

Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qniE_	 Alignment		99.8	21	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
2	c1fwxB_	 Alignment		99.8	11	PDB header: oxidoreductase Chain: B; PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
3	c3s8vA_	 Alignment		99.8	14	PDB header: signaling protein Chain: A; PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of Irp6-dkk1 complex
4	d1qnia2	 Alignment		99.7	17	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
5	c3bwsA_	 Alignment		99.7	26	PDB header: unknown function Chain: A; PDB Molecule: protein Ip49; PDBTitle: crystal structure of the leptospiral antigen Ip49
6	c3s94A_	 Alignment		99.7	13	PDB header: signaling protein Chain: A; PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of Irp6-e1e2
7	c5i5iA_	 Alignment		99.7	24	PDB header: oxidoreductase Chain: A; PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
8	c6gc1A_	 Alignment		99.7	22	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
9	c5f30B_	 Alignment		99.7	23	PDB header: oxidoreductase Chain: B; PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
10	c3sbrF_	 Alignment		99.7	10	PDB header: oxidoreductase Chain: F; PDB Molecule: nitrous-oxide reductase; PDBTitle: pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
11	c3u4yA_	 Alignment		99.7	14	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.

12	c6f0qB_	Alignment		99.7	53	PDB header: de novo protein Chain: B: PDB Molecule: pizza6-ayw; PDBTitle: crystal structure of pizza6-ayw
13	d1fwx2	Alignment		99.6	12	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
14	c2iwkB_	Alignment		99.6	20	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
15	c3hrpA_	Alignment		99.6	15	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
16	c4hw6D_	Alignment		99.6	17	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
17	c1n7dA_	Alignment		99.6	22	PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: extracellular domain of the ldl receptor
18	c1l0qC_	Alignment		99.6	44	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
19	c2iwaA_	Alignment		99.6	12	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: unbound glutaminyl cyclotransferase from carica papaya.
20	c1gq1B_	Alignment		99.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
21	d1jofa_	Alignment	not modelled	99.6	20	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-mucoante lactonizing enzyme Family: 3-carboxy-cis,cis-mucoante lactonizing enzyme
22	c3kyaA_	Alignment	not modelled	99.6	18	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
23	c3vh0C_	Alignment	not modelled	99.5	16	PDB header: protein binding/dna Chain: C: PDB Molecule: uncharacterized protein ynce; PDBTitle: crystal structure of e. coli ynce complexed with dna
24	c3nolA_	Alignment	not modelled	99.5	11	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
25	c2z2pA_	Alignment	not modelled	99.5	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
26	c3mbrX_	Alignment	not modelled	99.5	11	PDB header: transferase Chain: X: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of the glutaminyl cyclase from xanthomonas2 campestris
27	d2p4oa1	Alignment	not modelled	99.5	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like
28	c6fayA_	Alignment	not modelled	99.5	17	PDB header: cell adhesion Chain: A: PDB Molecule: od23 protein; PDBTitle: teneurin3 monomer
						Fold: Ferritin-like

29	d2g38a1	Alignment	not modelled	99.5	26	Superfamily: PE/PPE dimer-like Family: PE
30	c2g38A	Alignment	not modelled	99.5	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
31	c6fb3A	Alignment	not modelled	99.5	14	PDB header: cell adhesion Chain: A: PDB Molecule: teneurin-2; PDBTitle: teneurin 2 partial extracellular domain
32	c6rteB	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
33	c5xfsA	Alignment	not modelled	99.5	43	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
34	c1nnoA	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
35	d1jmb	Alignment	not modelled	99.5	23	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
36	c3fw0A	Alignment	not modelled	99.5	27	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)
37	d1qksa2	Alignment	not modelled	99.4	15	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	d1pjax	Alignment	not modelled	99.4	19	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
39	d1l0qa2	Alignment	not modelled	99.4	44	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
40	c5c2vB	Alignment	not modelled	99.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: hydrazine synthase beta subunit; PDBTitle: kueningenia stuttgartiensis hydrazine synthase
41	c3hfb	Alignment	not modelled	99.4	22	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.
42	c5d9bA	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: luciferin regenerating enzyme; PDBTitle: luciferin-regenerating enzyme solved by siras using xfel (refined2 against native data)
43	c2qc5A	Alignment	not modelled	99.4	11	PDB header: lyase Chain: A: PDB Molecule: streptogramin b lactonase; PDBTitle: streptogramin b lyase structure
44	c3sogA	Alignment	not modelled	99.4	13	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
45	c5tzt	Alignment	not modelled	99.4	16	PDB header: translation Chain: T: PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome
46	c2j57l	Alignment	not modelled	99.4	14	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.
47	d1pbyb	Alignment	not modelled	99.4	19	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
48	c2p9wA	Alignment	not modelled	99.3	21	PDB header: allergen Chain: A: PDB Molecule: mal s 1 allergenic protein; PDBTitle: crystal structure of the major malassezia sympodialis allergen mala s2 1
49	c3g4hB	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
50	c4qriA	Alignment	not modelled	99.3	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
51	c5i2tA	Alignment	not modelled	99.3	9	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
52	d1ri6a	Alignment	not modelled	99.3	17	Fold: 7-bladed beta-propeller Superfamily: Putative isomerase YbhE Family: Putative isomerase YbhE
53	c3fgbB	Alignment	not modelled	99.3	13	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. PDB header: hydrolase

