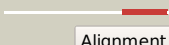
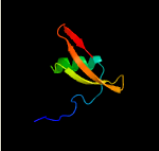
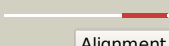

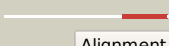
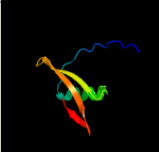

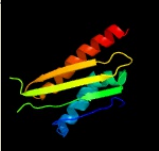

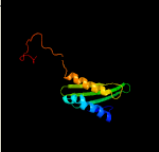



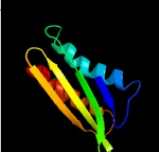



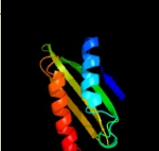

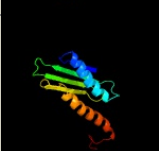





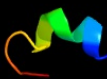
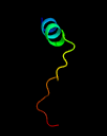
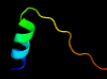





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0079 (-)_88201_89022
Date	Tue Jul 23 14:50:11 BST 2019
Unique Job ID	4f4dd0b5ff5b4c99

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ka5A_	 Alignment		99.7	15	PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
2	c3k2tA_	 Alignment		99.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
3	c3lyvF_	 Alignment		99.6	28	PDB header: chaperone Chain: F: PDB Molecule: ribosome-associated factor y; PDBTitle: crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
4	c6dzkY_	 Alignment		99.0	16	PDB header: ribosome Chain: Y: PDB Molecule: ribosome hibernation promoting factor; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
5	d1l4sa_	 Alignment		99.0	9	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
6	c3tqmD_	 Alignment		99.0	13	PDB header: protein binding Chain: D: PDB Molecule: ribosome-associated factor y; PDBTitle: structure of an ribosomal subunit interface protein from coxiella2 burnetii
7	d2ywqa1	 Alignment		98.9	16	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
8	c2rqlA_	 Alignment		98.9	13	PDB header: translation Chain: A: PDB Molecule: probable sigma-54 modulation protein; PDBTitle: solution structure of the e. coli ribosome hibernation2 promoting factor hpf
9	c4fylB_	 Alignment		98.9	14	PDB header: translation Chain: B: PDB Molecule: ribosome hibernation protein yhbh; PDBTitle: high-resolution x-ray structure of hpf from vibrio cholerae
10	c6qbzA_	 Alignment		98.8	10	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome hibernation promoting factor; PDBTitle: solution structure of the n-terminal domain of the staphylococcus2 aureus hibernation promoting factor
11	c5mmiy_	 Alignment		98.8	12	PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome

12	d1imua_	Alignment		98.7	14	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
13	d2k0bx1	Alignment		38.1	14	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
14	c4gi3C_	Alignment		31.9	30	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: greglin; PDBTitle: crystal structure of greglin in complex with subtilisin
15	c2jy8A_	Alignment		30.2	14	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-binding protein p62; PDBTitle: nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
16	c1oheA_	Alignment		28.8	27	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
17	d1ohea1	Alignment		27.0	27	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
18	c3a9lB_	Alignment		25.6	13	PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
19	c5boiA_	Alignment		22.8	29	PDB header: unknown function Chain: A: PDB Molecule: germination protein ypeb; PDBTitle: bacillus megaterium ypeb c-terminal domain
20	c1gsha_	Alignment		19.9	17	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
21	d2ae8a2	Alignment	not modelled	19.5	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
22	c6c0fv_	Alignment	not modelled	19.1	17	PDB header: ribosome Chain: V: PDB Molecule: 60s ribosomal protein l23-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
23	d1yrea1	Alignment	not modelled	18.3	7	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
24	c3cp3A_	Alignment	not modelled	16.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
25	c2j44A_	Alignment	not modelled	15.1	45	PDB header: carbohydrate-binding module Chain: A: PDB Molecule: alkaline amylopullulanase; PDBTitle: alpha-glucon binding by a streptococcal virulence factor
26	d2f1da2	Alignment	not modelled	15.0	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
27	c4k90B_	Alignment	not modelled	14.7	31	PDB header: hydrolase Chain: B: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
28	c2zkqi_	Alignment	not modelled	13.1	19	PDB header: ribosomal protein/rna Chain: I: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
						Fold: Ferredoxin-like

