

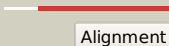

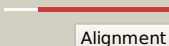




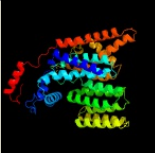


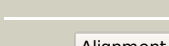
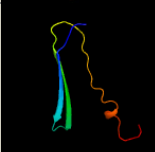
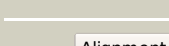

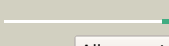
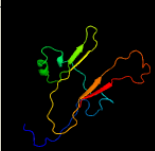

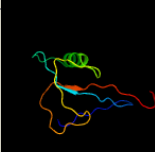

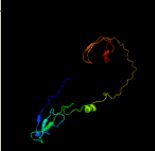


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3635 (-) _4073813_4075588
Date	Fri Aug 9 18:20:32 BST 2019
Unique Job ID	1c9d7fdafb339ee1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6p2rB_	 Alignment		99.7	16	PDB header: transferase Chain: B: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
2	c5f15A_	 Alignment		99.7	13	PDB header: transferase Chain: A: PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
3	c6p25A_	 Alignment		99.6	13	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
4	c3wajA_	 Alignment		99.3	12	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
5	c3rceA_	 Alignment		99.1	10	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
6	c6eznF_	 Alignment		98.8	13	PDB header: membrane protein Chain: F: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
7	d1lura_	 Alignment		56.4	17	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Aldose 1-epimerase (mutarotase)
8	d1wxma1	 Alignment		50.2	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
9	c4rdbA_	 Alignment		45.8	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: immunoreactive 32 kda antigen pg49; PDBTitle: crystal structure of an immunoreactive 32 kda antigen pg49 (pg_0181)2 from porphyromonas gingivalis w83 at 1.45 a resolution (psi community3 target, nakayama)
10	c5n1tM_	 Alignment		45.2	21	PDB header: oxidoreductase Chain: M: PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
11	c4adjB_	 Alignment		43.6	18	PDB header: viral protein Chain: B: PDB Molecule: e1 envelope glycoprotein; PDBTitle: crystal structure of the rubella virus glycoprotein e1 in its2 post-fusion form crystallized in presence of 1mm of calcium acetate

12	c6cd2C_	Alignment		37.9	14	PDB header: membrane protein/chaperone Chain: C: PDB Molecule: outer membrane usher protein papc; PDBTitle: crystal structure of the papc usher bound to the chaperone-adhesin2 papd-papg
13	c6nfqC_	Alignment		31.5	13	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
14	c3ohnA_	Alignment		30.2	15	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane usher protein fimd; PDBTitle: crystal structure of the fimd translocation domain
15	d2f2ha1	Alignment		29.2	28	Fold: Putative glucosidase YicI, C-terminal domain Superfamily: Putative glucosidase YicI, C-terminal domain Family: Putative glucosidase YicI, C-terminal domain
16	c4dipD_	Alignment		24.5	18	PDB header: isomerase Chain: D: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp14
17	c2w1wB_	Alignment		22.1	13	PDB header: hydrolase Chain: B: PDB Molecule: lipolytic enzyme, g-d-s-l; PDBTitle: native structure of a family 35 carbohydrate binding module2 from clostridium thermocellum
18	c5yxiA_	Alignment		21.3	23	PDB header: de novo protein Chain: A: PDB Molecule: drafx6; PDBTitle: designed protein drafx6
19	c3k8rA_	Alignment		19.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
20	c4jjaA_	Alignment		19.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1343 family protein (bf0379) from2 bacteroides fragilis nctc 9343 at 1.30 a resolution
21	c2yevB_	Alignment	not modelled	18.9	17	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
22	c6gszA_	Alignment	not modelled	17.6	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-l-rhamnosidase; PDBTitle: crystal structure of native alfa-l-rhamnosidase from aspergillus2 terreus
23	c2kzbA_	Alignment	not modelled	17.4	10	PDB header: protein transport Chain: A: PDB Molecule: autophagy-related protein 19; PDBTitle: solution structure of alpha-mannosidase binding domain of atg19
24	c4mspB_	Alignment	not modelled	16.8	18	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp222 (aka fkbp14) containing two ef-hand motifs
25	d1nsza_	Alignment	not modelled	16.7	17	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Aldose 1-epimerase (mutarotase)
26	c2okxB_	Alignment	not modelled	16.5	18	PDB header: hydrolase Chain: B: PDB Molecule: rhamnosidase b; PDBTitle: crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
27	d1ulva2	Alignment	not modelled	16.2	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
28	c2vzqA_	Alignment	not modelled	16.1	16	PDB header: hydrolase Chain: A: PDB Molecule: exo-beta-d-glucosaminidase; PDBTitle: c-terminal cbm35 from amycolatopsis orientalis exo-chitosanase csxa in2 complex with digalacturonic acid PDB header: oxidoreductase