54	c3tc9B_	Alignment	not modelled	99.3	14	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
55	d2ghsa1	Alignment	not modelled	99.3	16	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
56	c2ghsA_	Alignment	not modelled	99.3	16	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
57	c3dsmA_	Alignment	not modelled	99.3	16	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.
58	c2i0tB_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
59	c2h47F_	Alignment	not modelled	99.3	17	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)
60	d1ijqa1	Alignment	not modelled	99.3	18	Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
61	c3c75J_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
62	c4nsxA_	Alignment	not modelled	99.3	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
63	d1npea_	Alignment	not modelled	99.3	18	Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
64	c3dr2A_	Alignment	not modelled	99.3	9	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
65	c2qe8B_	Alignment	not modelled	99.3	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
66	d2dgl1a1	Alignment	not modelled	99.3	21	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
67	d1v04a_	Alignment	not modelled	99.3	20	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: Serum paraoxonase/arylesterase 1, PON1
68	d1rwia_	Alignment	not modelled	99.3	31	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
69	d1nira2	Alignment	not modelled	99.3	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
70	c6ck1C_	Alignment	not modelled	99.3	16	PDB header: metal binding protein Chain: C: PDB Molecule: a1b2f4 protein; PDBTitle: crystal structure of paracoccus denitrificans aztD
71	c6cmkB_	Alignment	not modelled	99.3	14	PDB header: metal binding protein Chain: B: PDB Molecule: aztD protein; PDBTitle: crystal structure of citrobacter koseri aztD
72	c5a1vL_	Alignment	not modelled	99.2	16	PDB header: transport protein Chain: L: PDB Molecule: coatomer subunit beta; PDBTitle: the structure of the copi coat linkage i
73	c6nd4T_	Alignment	not modelled	99.2	16	PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
74	c6d69A_	Alignment	not modelled	99.2	19	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
75	d2madh_	Alignment	not modelled	99.2	11	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
76	c2fp8A_	Alignment	not modelled	99.2	19	PDB header: lyase Chain: A: PDB Molecule: strictosidine synthase; PDBTitle: structure of strictosidine synthase, the biosynthetic entry to the2 monoterpene indole alkaloid family
77	c6nd4O_	Alignment	not modelled	99.2	8	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
78	c5nzvC_	Alignment	not modelled	99.2	17	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage iv
						Fold: 7-bladed beta-propeller

