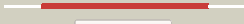



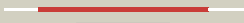



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3006_(lppZ)_3364719_3365840
Date	Thu Aug 8 16:20:17 BST 2019
Unique Job ID	aa3ae08c5e76533c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ho5B_	 Alignment		100.0	17	PDB header: signaling protein Chain: B: PDB Molecule: hedgehog-interacting protein; PDBTitle: crystal structure of hedgehog-interacting protein (hhp) and sonic2 hedgehog (shh) complex
2	c2wg3C_	 Alignment		100.0	18	PDB header: signaling protein Chain: C: PDB Molecule: hedgehog-interacting protein; PDBTitle: crystal structure of the complex between human hedgehog-2 interacting protein hip and desert hedgehog without calcium
3	d1crua_	 Alignment		100.0	24	Fold: 6-bladed beta-propeller Superfamily: Soluble quinoprotein glucose dehydrogenase Family: Soluble quinoprotein glucose dehydrogenase
4	c3a9gA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pqq-dependent sugar dehydrogenase apo-form
5	c2ismA_	 Alignment		100.0	24	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
6	c3dasA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the pqq-bound form of aldose sugar2 dehydrogenase (adh) from streptomyces coelicolor
7	c2q8sB_	 Alignment		100.0	22	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
8	c2qe8B_	 Alignment		99.8	13	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
9	d1pjxa_	 Alignment		99.8	12	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
10	d2p4oa1	 Alignment		99.7	15	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: All0351-like
11	d2dg1a1	 Alignment		99.7	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like

12	c3dr2A_	Alignment		99.7	11	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
13	c6fb3A_	Alignment		99.7	17	PDB header: cell adhesion Chain: A: PDB Molecule: teneurin-2; PDBTitle: teneurin 2 partial extracellular domain
14	c3g4hB_	Alignment		99.7	11	PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
15	c3e5zA_	Alignment		99.7	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.
16	c5d9bA_	Alignment		99.7	10	PDB header: hydrolase Chain: A: PDB Molecule: luciferin regenerating enzyme; PDBTitle: luciferin-regenerating enzyme solved by siras using xfel (refined2 against native data)
17	c2ghsA_	Alignment		99.6	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
18	d2ghsa1	Alignment		99.6	14	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
19	c6gc1A_	Alignment		99.6	15	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
20	c2z2pA_	Alignment		99.5	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
21	c2qc5A_	Alignment	not modelled	99.5	18	PDB header: lyase Chain: A: PDB Molecule: streptogramin b lactonase; PDBTitle: streptogramin b lyase structure
22	c6fayA_	Alignment	not modelled	99.5	18	PDB header: cell adhesion Chain: A: PDB Molecule: odz3 protein; PDBTitle: teneurin3 monomer
23	d1v04a_	Alignment	not modelled	99.5	10	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: Serum paraoxonase/arylesterase 1, PON1
24	c3s94A_	Alignment	not modelled	99.5	14	PDB header: signaling protein Chain: A: PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of lrp6-e1e2
25	c1n7dA_	Alignment	not modelled	99.4	11	PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: extracellular domain of the ldl receptor
26	c3soqA_	Alignment	not modelled	99.4	14	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
27	c3fw0A_	Alignment	not modelled	99.4	13	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)
28	c6f0qB_	Alignment	not modelled	99.3	16	PDB header: de novo protein Chain: B: PDB Molecule: pizza6-ayw; PDBTitle: crystal structure of pizza6-ayw

