
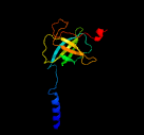
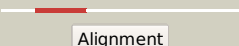

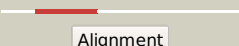
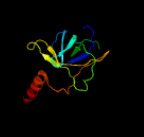
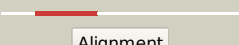


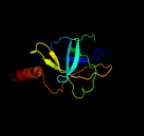
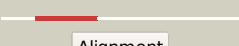
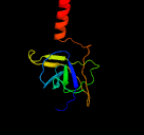
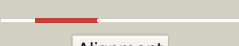
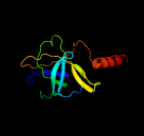

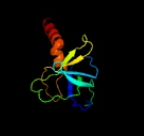

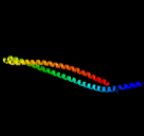

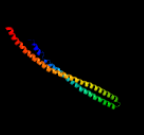

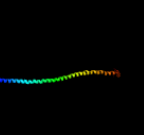
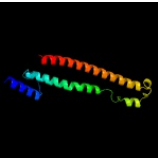
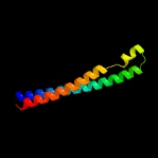


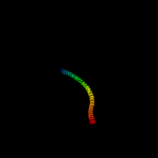

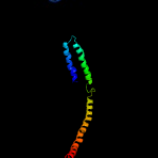

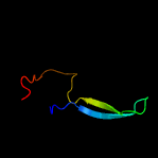


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1968_(mce3C)_2211634_2212866
 Date Mon Aug 5 13:25:06 BST 2019
 Unique Job ID 0e3d33bdbd980033

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	30	PDB header: protein transport Chain: C: PDB Molecule: toluene tolerance efflux transporter (abc superfamily, PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	c5uw8C_	 Alignment		99.8	20	PDB header: transport protein Chain: C: PDB Molecule: probable phospholipid abc transporter-binding protein mlad; PDBTitle: structure of e. coli mce protein mlad, core mce domain
3	c5uvnD_	 Alignment		99.6	23	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnA_	 Alignment		99.6	23	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnC_	 Alignment		99.6	23	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnE_	 Alignment		99.6	23	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnF_	 Alignment		99.6	23	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnB_	 Alignment		99.6	23	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c3g67A_	 Alignment		95.2	7	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
10	c1qu7A_	 Alignment		93.9	8	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
11	c3vkhA_	 Alignment		88.8	7	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain

12	c6b7nC_	Alignment		87.0	10	PDB header: viral protein Chain: C; PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
13	c2ieqC_	Alignment		86.3	11	PDB header: viral protein Chain: C; PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
14	c6e6aB_	Alignment		85.3	17	PDB header: protein binding Chain: B; PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
15	c3lnrA_	Alignment		84.7	18	PDB header: signaling protein Chain: A; PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
16	c3zx6A_	Alignment		83.9	11	PDB header: signaling Chain: A; PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
17	d1eq1a_	Alignment		83.7	11	Fold: Apolipoprotein-III Superfamily: Apolipoprotein-III Family: Apolipoprotein-III
18	c5u0pU_	Alignment		83.6	11	PDB header: transcription Chain: U; PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
19	c2ch7A_	Alignment		82.5	12	PDB header: chemotaxis Chain: A; PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
20	c2j5uB_	Alignment		79.5	12	PDB header: cell shape regulation Chain: B; PDB Molecule: imrec protein; PDBTitle: mreC lysteria monocytogenes
21	c2d4yA_	Alignment	not modelled	79.4	13	PDB header: structural protein Chain: A; PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
22	c6ezvX_	Alignment	not modelled	77.5	11	PDB header: toxin Chain: X; PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
23	d1st6a4	Alignment	not modelled	77.0	14	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
24	c1deqO_	Alignment	not modelled	73.1	9	PDB header: blood clotting Chain: O; PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
25	c6gajA_	Alignment	not modelled	72.7	9	PDB header: viral protein Chain: A; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1I reovirus sigma1 coiled coil tail (iodide)
26	c2wpqA_	Alignment	not modelled	72.5	5	PDB header: membrane protein Chain: A; PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (sadaK3, in-2 register fusion)
27	c3ojaB_	Alignment	not modelled	71.5	13	PDB header: protein binding Chain: B; PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
28	c6nb3B_	Alignment	not modelled	70.2	17	PDB header: virus Chain: B; PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)