79	d2bbkh_	Alignment	not modelled	99.2	24	Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
80	c3iytG_	Alignment	not modelled	99.2	8	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
81	c5a1uC_	Alignment	not modelled	99.2	12	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat triad
82	c5a1vK_	Alignment	not modelled	99.2	10	PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
83	c3mkqA_	Alignment	not modelled	99.2	16	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
84	c3nokB_	Alignment	not modelled	99.1	9	PDB header: transferase Chain: B: PDB Molecule: glutaminy cyclase; PDBTitle: crystal structure of myxococcus xanthus glutaminy cyclase
85	c3qqzA_	Alignment	not modelled	99.1	9	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 from <i>Escherichia coli</i> cft073
86	c2ymuA_	Alignment	not modelled	99.1	19	PDB header: unknown function Chain: A: PDB Molecule: wd-40 repeat protein; PDBTitle: structure of a highly repetitive propeller structure
87	d1q7fa_	Alignment	not modelled	99.1	15	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
88	c3e5zA_	Alignment	not modelled	99.1	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.
89	c6igbB_	Alignment	not modelled	99.1	16	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic gluconolactonase, ppgl; PDBTitle: the structure of pseudomonas aeruginosa periplasmic gluconolactonase,2 ppgl
90	c5juyB_	Alignment	not modelled	99.1	8	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
91	c3dm0A_	Alignment	not modelled	99.1	9	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 <i>A. thaliana</i>
92	c1ijqA_	Alignment	not modelled	99.1	22	PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: crystal structure of the ldl receptor ywtd-egf domain pair
93	c6nd4Q_	Alignment	not modelled	99.1	10	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
94	c6fqIA_	Alignment	not modelled	99.1	25	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
95	c4wjsA_	Alignment	not modelled	99.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: rsa4; PDBTitle: crystal structure of rsa4 from chaetomium thermophilum
96	d1crua_	Alignment	not modelled	99.0	19	Fold: 6-bladed beta-propeller Superfamily: Soluble quinoprotein glucose dehydrogenase Family: Soluble quinoprotein glucose dehydrogenase
97	c4wjuB_	Alignment	not modelled	99.0	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: ribosome assembly protein 4; PDBTitle: crystal structure of rsa4 from saccharomyces cerevisiae
98	c1nr0A_	Alignment	not modelled	99.0	13	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).
99	c5thaA_	Alignment	not modelled	99.0	15	PDB header: rna binding protein Chain: A: PDB Molecule: gem-associated protein 5; PDBTitle: gemin5 wd40 repeats in complex with a guanosyl moiety
100	c5cvoD_	Alignment	not modelled	99.0	9	PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
101	c2oaiA_	Alignment	not modelled	99.0	13	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: protein sni1; PDBTitle: crystal structure of sno7 from <i>S. cerevisiae</i>
102	d1ospo_	Alignment	not modelled	99.0	6	Fold: open-sided beta-meander Superfamily: Outer surface protein Family: Outer surface protein
103	c5ch2A_	Alignment	not modelled	99.0	13	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
104	d1t2a_	Alignment	not modelled	98.9	14	Fold: 5-bladed beta-propeller Superfamily: Tachylectin-2 Family: Tachylectin-2
105	c5cvoA_	Alignment	not modelled	98.9	10	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex

106	c3a9gA_	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pqq-dependent sugar dehydrogenase apo-form
107	c5a5uB_	Alignment	not modelled	98.9	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
108	c2w18A_	Alignment	not modelled	98.8	14	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
109	c5k1bB_	Alignment	not modelled	98.8	10	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
110	c6nd4S_	Alignment	not modelled	98.8	13	PDB header: ribosome Chain: S: PDB Molecule: utp18; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
111	c1n6dE_	Alignment	not modelled	98.8	9	PDB header: hydrolase Chain: E: PDB Molecule: tricorn protease; PDBTitle: tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
112	c1k32E_	Alignment	not modelled	98.8	9	PDB header: hydrolase Chain: E: PDB Molecule: tricorn protease; PDBTitle: crystal structure of the tricorn protease
113	c4yczA_	Alignment	not modelled	98.8	12	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)
114	c4yhCA_	Alignment	not modelled	98.8	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
115	c2aq5A_	Alignment	not modelled	98.8	16	PDB header: structural protein Chain: A: PDB Molecule: coronin-1a; PDBTitle: crystal structure of murine coronin-1
116	c1pi6A_	Alignment	not modelled	98.8	10	PDB header: protein binding Chain: A: PDB Molecule: actin interacting protein 1; PDBTitle: yeast actin interacting protein 1 (aip1), orthorhombic crystal form
117	c6nd4H_	Alignment	not modelled	98.8	11	PDB header: ribosome Chain: H: PDB Molecule: utp17; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
118	c3j65q_	Alignment	not modelled	98.7	15	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.
119	c5cvlA_	Alignment	not modelled	98.7	10	PDB header: protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48 (uaf-1), residues 2-580
120	c4xfvA_	Alignment	not modelled	98.7	12	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 2; PDBTitle: crystal structure of elp2