29	c3hrpA	Alignment	not modelled	99.3	17	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
30	c3s8vA	Alignment	not modelled	99.3	13	PDB header: signaling protein Chain: A: PDB Molecule: low-density lipoprotein receptor-related protein 6; PDBTitle: crystal structure of lrp6-dkk1 complex
31	c3qqzA	Alignment	not modelled	99.3	13	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
32	d1npea	Alignment	not modelled	99.3	12	Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
33	d1ijqa1	Alignment	not modelled	99.2	10	Fold: 6-bladed beta-propeller Superfamily: YWTD domain Family: YWTD domain
34	c1ijqA	Alignment	not modelled	99.2	11	PDB header: lipid transport Chain: A: PDB Molecule: low-density lipoprotein receptor; PDBTitle: crystal structure of the ldl receptor ywtd-egf domain pair
35	c3u4yA	Alignment	not modelled	99.2	12	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.
36	c3kyaA	Alignment	not modelled	99.2	9	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
37	c3tc9B	Alignment	not modelled	99.1	12	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
38	c3vh0C	Alignment	not modelled	99.1	9	PDB header: protein binding/dna Chain: C: PDB Molecule: uncharacterized protein ynce; PDBTitle: crystal structure of e. coli ynce complexed with dna
39	d1rwia	Alignment	not modelled	99.1	21	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
40	c6d69A	Alignment	not modelled	99.1	10	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
41	c2p9wA	Alignment	not modelled	99.1	12	PDB header: allergen Chain: A: PDB Molecule: mal s 1 allergenic protein; PDBTitle: crystal structure of the major malassezia sympodialis allergen mala s2 1
42	c2fp8A	Alignment	not modelled	99.0	15	PDB header: lyase Chain: A: PDB Molecule: strictosidine synthase; PDBTitle: structure of strictosidine synthase, the biosynthetic entry to the2 monoterpenoid indole alkaloid family
43	c4hw6D	Alignment	not modelled	99.0	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
44	c3hfgB	Alignment	not modelled	98.9	11	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.
45	c3mbrX	Alignment	not modelled	98.5	9	PDB header: transferase Chain: X: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of the glutaminyl cyclase from xanthomonas2 campestris
46	c4qriA	Alignment	not modelled	98.5	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
47	c6rteB	Alignment	not modelled	98.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
48	d1q7fa	Alignment	not modelled	98.5	11	Fold: 6-bladed beta-propeller Superfamily: NHL repeat Family: NHL repeat
49	c3nola	Alignment	not modelled	98.3	14	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
50	c3fgbB	Alignment	not modelled	98.3	9	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.
51	c3bwsA	Alignment	not modelled	98.2	11	PDB header: unknown function Chain: A: PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
52	c6iqbB	Alignment	not modelled	98.2	12	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic gluconolactonase, ppgl; PDBTitle: the structure of pseudomonas aeruginosa periplasmic gluconolactonase,2 ppgl
53	c3sbrF	Alignment	not modelled	98.2	12	PDB header: oxidoreductase Chain: F: PDB Molecule: nitrous-oxide reductase; PDBTitle: pseudomonas stutzeri nitrous oxide reductase, p1 crystal

						form with2 substrate
54	c2iwaA	Alignment	not modelled	98.1	19	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: unbound glutaminyl cyclotransferase from carica papaya.
55	d1jofa	Alignment	not modelled	98.1	12	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-mucoante lactonizing enzyme Family: 3-carboxy-cis,cis-mucoante lactonizing enzyme
56	c5f30B	Alignment	not modelled	98.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
57	d1t2a	Alignment	not modelled	98.0	17	Fold: 5-bladed beta-propeller Superfamily: Tachylectin-2 Family: Tachylectin-2
58	d1fwxa2	Alignment	not modelled	98.0	14	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
59	c2i0tB	Alignment	not modelled	98.0	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
60	c6cmkB	Alignment	not modelled	97.8	10	PDB header: metal binding protein Chain: B: PDB Molecule: aztd protein; PDBTitle: crystal structure of citrobacter koseri aztd
61	d1ri6a	Alignment	not modelled	97.8	11	Fold: 7-bladed beta-propeller Superfamily: Putative isomerase YbhE Family: Putative isomerase YbhE
62	c1fwxB	Alignment	not modelled	97.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrous oxide reductase; PDBTitle: crystal structure of nitrous oxide reductase from p. denitrificans
63	c1nnoA	Alignment	not modelled	97.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
64	c1qniE	Alignment	not modelled	97.6	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
65	c1gq1B	Alignment	not modelled	97.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
66	d1qnia2	Alignment	not modelled	97.6	16	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
67	c5i5iA	Alignment	not modelled	97.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
68	d1jmxB	Alignment	not modelled	97.5	9	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
69	d2bbkh	Alignment	not modelled	97.4	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
70	c2j57J	Alignment	not modelled	97.3	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.
71	d1qksa2	Alignment	not modelled	97.3	11	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
72	c6ck1C	Alignment	not modelled	97.3	11	PDB header: metal binding protein Chain: C: PDB Molecule: a1b2f4 protein; PDBTitle: crystal structure of paracoccus denitrificans aztd
73	c2h47F	Alignment	not modelled	97.2	8	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)
74	c3c75J	Alignment	not modelled	97.1	14	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
75	c6fqIA	Alignment	not modelled	97.0	9	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
76	c3nokB	Alignment	not modelled	97.0	15	PDB header: transferase Chain: B: PDB Molecule: glutaminyl cyclase; PDBTitle: crystal structure of myxococcus xanthus glutaminyl cyclase
77	d1nira2	Alignment	not modelled	97.0	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
78	d2madh	Alignment	not modelled	97.0	10	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
						PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bacuni_02894;

79	c3dsmA_	Alignment	not modelled	97.0	11	PDBTitle: crystal structure of the surface layer protein bacuni_02894 from2 bacteroides uniformis, northeast structural genomics consortium3 target btr193d.
80	c1l0qC_	Alignment	not modelled	96.8	15	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
81	d2bgra1	Alignment	not modelled	96.5	12	Fold: 8-bladed beta-propeller Superfamily: DPP6 N-terminal domain-like Family: DPP6 N-terminal domain-like
82	c6qk7A_	Alignment	not modelled	96.4	12	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 1; PDBTitle: elongator catalytic subcomplex elp123 lobe
83	c4e54B_	Alignment	not modelled	96.3	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
84	c2iwkB_	Alignment	not modelled	96.3	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
85	c3no2A_	Alignment	not modelled	96.1	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein of unknown function (baccac_01654) from2 bacteroides caccae at 1.35 a resolution
86	c3zwb_	Alignment	not modelled	96.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase phox; PDBTitle: pseudomonas fluorescens phox in complex with vanadate, a2 transition state analogue
87	c2ivzD_	Alignment	not modelled	96.0	11	PDB header: protein transport/hydrolase Chain: D: PDB Molecule: protein tolB; PDBTitle: structure of tolB in complex with a peptide of the colicin2 e9 t-domain
88	c5c2mA_	Alignment	not modelled	96.0	18	PDB header: structural protein Chain: A: PDB Molecule: predicted protein; PDBTitle: the de novo evolutionary emergence of a symmetrical protein is shaped2 by folding constraints
89	c5hrmB_	Alignment	not modelled	95.7	12	PDB header: hydrolase Chain: B: PDB Molecule: haloalkylphosphorus hydrolase; PDBTitle: crystal structure of phosphotriesterase from sphingobium sp. tcm1
90	c6nd4H_	Alignment	not modelled	94.9	9	PDB header: ribosome Chain: H: PDB Molecule: utp17; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
91	c2ecfA_	Alignment	not modelled	94.9	13	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
92	c2w8bB_	Alignment	not modelled	94.7	10	PDB header: protein transport/membrane protein Chain: B: PDB Molecule: protein tolB; PDBTitle: crystal structure of processed tolB in complex with pal
93	c5c2vB_	Alignment	not modelled	94.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: hydrazine synthase beta subunit; PDBTitle: kueningenia stuttgartiensis hydrazine synthase
94	c5ch2A_	Alignment	not modelled	94.0	17	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
95	c3ottB_	Alignment	not modelled	93.8	11	PDB header: transcription Chain: B: PDB Molecule: two-component system sensor histidine kinase; PDBTitle: crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron
96	d1orva1	Alignment	not modelled	93.7	12	Fold: 8-bladed beta-propeller Superfamily: DPP6 N-terminal domain-like Family: DPP6 N-terminal domain-like
97	c6nd4S_	Alignment	not modelled	93.6	10	PDB header: ribosome Chain: S: PDB Molecule: utp18; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
98	c5a5uB_	Alignment	not modelled	93.4	15	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
99	d1xfda1	Alignment	not modelled	93.3	9	Fold: 8-bladed beta-propeller Superfamily: DPP6 N-terminal domain-like Family: DPP6 N-terminal domain-like
100	c5a1vK_	Alignment	not modelled	92.7	12	PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the cop1 coat linkage i
101	c6nd4O_	Alignment	not modelled	92.1	10	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
102	c5yznA_	Alignment	not modelled	92.1	11	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
103	c4yczA_	Alignment	not modelled	91.9	9	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)
104	c3q6kA_	Alignment	not modelled	91.2	17	PDB header: protein binding Chain: A: PDB Molecule: 43.2 kda salivary protein; PDBTitle: salivary protein from lutzomyia longipalpis