29	c5ir6B_	Alignment	not modelled	15.9	7	Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
30	c3mwxA_	Alignment	not modelled	15.9	12	PDB header: isomerase Chain: A: PDB Molecule: aldose 1-epimerase; PDBTitle: crystal structure of a putative galactose mutarotase (bsu18360) from2 bacillus subtilis at 1.45 a resolution
31	d1j0ha2	Alignment	not modelled	15.6	20	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
32	d2o34a1	Alignment	not modelled	15.4	23	Fold: T-fold Superfamily: AppE-like Family: DVU1097-like
33	c3nreB_	Alignment	not modelled	14.9	13	PDB header: isomerase Chain: B: PDB Molecule: aldose 1-epimerase; PDBTitle: crystal structure of a putative aldose 1-epimerase (b2544) from2 escherichia coli k12 at 1.59 a resolution
34	d1ix2a_	Alignment	not modelled	14.8	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
35	c4dtfA_	Alignment	not modelled	14.7	16	PDB header: toxin Chain: A: PDB Molecule: vgrg protein; PDBTitle: structure of a vgrg vibrio cholerae toxin acd domain in complex with2 amp-pnp and mg++
36	c4gxB_	Alignment	not modelled	14.6	25	PDB header: protein transport/cell adhesion Chain: A: PDB Molecule: sorting nexin-17; PDBTitle: structure of the snx17 atypical ferm domain bound to the npxy motif of2 p-selectin
37	c3i31A_	Alignment	not modelled	14.6	19	PDB header: rna binding protein,hydrolase Chain: A: PDB Molecule: heat resistant rna dependent atpase; PDBTitle: hera helicase rna binding domain is an rrm fold
38	c3dcdA_	Alignment	not modelled	14.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: galactose mutarotase related enzyme; PDBTitle: x-ray structure of the galactose mutarotase related enzyme q5fkd7 from2 lactobacillus acidophilus at the resolution 1.9a. northeast3 structural genomics consortium target lar33.
39	c2bgpA_	Alignment	not modelled	14.6	11	PDB header: carbohydrate binding protein Chain: A: PDB Molecule: endo-b1,4-mannanase 5c; PDBTitle: mannan binding module from man5c in bound conformation
40	c5w21B_	Alignment	not modelled	14.2	21	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: fibroblast growth factor 23; PDBTitle: crystal structure of a 1:1:1 fgf23-fgfr1c-aklotho ternary complex
41	c2w3jA_	Alignment	not modelled	14.2	16	PDB header: sugar-binding protein Chain: A: PDB Molecule: carbohydrate binding module; PDBTitle: structure of a family 35 carbohydrate binding module from2 an environmental isolate
42	c4k05B_	Alignment	not modelled	14.1	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical exported protein; PDBTitle: crystal structure of a duf1343 family protein (bf0371) from2 bacteroides fragilis nctc 9343 at 1.65 a resolution
43	c3rfuC_	Alignment	not modelled	13.7	18	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
44	c6e14D_	Alignment	not modelled	13.7	13	PDB header: membrane protein Chain: D: PDB Molecule: fimbrial biogenesis outer membrane usher protein; PDBTitle: handover mechanism of the growing pilus by the bacterial outer2 membrane usher fimd
45	d1c3ga2	Alignment	not modelled	13.4	19	Fold: HSP40/DnaJ peptide-binding domain Superfamily: HSP40/DnaJ peptide-binding domain Family: HSP40/DnaJ peptide-binding domain
46	c6e8aA_	Alignment	not modelled	13.3	19	PDB header: unknown function Chain: A: PDB Molecule: duf1795 domain-containing protein; PDBTitle: crystal structure of dcrb from salmonella enterica at 1.92 angstroms2 resolution
47	c4rnlB_	Alignment	not modelled	12.9	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: possible galactose mutarotase; PDBTitle: the crystal structure of a possible galactose mutarotase from2 streptomyces platensis subsp. rosaceus
48	d1od3a_	Alignment	not modelled	12.7	19	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
49	d1i5pa1	Alignment	not modelled	12.7	19	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: delta-Endotoxin, C-terminal domain
50	c2hbpA_	Alignment	not modelled	12.2	18	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
51	c3oisA_	Alignment	not modelled	12.2	6	PDB header: hydrolase Chain: A: PDB Molecule: cysteine protease; PDBTitle: crystal structure xylellain, a cysteine protease from xylella2 fastidiosa
52	c5xyiD_	Alignment	not modelled	12.0	21	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s3, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
53	d2i6va1	Alignment	not modelled	11.9	26	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
54	c2auwB_	Alignment	not modelled	11.8	16	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718 PDB header: membrane protein