29	c1deqF_	Alignment	not modelled	69.4	13	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
30	c1ei3E_	Alignment	not modelled	68.2	14	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
31	c4rh7A_	Alignment	not modelled	68.1	9	PDB header: motor protein Chain: A: PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
32	c5zhyA_	Alignment	not modelled	65.7	13	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
33	c5xbjA_	Alignment	not modelled	61.8	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
34	c4ut1A_	Alignment	not modelled	61.7	18	PDB header: motor protein Chain: A: PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
35	c2qihA_	Alignment	not modelled	60.7	11	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
36	c6o7ua_	Alignment	not modelled	59.4	11	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
37	d1g4us1	Alignment	not modelled	58.6	12	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
38	c3cwgA_	Alignment	not modelled	57.1	11	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
39	c6gapB_	Alignment	not modelled	54.5	13	PDB header: viral protein Chain: B: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
40	c1kmiZ_	Alignment	not modelled	53.8	10	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
41	c2kbbA_	Alignment	not modelled	49.8	13	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
42	c6gaoC_	Alignment	not modelled	47.0	9	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail and body
43	d1st6a3	Alignment	not modelled	45.1	14	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
44	c2p22A_	Alignment	not modelled	44.6	12	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast escrt-i heterotetramer core
45	c5n76C_	Alignment	not modelled	43.8	15	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
46	c2qf4A_	Alignment	not modelled	43.7	14	PDB header: structural protein Chain: A: PDB Molecule: cell shape determining protein mrec; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
47	c2yfaA_	Alignment	not modelled	43.3	10	PDB header: receptor Chain: A: PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
48	c2dq3A_	Alignment	not modelled	42.9	10	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
49	c5cwsj_	Alignment	not modelled	42.7	10	PDB header: protein transport Chain: J: PDB Molecule: nucleoporin nup49; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
50	d1ykhb1	Alignment	not modelled	42.4	11	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
51	d1h9ma2	Alignment	not modelled	41.4	23	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
52	c5j65A_	Alignment	not modelled	41.2	9	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
53	c5zuvB_	Alignment	not modelled	40.4	4	PDB header: viral protein, inhibitor Chain: B: PDB Molecule: spike glycoprotein,spike glycoprotein,inhibitor ek1; PDBTitle: crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
54	c3i6vL_	Alignment	not modelled	40.0	18	PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial;

54	c3jvtE_	Alignment	not modelled	40.0	10	PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial 2 ribosome
55	d1st6a5	Alignment	not modelled	39.7	16	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
56	c3ur1C_	Alignment	not modelled	39.3	9	PDB header: immune system Chain: C: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: the structure of a ternary complex between chea domains p4 and p5 with 2 chew and with a truncated fragment of tm14, a chemoreceptor analog 3 from thermotoga maritima.
57	d1quua1	Alignment	not modelled	39.1	11	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
58	c2vs0B_	Alignment	not modelled	39.1	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus 2 virulence factor esxa
59	c3ghgl_	Alignment	not modelled	38.3	14	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
60	c4lwsA_	Alignment	not modelled	37.6	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
61	c4njlA_	Alignment	not modelled	37.3	10	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
62	c1ei3C_	Alignment	not modelled	37.2	14	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
63	d2uubl1	Alignment	not modelled	36.9	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
64	d1h9ra2	Alignment	not modelled	36.5	20	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
65	c1bf5A_	Alignment	not modelled	34.9	8	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
66	d1h9ma1	Alignment	not modelled	34.5	23	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
67	d1guta_	Alignment	not modelled	34.4	16	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
68	c2nrjA_	Alignment	not modelled	34.2	11	PDB header: toxin Chain: A: PDB Molecule: hbl b protein; PDBTitle: crystal structure of hemolysin binding component from 2 bacillus cereus
69	c6grjG_	Alignment	not modelled	34.1	10	PDB header: toxin Chain: G: PDB Molecule: ahlb; PDBTitle: structure of the ahlb pore of the tripartite alpha-pore forming toxin, 2 ahl, from aeromonas hydrophila.
70	c1zn1L_	Alignment	not modelled	33.9	21	PDB header: biosynthetic/structural protein/rna Chain: L: PDB Molecule: 30s ribosomal protein s12; PDBTitle: coordinates of rrf fitted into cryo-em map of the 70s post-termination 2 complex
71	c4abxB_	Alignment	not modelled	33.1	12	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
72	c1wnce_	Alignment	not modelled	32.6	20	PDB header: viral protein Chain: E: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of the sars-cov spike protein fusion core
73	c5yfpG_	Alignment	not modelled	32.2	14	PDB header: exocytosis Chain: G: PDB Molecule: exocyst complex component exo70; PDBTitle: cryo-em structure of the exocyst complex
74	c1quua_	Alignment	not modelled	31.5	14	PDB header: contractile protein Chain: A: PDB Molecule: human skeletal muscle alpha-actinin 2; PDBTitle: crystal structure of two central spectrin-like repeats from alpha-2 actinin
75	c5j2lB_	Alignment	not modelled	31.3	14	PDB header: de novo protein Chain: B: PDB Molecule: protein design 2l4hc2_11; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond 2 network-mediated specificity
76	c5c3lC_	Alignment	not modelled	30.8	14	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup62; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
77	c5x5bB_	Alignment	not modelled	30.5	14	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
78	c6nzkB_	Alignment	not modelled	29.3	10	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid 2 receptors
79	c6ewyA_	Alignment	not modelled	29.2	11	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
80	c5yfpB_	Alignment	not modelled	29.0	14	PDB header: exocytosis Chain: B: PDB Molecule: exocyst complex component sec5; PDBTitle: cryo-em structure of the exocyst complex

81	c6cs2A_	Alignment	not modelled	28.4	13	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
82	d2qall1	Alignment	not modelled	27.7	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
83	c5ew5C_	Alignment	not modelled	27.6	8	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
84	c2bezC_	Alignment	not modelled	27.2	11	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolitically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
85	d1i94I_	Alignment	not modelled	27.1	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
86	c2gl2B_	Alignment	not modelled	27.1	11	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
87	d1hcia4	Alignment	not modelled	26.8	9	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
88	c5i08A_	Alignment	not modelled	26.5	14	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
89	d2cp6a1	Alignment	not modelled	26.2	23	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
90	c5xlrC_	Alignment	not modelled	25.9	14	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
91	c4wsrA_	Alignment	not modelled	24.7	18	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
92	c5nugB_	Alignment	not modelled	24.7	13	PDB header: motor protein Chain: B: PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
93	d1fr3a_	Alignment	not modelled	24.6	18	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
94	c3ghgK_	Alignment	not modelled	23.8	8	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
95	c2q13A_	Alignment	not modelled	23.6	9	PDB header: protein transport Chain: A: PDB Molecule: dcc-interacting protein 13 alpha; PDBTitle: crystal structure of bar-ph domain of appl1
96	c1cz5A_	Alignment	not modelled	21.9	12	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
97	c1yvlB_	Alignment	not modelled	21.8	9	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
98	c5gasN_	Alignment	not modelled	21.8	14	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
99	c1bg1A_	Alignment	not modelled	21.6	10	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
100	c4iogD_	Alignment	not modelled	21.3	11	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
101	c5szsC_	Alignment	not modelled	21.2	12	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
102	c3qr8A_	Alignment	not modelled	20.7	15	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
103	c5cwsC_	Alignment	not modelled	20.6	17	PDB header: protein transport Chain: C: PDB Molecule: nucleoporin nsp1; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
104	c5n9yB_	Alignment	not modelled	20.3	13	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb