
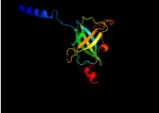
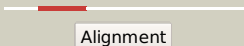
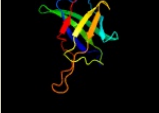
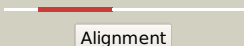








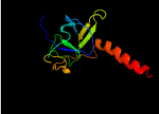



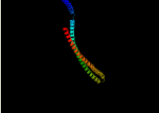

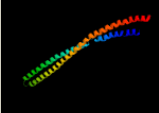


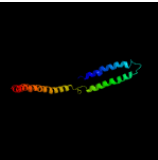
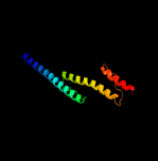

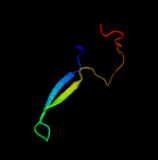


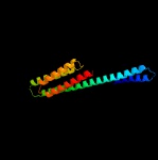
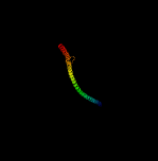
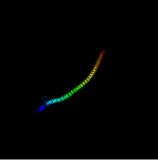


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3496c_(mce4D)_3914710_3916065
 Date Fri Aug 9 18:20:17 BST 2019
 Unique Job ID e57e37694a9e4e3c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.8	18	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		99.7	21	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	c5uvnB_	 Alignment		99.4	13	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnD_	 Alignment		99.4	13	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnC_	 Alignment		99.4	13	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		99.4	13	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		99.4	13	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnA_	 Alignment		99.4	13	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c3g67A_	 Alignment		94.9	9	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		94.7	9	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	c2d4yA_	 Alignment		90.3	15	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)

12	c5u0pU_	Alignment		85.4	10	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
13	c3lnrA_	Alignment		85.1	11	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
14	c3zx6A_	Alignment		84.3	16	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
15	c2j5uB_	Alignment		83.8	12	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
16	c2ieqC_	Alignment		83.5	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
17	c2wpgA_	Alignment		81.8	5	PDB header: membrane protein Chain: A: PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (sada3, in-2 register fusion)
18	c2yfaA_	Alignment		81.4	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
19	c2qihA_	Alignment		81.3	11	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
20	c2ch7A_	Alignment		80.7	8	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
21	c4abxB_	Alignment	not modelled	76.4	14	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
22	c1kmiZ_	Alignment	not modelled	76.1	14	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
23	c1bf5A_	Alignment	not modelled	73.9	9	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
24	c6e6aB_	Alignment	not modelled	73.7	15	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
25	c6nzkB_	Alignment	not modelled	72.9	16	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
26	c2vs0B_	Alignment	not modelled	72.6	17	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
27	c5x5bB_	Alignment	not modelled	71.6	15	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
28	c4ut1A_	Alignment	not modelled	71.5	14	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 PDB header: motor protein

29	c4rh7A_	Alignment	not modelled	70.8	8	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
30	c5i08A_	Alignment	not modelled	67.9	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
31	c5xlrC_	Alignment	not modelled	67.2	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
32	c6gaoC_	Alignment	not modelled	67.0	10	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
33	c1deqF_	Alignment	not modelled	66.6	8	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
34	c5wrgB_	Alignment	not modelled	65.6	15	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
35	c6nb3B_	Alignment	not modelled	64.7	18	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
36	c3cwgA_	Alignment	not modelled	64.6	8	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
37	c2qf4A_	Alignment	not modelled	64.2	10	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)
38	c4lwsB_	Alignment	not modelled	64.1	7	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
39	c6gajA_	Alignment	not modelled	64.0	5	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
40	c5zhyA_	Alignment	not modelled	63.9	7	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
41	c3jclC_	Alignment	not modelled	63.8	12	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
42	c6b7nC_	Alignment	not modelled	62.6	14	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
43	c1h4uA_	Alignment	not modelled	62.3	20	PDB header: extracellular matrix protein Chain: A: PDB Molecule: nidogen-1; PDBTitle: domain g2 of mouse nidogen-1
44	c3ojaB_	Alignment	not modelled	62.1	8	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
45	c4iogD_	Alignment	not modelled	61.9	13	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
46	c1ei3E_	Alignment	not modelled	61.6	11	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
47	c4lwsA_	Alignment	not modelled	61.5	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
48	c3gvmA_	Alignment	not modelled	59.6	22	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
49	c6gapB_	Alignment	not modelled	58.9	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
50	c5x5fC_	Alignment	not modelled	58.5	18	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
51	c5szsC_	Alignment	not modelled	57.8	15	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
52	d1h9ra2	Alignment	not modelled	57.0	20	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
53	c3vkbA_	Alignment	not modelled	56.8	14	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
54	c3ghgK_	Alignment	not modelled	56.2	12	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen

55	c6cs2A_	Alignment	not modelled	55.9	15	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
56	c6cv0C_	Alignment	not modelled	55.1	10	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
57	c3j99M_	Alignment	not modelled	54.6	5	PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iib)
58	d1h9ma2	Alignment	not modelled	54.2	16	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
59	c5cwsC_	Alignment	not modelled	54.2	16	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
60	c1ei3C_	Alignment	not modelled	51.9	9	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
61	c5yfpG_	Alignment	not modelled	51.5	10	PDB header: exocytosis Chain: G: PDB Molecule: exocyst complex component exo70; PDBTitle: cryo-em structure of the exocyst complex
62	d1guta_	Alignment	not modelled	51.3	8	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
63	c1deqO_	Alignment	not modelled	50.3	10	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
64	c5xbjA_	Alignment	not modelled	49.3	11	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
65	d1szia_	Alignment	not modelled	48.7	14	Fold: Four-helical up-and-down bundle Superfamily: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain Family: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
66	d1h9ma1	Alignment	not modelled	48.4	8	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
67	c6ezvX_	Alignment	not modelled	48.3	10	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
68	d1gl4a1	Alignment	not modelled	47.7	23	Fold: GFP-like Superfamily: GFP-like Family: Domain G2 of nidogen-1
69	d1wa8a1	Alignment	not modelled	46.9	11	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
70	d1quua1	Alignment	not modelled	46.8	11	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
71	c4n21E_	Alignment	not modelled	45.9	6	PDB header: viral protein Chain: E: PDB Molecule: gp2 ectodomain; PDBTitle: crystal structure of the gp2 core domain from the california academy2 of science virus
72	c4e40A_	Alignment	not modelled	45.8	12	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
73	c5yfpD_	Alignment	not modelled	45.7	9	PDB header: exocytosis Chain: D: PDB Molecule: exocyst complex component sec8; PDBTitle: cryo-em structure of the exocyst complex
74	d1ykhb1	Alignment	not modelled	45.2	8	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
75	c1quua_	Alignment	not modelled	45.0	8	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
76	c4f7gB_	Alignment	not modelled	44.8	15	PDB header: cell adhesion Chain: B: PDB Molecule: tal1n-1; PDBTitle: crystal structure of talin autoinhibition complex
77	c6grjG_	Alignment	not modelled	43.5	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.
78	c1bg1A_	Alignment	not modelled	42.5	10	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
79	c3j6vL_	Alignment	not modelled	41.9	22	PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
80	c3zbcC_	Alignment	not modelled	41.6	9	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
						Fold: OB-fold

81	d2uubl1	Alignment	not modelled	41.4	16	Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
82	d2j9ua1	Alignment	not modelled	41.0	9	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like
83	c2nrjA	Alignment	not modelled	40.9	17	PDB header: toxin Chain: A: PDB Molecule: hbl b protein; PDBTitle: crystal structure of hemolysin binding component from2 bacillus cereus
84	c4wsrA	Alignment	not modelled	40.4	12	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
85	d1fr3a	Alignment	not modelled	40.2	18	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
86	c5n76C	Alignment	not modelled	40.2	13	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
87	c3euhB	Alignment	not modelled	40.1	10	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
88	c4njjA	Alignment	not modelled	39.9	15	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
89	c5svaT	Alignment	not modelled	38.8	15	PDB header: transcription, transferase/dna Chain: T: PDB Molecule: mediator of rna polymerase ii transcription subunit 4; PDBTitle: mediator-rna polymerase ii pre-initiation complex
90	c1zn1L	Alignment	not modelled	38.4	16	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-termination2 complex
91	c6ewyA	Alignment	not modelled	37.6	9	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
92	c5dfzA	Alignment	not modelled	34.9	11	PDB header: transferase Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 38; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
93	c4fiuC	Alignment	not modelled	34.1	11	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
94	d1st6a4	Alignment	not modelled	33.5	12	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
95	c3ur1C	Alignment	not modelled	33.4	8	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 with2 chew and with a truncated fragment of tm14, a chemoreceptor analog3 from thermotoga maritima.
96	d1eq1a	Alignment	not modelled	33.4	15	Fold: Apolipoprotein-III Superfamily: Apolipoprotein-III Family: Apolipoprotein-III
97	c3qr8A	Alignment	not modelled	32.9	10	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
98	d2qall1	Alignment	not modelled	32.1	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
99	c6gy6Q	Alignment	not modelled	31.8	8	PDB header: toxin Chain: Q: PDB Molecule: xaxa; PDBTitle: xaxab pore complex from xenorhabdus nematophila
100	c4cjdA	Alignment	not modelled	31.0	27	PDB header: cell adhesion Chain: A: PDB Molecule: nada; PDBTitle: crystal structure of neisseria meningitidis trimeric2 autotransporter and vaccine antigen nada
101	c2j9wB	Alignment	not modelled	30.8	14	PDB header: protein transport Chain: B: PDB Molecule: vps28-prov protein; PDBTitle: structural insight into the escrt-i-ii link and its role in mvb2 trafficking
102	c6b3oB	Alignment	not modelled	30.5	12	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
103	d1i94l	Alignment	not modelled	30.4	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
104	c2q13A	Alignment	not modelled	30.1	9	PDB header: protein transport Chain: A: PDB Molecule: dcc-interacting protein 13 alpha; PDBTitle: crystal structure of bar-ph domain of app1
105	c1ha0A	Alignment	not modelled	29.9	16	PDB header: viral protein Chain: A: PDB Molecule: protein (hemagglutinin precursor); PDBTitle: hemagglutinin precursor ha0
106	c2wr2B	Alignment	not modelled	29.7	14	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
107	c6j9rA	Alignment	not modelled	29.4	9	PDB header: translation Chain: A: PDB Molecule: brain tumor protein;

						PDBTitle: coiled-coil domain of drosophila trim protein brat
108	c1h9mB_	Alignment	not modelled	29.1	21	PDB header: binding protein Chain: B: PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. pegrown form with4 molybdate bound
109	c3bt6B_	Alignment	not modelled	28.9	11	PDB header: viral protein Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
110	c2ql2B_	Alignment	not modelled	28.4	8	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
111	c2dq3A_	Alignment	not modelled	28.3	16	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
112	c2p22A_	Alignment	not modelled	28.1	8	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast escrt-i heterotetramer core
113	d1g4us1	Alignment	not modelled	27.8	15	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
114	c1h9sA_	Alignment	not modelled	27.5	20	PDB header: transcription regulator Chain: A: PDB Molecule: molybdenum transport protein mode; PDBTitle: molybdate bound complex of dimop domain of mode from e.coli
115	c5zuvB_	Alignment	not modelled	27.2	13	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
116	d2vzsa2	Alignment	not modelled	27.2	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
117	c5tpjA_	Alignment	not modelled	27.2	16	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
118	d2cu6a1	Alignment	not modelled	27.1	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
119	c5dmaA_	Alignment	not modelled	26.6	13	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcra; PDBTitle: crystal structure of c-terminal tudor domain in pcra/uvrd helicase
120	c1pkvB_	Alignment	not modelled	26.4	11	PDB header: transferase Chain: B: PDB Molecule: riboflavin synthase alpha chain; PDBTitle: the n-terminal domain of riboflavin synthase in complex with2 riboflavin