55	c1xrdA_	Alignment	not modelled	11.7	30	Chain: A: PDB Molecule: light-harvesting protein b-880, alpha chain; PDBTitle: light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
56	d1xrda1	Alignment	not modelled	11.7	30	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
57	c5awqA_	Alignment	not modelled	11.6	10	PDB header: hydrolase Chain: A: PDB Molecule: isomaltodextranase; PDBTitle: arthrobacter globiformis t6 isomalto-dextranase complexed with panose
58	c5hj1A_	Alignment	not modelled	11.6	25	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase c protein; PDBTitle: crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
59	c6et5b_	Alignment	not modelled	11.6	27	PDB header: photosynthesis Chain: B: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
60	c3imhB_	Alignment	not modelled	11.4	14	PDB header: isomerase Chain: B: PDB Molecule: galactose-1-epimerase; PDBTitle: crystal structure of galactose 1-epimerase from lactobacillus2 acidophilus ncfm
61	c3n6yA_	Alignment	not modelled	11.4	13	PDB header: unknown function Chain: A: PDB Molecule: immunoglobulin-like protein; PDBTitle: crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
62	c1sr9A_	Alignment	not modelled	11.3	13	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
63	d2c9qa1	Alignment	not modelled	11.3	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
64	d2azeb1	Alignment	not modelled	11.3	3	Fold: E2F-DP heterodimerization region Superfamily: E2F-DP heterodimerization region Family: E2F dimerization segment
65	c2xznC_	Alignment	not modelled	11.1	17	PDB header: ribosome Chain: C: PDB Molecule: kh domain containing protein; 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 2
66	c2vqiA_	Alignment	not modelled	11.1	6	PDB header: transport Chain: A: PDB Molecule: outer membrane usher protein papc; PDBTitle: structure of the p pilus usher (papc) translocation pore
67	c4hs5B_	Alignment	not modelled	10.8	12	PDB header: metal binding protein Chain: B: PDB Molecule: protein cyay; PDBTitle: frataxin from psychromonas ingrahamii as a model to study stability2 modulation within cyay protein family
68	d1dp4a_	Alignment	not modelled	10.6	27	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
69	d1t3qa2	Alignment	not modelled	10.6	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
70	c4ifdE_	Alignment	not modelled	10.5	27	PDB header: hydrolase/rna Chain: E: PDB Molecule: exosome complex component rrp42; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
71	c3i38E_	Alignment	not modelled	10.5	19	PDB header: chaperone Chain: E: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
72	c3i38C_	Alignment	not modelled	10.5	19	PDB header: chaperone Chain: C: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
73	c4v1ao_	Alignment	not modelled	10.4	10	PDB header: ribosome Chain: O: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
74	c2wzpR_	Alignment	not modelled	10.3	16	PDB header: viral protein Chain: R: PDB Molecule: lactococcal phage p2 orf16; PDBTitle: structures of lactococcal phage p2 baseplate shed light on2 a novel mechanism of host attachment and activation in3 siphoviridae
75	c2kijA_	Alignment	not modelled	10.3	14	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the actuator domain of the copper-2 transporting atpase atp7a
76	c4jpdA_	Alignment	not modelled	10.3	18	PDB header: metal binding protein Chain: A: PDB Molecule: protein cyay; PDBTitle: the structure of cyay from burkholderia cenocepacia
77	c1fftG_	Alignment	not modelled	10.2	16	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
78	c2a8B_	Alignment	not modelled	10.2	12	PDB header: hydrolase Chain: B: PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human taspase1 (t234a mutant)
79	c3ccjU_	Alignment	not modelled	10.2	25	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24e; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u
80	d1vqou1	Alignment	not modelled	10.2	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Ribosomal protein L24e

81	c6adqW_	Alignment	not modelled	10.2	20	PDB header: electron transport Chain: W: PDB Molecule: lpqe protein; PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
82	c2zkru_	Alignment	not modelled	10.1	44	PDB header: ribosomal protein/rna Chain: U: PDB Molecule: rna expansion segment es41; 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
83	c3zeyX_	Alignment	not modelled	10.1	17	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s3, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
84	c3ggqA_	Alignment	not modelled	10.1	18	PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: dimerization of hepatitis e virus capsid protein e2s domain is2 essential for virus-host interaction
85	d1wf9a1	Alignment	not modelled	10.1	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
86	c3fljA_	Alignment	not modelled	10.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein conserved in bacteria with a PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
87	d1kn0a_	Alignment	not modelled	10.0	13	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: The homologous-pairing domain of Rad52 recombinase
88	c2x8nA_	Alignment	not modelled	10.0	13	PDB header: structural genomics Chain: A: PDB Molecule: cv0863; PDBTitle: solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. ocsf target cv0863.
89	c3wmmY_	Alignment	not modelled	10.0	28	PDB header: photosynthesis Chain: Y: PDB Molecule: lh1 alpha polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
90	c1hyoB_	Alignment	not modelled	9.9	19	PDB header: hydrolase Chain: B: PDB Molecule: fumarylacetoacetate hydrolase; PDBTitle: crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
91	d1hdgo2	Alignment	not modelled	9.9	42	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
92	d1ew4a_	Alignment	not modelled	9.9	15	Fold: N domain of copper amine oxidase-like Superfamily: Fratxin/Nqo15-like Family: Fratxin-like
93	c3o1hB_	Alignment	not modelled	9.9	12	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
94	d1uy4a_	Alignment	not modelled	9.9	12	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
95	c1s1iS_	Alignment	not modelled	9.8	19	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l24-a; 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, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
96	d1pjxa_	Alignment	not modelled	9.8	5	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase Family: SGL-like
97	c1s1hC_	Alignment	not modelled	9.8	21	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s3; 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.
98	c3izbB_	Alignment	not modelled	9.8	21	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein rps3 (s3p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
99	c4go6C_	Alignment	not modelled	9.8	35	PDB header: protein binding Chain: C: PDB Molecule: hcf n-terminal chain 1; PDBTitle: crystal structure of hcf-1 self-association sequence 1