105	d1l0qa2	Alignment	not modelled	90.9	14	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
106	c5yyIA	Alignment	not modelled	90.2	15	PDB header: signaling protein Chain: A: PDB Molecule: major royal jelly protein 1; PDBTitle: structure of major royal jelly protein 1 oligomer
107	d1h6la	Alignment	not modelled	90.2	14	Fold: 6-bladed beta-propeller Superfamily: Thermostable phytase (3-phytase) Family: Thermostable phytase (3-phytase)
108	c5i2tA	Alignment	not modelled	89.5	15	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
109	c5oljA	Alignment	not modelled	89.4	10	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
110	d1pbyb	Alignment	not modelled	89.2	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
111	c2j04B	Alignment	not modelled	87.3	11	PDB header: transcription Chain: B: PDB Molecule: ydr362cp; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor iiic
112	c4wjIB	Alignment	not modelled	86.2	12	PDB header: membrane protein Chain: B: PDB Molecule: inactive dipeptidyl peptidase 10; PDBTitle: structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels
113	c6nd4W	Alignment	not modelled	85.7	11	PDB header: ribosome Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
114	c6em5m	Alignment	not modelled	85.3	9	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
115	c4xfvA	Alignment	not modelled	84.9	8	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 2; PDBTitle: crystal structure of elp2
116	c3dm0A	Alignment	not modelled	84.5	14	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
117	c4a2ID	Alignment	not modelled	83.5	11	PDB header: transcription Chain: D: PDB Molecule: two-component system sensor histidine kinase/response; PDBTitle: structure of the periplasmic domain of the heparin and heparan2 sulphate sensing hybrid two component system bt4663 in apo and3 ligand bound forms
118	c1k32E	Alignment	not modelled	83.5	8	PDB header: hydrolase Chain: E: PDB Molecule: tricorn protease; PDBTitle: crystal structure of the tricorn protease
119	c6iyyA	Alignment	not modelled	82.9	10	PDB header: lipid binding protein Chain: A: PDB Molecule: wd repeat domain phosphoinositide-interacting protein 3; PDBTitle: crystal structure of human wipi3,loop deletion mutant
120	c3kifD	Alignment	not modelled	82.6	15	PDB header: sugar binding protein Chain: D: PDB Molecule: 5-bladed beta-propeller lectin; PDBTitle: the crystal structures of two fragments truncated from 5-bladed beta-2 propeller lectin, tachylectin-2 (lib1-b7-18 and lib2-d2-15)