29	d2bm0a4	Alignment	not modelled	13.0	29	Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
30	d1m0wa1	Alignment	not modelled	12.8	28	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Eukaryotic glutathione synthetase, substrate-binding domain
31	c4v19W_	Alignment	not modelled	12.0	28	PDB header: ribosome Chain: W; PDB Molecule: mitoribosomal protein ul22m, mrp122; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
32	c3r9jD_	Alignment	not modelled	11.9	10	PDB header: cell cycle,hydrolase/cell cycle Chain: D; PDB Molecule: cell division topological specificity factor; PDBTitle: 4.3a resolution structure of a mind-mine(i24n) protein complex
33	c2f46A_	Alignment	not modelled	11.8	12	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
34	d1kyqa2	Alignment	not modelled	11.7	4	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
35	c2m2kA_	Alignment	not modelled	11.5	15	PDB header: transport protein Chain: A; PDB Molecule: hasb protein; PDBTitle: the structure of hasb ctd
36	c3be3A_	Alignment	not modelled	11.4	43	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
37	c2j43A_	Alignment	not modelled	11.3	18	PDB header: carbohydrate-binding module Chain: A; PDB Molecule: spydx; PDBTitle: alpha-glucan recognition by family 41 carbohydrate-binding2 modules from streptococcal virulence factors
38	d1ev0a_	Alignment	not modelled	11.2	9	Fold: Cell division protein MinE topological specificity domain Superfamily: Cell division protein MinE topological specificity domain Family: Cell division protein MinE topological specificity domain
39	d1rhya2	Alignment	not modelled	11.0	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Imidazole glycerol phosphate dehydratase
40	c4iwyA_	Alignment	not modelled	10.5	27	PDB header: ligase Chain: A; PDB Molecule: ribosomal protein s6 modification protein; PDBTitle: semet-substituted rimk structure
41	c4l6wA_	Alignment	not modelled	10.3	21	PDB header: ligase Chain: A; PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
42	c4c1aC_	Alignment	not modelled	10.2	15	PDB header: hydrolase Chain: C; PDB Molecule: orf1-encoded protein; PDBTitle: coiled coil domain of the zfl2-1 orf1 protein from the2 zebrafish zfl2-1 retrotransposon
43	c4c1aB_	Alignment	not modelled	10.2	15	PDB header: hydrolase Chain: B; PDB Molecule: orf1-encoded protein; PDBTitle: coiled coil domain of the zfl2-1 orf1 protein from the2 zebrafish zfl2-1 retrotransposon
44	c4c1aA_	Alignment	not modelled	10.2	15	PDB header: hydrolase Chain: A; PDB Molecule: orf1-encoded protein; PDBTitle: coiled coil domain of the zfl2-1 orf1 protein from the2 zebrafish zfl2-1 retrotransposon
45	d1fx7a3	Alignment	not modelled	10.0	28	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
46	c3rxxA_	Alignment	not modelled	9.9	15	PDB header: ligase Chain: A; PDB Molecule: biotin-[acetyl-coa-carboxylase] ligase; PDBTitle: structural characterisation of staphylococcus aureus biotin protein2 ligase
47	c3n6rF_	Alignment	not modelled	9.8	22	PDB header: ligase Chain: F; PDB Molecule: propionyl-coa carboxylase, beta subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
48	c5xw4A_	Alignment	not modelled	9.8	27	PDB header: cell cycle Chain: A; PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
49	c2ftcM_	Alignment	not modelled	9.7	28	PDB header: ribosome Chain: M; PDB Molecule: mitochondrial ribosomal protein l22 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
50	d2dy1a4	Alignment	not modelled	9.5	25	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
51	c3jywN_	Alignment	not modelled	9.4	6	PDB header: ribosome Chain: N; PDB Molecule: 60s ribosomal protein l17(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
52	c1s1hl_	Alignment	not modelled	9.2	27	PDB header: ribosome Chain: l; PDB Molecule: 40s ribosomal protein s16; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
53	c3fkhB_	Alignment	not modelled	9.1	17	PDB header: oxidoreductase Chain: B; PDB Molecule: putative pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution

54	c4a17Q_	Alignment	not modelled	8.9	15	PDB header: ribosome Chain: Q: PDB Molecule: rpl17; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
55	c1vw4O_	Alignment	not modelled	8.9	17	PDB header: ribosome Chain: O: PDB Molecule: 54s ribosomal protein l22, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
56	d2zjrp1	Alignment	not modelled	8.9	11	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
57	d2vqe1	Alignment	not modelled	8.7	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
58	c2ph7B_	Alignment	not modelled	8.5	42	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_2093; PDBTitle: crystal structure of af2093 from archaeoglobus fulgidus
59	c5xyiQ_	Alignment	not modelled	8.4	23	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
60	c2odkD_	Alignment	not modelled	8.3	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
61	c1kyqC_	Alignment	not modelled	8.1	4	PDB header: oxidoreductase, lyase Chain: C: PDB Molecule: siroheme biosynthesis protein met8; PDBTitle: met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
62	d2gy9i1	Alignment	not modelled	8.1	23	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
63	c5oevD_	Alignment	not modelled	8.1	19	PDB header: transferase Chain: D: PDB Molecule: glutathione synthetase-like effector 22 (gpa-gss22-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss22) from2 globodera pallida in apoform.
64	c3zf7R_	Alignment	not modelled	8.0	8	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l17, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
65	c5o5jl_	Alignment	not modelled	7.8	31	PDB header: ribosome Chain: I: PDB Molecule: 30s ribosomal protein s9; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
66	c1u8xX_	Alignment	not modelled	7.7	15	PDB header: hydrolase Chain: X: PDB Molecule: maltose-6'-phosphate glucosidase; PDBTitle: crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
67	c4ce4W_	Alignment	not modelled	7.7	28	PDB header: ribosome Chain: W: PDB Molecule: mrpl22; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
68	c5onkA_	Alignment	not modelled	7.7	24	PDB header: hydrolase Chain: A: PDB Molecule: yndl; PDBTitle: native yndl
69	c2xzm1_	Alignment	not modelled	7.6	19	PDB header: ribosome Chain: I: PDB Molecule: rps16e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
70	d1j0ha2	Alignment	not modelled	7.6	21	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
71	c3nqyA_	Alignment	not modelled	7.6	50	PDB header: hydrolase Chain: A: PDB Molecule: secreted metalloprotease mcp02; PDBTitle: crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a
72	d2a7sa2	Alignment	not modelled	7.5	21	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
73	c3bbn1_	Alignment	not modelled	7.5	35	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein s9; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
74	c3zeyK_	Alignment	not modelled	7.4	23	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s16, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
75	c5o60T_	Alignment	not modelled	7.4	11	PDB header: ribosome Chain: T: PDB Molecule: 50s ribosomal protein l22; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
76	d1lr0a_	Alignment	not modelled	7.3	16	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: ToIA
77	d2gycq1	Alignment	not modelled	7.3	17	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
78	c3j21S_	Alignment	not modelled	7.2	15	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l22p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins) PDB header: ribosomal protein/rna Chain: R: PDB Molecule: rna expansion segment es39 part i;

79	c2zkr_	Alignment	not modelled	7.1	8	PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
80	c2pfiA_	Alignment	not modelled	7.1	13	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein clc-ka; PDBTitle: crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
81	c4f8bE_	Alignment	not modelled	7.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh-dependent 7-cyano-7-deazaguanine reductase; PDBTitle: crystal structure of the covalent thioimide intermediate of unimodular2 nitrile reductase quef
82	c3j20K_	Alignment	not modelled	7.0	35	PDB header: ribosome Chain: K: PDB Molecule: 30s ribosomal protein s9p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
83	c3fwrB_	Alignment	not modelled	6.9	12	PDB header: transcription Chain: B: PDB Molecule: yqzb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
84	d2odka1	Alignment	not modelled	6.9	16	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
85	d2fsra1	Alignment	not modelled	6.9	21	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
86	c2a7yA_	Alignment	not modelled	6.8	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2302/mt2359; PDBTitle: solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
87	d2a7ya1	Alignment	not modelled	6.8	31	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Rv2302-like
88	c2nvgA_	Alignment	not modelled	6.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
89	c4pr3A_	Alignment	not modelled	6.7	26	PDB header: hydrolase Chain: A: PDB Molecule: 5'-methylthioadenosine nucleosidase / s- PDBTitle: crystal structure of brucella melitensis 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase
90	c2m3vA_	Alignment	not modelled	6.7	11	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from pseudomonas aeruginosa
91	d1i4ja_	Alignment	not modelled	6.6	11	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
92	c5fifD_	Alignment	not modelled	6.5	24	PDB header: ligase Chain: D: PDB Molecule: carboxylase; PDBTitle: carboxyltransferase domain of a single-chain bacterial carboxylase
93	d1vqor1	Alignment	not modelled	6.5	23	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
94	c1on3E_	Alignment	not modelled	6.5	24	PDB header: transferase Chain: E: PDB Molecule: methylmalonyl-coa carboxyltransferase 12s PDBTitle: transcarboxylase 12s crystal structure: hexamer assembly2 and substrate binding to a multienzyme core (with3 methylmalonyl-coenzyme a and methylmalonic acid bound)
95	c4chfB_	Alignment	not modelled	6.4	44	PDB header: viral protein Chain: B: PDB Molecule: polymerase basic protein 2; PDBTitle: crystal structure of the putative cap-binding domain of the2 pb2 subunit of thogoto virus polymerase (form 2)
96	c2a7sD_	Alignment	not modelled	6.4	22	PDB header: ligase Chain: D: PDB Molecule: probable propionyl-coa carboxylase beta chain 5; PDBTitle: crystal structure of the acyl-coa carboxylase, accd5, from2 mycobacterium tuberculosis
97	c3j3wS_	Alignment	not modelled	6.2	11	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l22; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
98	c5kc1H_	Alignment	not modelled	6.2	31	PDB header: endocytosis Chain: H: PDB Molecule: autophagy-related protein 38; PDBTitle: structure of the c-terminal dimerization domain of atg38
99	c3ts3D_	Alignment	not modelled	6.0	23	PDB header: viral protein Chain: D: PDB Molecule: capsid polyprotein; PDBTitle: crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution