 PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex

55	c5cvoA_	Alignment	not modelled	99.8	10	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
56	c1qniE_	Alignment	not modelled	99.8	12	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
57	d1fwxa2	Alignment	not modelled	99.8	14	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
58	c5nzcC_	Alignment	not modelled	99.8	7	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage iv
59	c5k1bB_	Alignment	not modelled	99.8	11	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
60	c5a1vL_	Alignment	not modelled	99.8	7	PDB header: transport protein Chain: L: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage i
61	c3dsmA_	Alignment	not modelled	99.8	11	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.
62	c6rteB_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
63	c4u1fA_	Alignment	not modelled	99.8	9	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of middle domain of eukaryotic translation2 initiation factor eif3b
64	c3vh0C_	Alignment	not modelled	99.8	12	PDB header: protein binding/dna Chain: C: PDB Molecule: uncharacterized protein ynce; PDBTitle: crystal structure of e. coli ynce complexed with dna
65	c5cvlA_	Alignment	not modelled	99.8	11	PDB header: protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48 (uaf-1), residues 2-580
66	c4wjsA_	Alignment	not modelled	99.8	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: rsa4; PDBTitle: crystal structure of rsa4 from chaetomium thermophilum
67	c6nd4W_	Alignment	not modelled	99.8	7	PDB header: ribosome Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
68	c5dfzB_	Alignment	not modelled	99.8	8	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
69	c4noxA_	Alignment	not modelled	99.8	10	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of the nine-bladed beta-propeller of eif3b
70	c1gq1B_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
71	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)
72	c4qriA_	Alignment	not modelled	99.8	11	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
73	d1qnia2	Alignment	not modelled	99.8	10	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
74	c1l0qC_	Alignment	not modelled	99.8	17	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
75	c2g8sB_	Alignment	not modelled	99.8	14	PDB header: sugar binding protein Chain: B: PDB Molecule: glucose/sorbose dehydrogenases; PDBTitle: crystal structure of the soluble aldose sugar dehydrogenase2 (asd) from escherichia coli in the apo-form
76	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
77	c2ymuA_	Alignment	not modelled	99.8	26	PDB header: unknown function Chain: A: PDB Molecule: wd-40 repeat protein; PDBTitle: structure of a highly repetitive propeller structure
78	c1fwxB_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
79	c6nd4Q_	Alignment	not modelled	99.8	8	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
80	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.
81	c5c2vB_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: hydrazine synthase beta subunit; PDBTitle: kueningenia stuttgartiensis hydrazine synthase
82	c1nr0A_	Alignment	not modelled	99.8	9	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).
83	c1nnoA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
84	c3sbrF_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: F: PDB Molecule: nitrous-oxide reductase; PDBTitle: pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
85	c2j57J_	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: x-ray reduced paracoccus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
86	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
87	c5a1uC_	Alignment	not modelled	99.7	6	PDB header: transport protein Chain: C: PDB Molecule: coatomeer subunit alpha; PDBTitle: the structure of the cop1 coat triad
88	d1gxra_	Alignment	not modelled	99.7	9	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
89	c5i2tA_	Alignment	not modelled	99.7	17	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
90	c5n4aA_	Alignment	not modelled	99.7	10	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 80; PDBTitle: crystal structure of chlamydomonas ift80
91	d1l0qa2	Alignment	not modelled	99.7	16	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
92	c5wbiA_	Alignment	not modelled	99.7	8	PDB header: protein binding Chain: A: PDB Molecule: regulatory-associated protein of tor 1; PDBTitle: crystal structure of the arabidopsis thaliana raptor
93	c4e54B_	Alignment	not modelled	99.7	10	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
94	c3mkqA_	Alignment	not modelled	99.7	7	PDB header: transport protein Chain: A: PDB Molecule: coatomeer beta'-subunit; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
95	d1v04a_	Alignment	not modelled	99.7	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: Serum paraoxonase/arylesterase 1, PON1
96	c4nsxA_	Alignment	not modelled	99.7	9	PDB header: protein binding Chain: A: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: crystal structure of the utp21 tandem wd domain
97	c3j65q_	Alignment	not modelled	99.7	18	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
98	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)
99	c3iytG_	Alignment	not modelled	99.7	8	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
100	d2madh_	Alignment	not modelled	99.7	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
101	c6eojD_	Alignment	not modelled	99.7	10	PDB header: rna binding protein Chain: D: PDB Molecule: polyadenylation factor subunit 2,polyadenylation factor PDBTitle: poly polymerase module of the cleavage and polyadenylation factor2 (cpf) from saccharomyces cerevisiae
102	c6em5m_	Alignment	not modelled	99.7	6	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
103	c6nd4L_	Alignment	not modelled	99.7	7	PDB header: ribosome Chain: L: PDB Molecule: utp5; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
104	c4bzkA_	Alignment	not modelled	99.7	15	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec31; PDBTitle: the structure of the cop1 coat assembled on membranes
105	c2i0tB_	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: B: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
106	c1pi6A_	Alignment	not modelled	99.7	15	PDB header: protein binding Chain: A: PDB Molecule: actin interacting protein 1; PDBTitle: yeast actin interacting protein 1 (aip1), orthorhombic

						crystal form
107	c6e29C_	Alignment	not modelled	99.7	6	PDB header: protein binding Chain: C: PDB Molecule: swd1-like protein; PDBTitle: crystal structure of myceliophtheria_thermophila cps50 (swd1) beta-2 propeller domain
108	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
109	c6mzcG_	Alignment	not modelled	99.7	9	PDB header: transcription Chain: G: PDB Molecule: transcription initiation factor tfiid subunit 5; PDBTitle: human tfiid bc core
110	c6f3tD_	Alignment	not modelled	99.7	10	PDB header: transcription Chain: D: PDB Molecule: transcription initiation factor tfiid subunit 5; PDBTitle: crystal structure of the human taf5-taf6-taf9 complex
111	d1jofa_	Alignment	not modelled	99.7	14	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-mucoante lactonizing enzyme Family: 3-carboxy-cis,cis-mucoante lactonizing enzyme
112	c6iczW_	Alignment	not modelled	99.7	9	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
113	c2j04B_	Alignment	not modelled	99.7	10	PDB header: transcription Chain: B: PDB Molecule: ydr362cp; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor iiic
114	d1ri6a_	Alignment	not modelled	99.6	12	Fold: 7-bladed beta-propeller Superfamily: Putative isomerase YbhE Family: Putative isomerase YbhE
115	c5mzhB_	Alignment	not modelled	99.6	9	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	c6nd4N_	Alignment	not modelled	99.6	10	PDB header: ribosome Chain: N: PDB Molecule: utp4; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
117	c6chgD_	Alignment	not modelled	99.6	7	PDB header: transferase Chain: D: PDB Molecule: klla0a08800p; PDBTitle: crystal structure of the yeast compass catalytic module
118	c2iwaA_	Alignment	not modelled	99.6	11	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: unbound glutaminyl cyclotransferase from carica papaya.
119	c6qk7A_	Alignment	not modelled	99.6	12	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 1; PDBTitle: elongator catalytic subcomplex elp123 lobe
120	c4o9dA_	Alignment	not modelled	99.6	11	PDB header: gene regulation Chain: A: PDB Molecule: rik1-associated factor 1; PDBTitle: structure of dos1 propeller