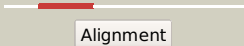
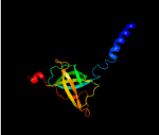
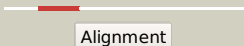
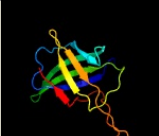
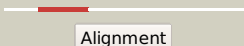

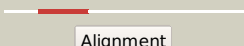
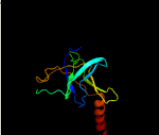
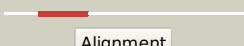
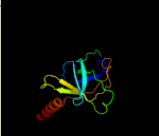
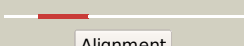

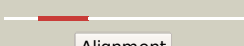
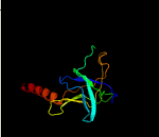



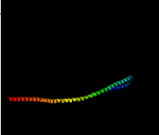

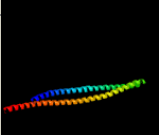

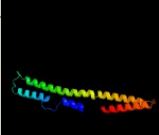

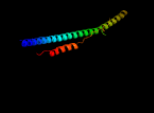

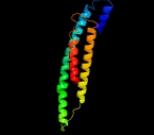
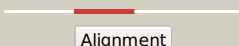
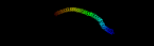
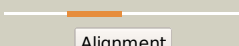

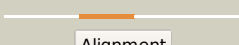
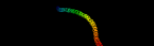
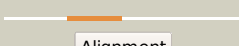

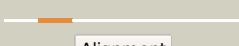
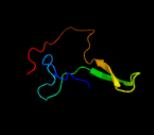



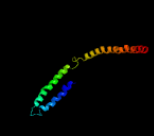


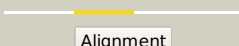
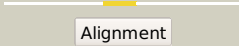
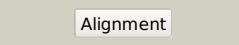
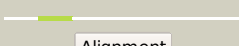
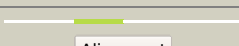
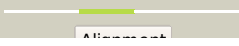


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0174_(mce1F)_205229_206776
 Date Tue Jul 23 14:50:22 BST 2019
 Unique Job ID a10e320af6aad4cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	28	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	23	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		99.3	19	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnE_	 Alignment		99.3	19	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnB_	 Alignment		99.3	19	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnA_	 Alignment		99.3	19	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnF_	 Alignment		99.3	19	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnC_	 Alignment		99.3	19	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		96.0	11	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
10	c3g67A_	 Alignment		93.7	9	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c5xbjA_	 Alignment		93.0	16	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

12	c1wyyB_	 Alignment		91.5	10	PDB header: viral protein Chain: B; PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
13	c3cwgA_	 Alignment		90.2	12	PDB header: transcription Chain: A; PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
14	c2ch7A_	 Alignment		90.0	11	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
15	c4ut1A_	 Alignment		88.0	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
16	c3zx6A_	 Alignment		86.9	12	PDB header: signaling Chain: A; PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
17	c2d4yA_	 Alignment		84.5	15	PDB header: structural protein Chain: A; PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
18	c2j5uB_	 Alignment		84.1	29	PDB header: cell shape regulation Chain: B; PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
19	c6e6aB_	 Alignment		83.7	17	PDB header: protein binding Chain: B; PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
20	c5u0pU_	 Alignment		82.2	9	PDB header: transcription Chain: U; PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
21	c2wpgA_	 Alignment	not modelled	80.9	8	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)
22	c2yfaA_	 Alignment	not modelled	80.9	12	PDB header: receptor Chain: A; PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
23	c3lnrA_	 Alignment	not modelled	77.6	15	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
24	c2vs0B_	 Alignment	not modelled	76.5	13	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
25	c1deqF_	 Alignment	not modelled	74.9	8	PDB header: blood clotting Chain: F; PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
26	c2qf4A_	 Alignment	not modelled	69.4	17	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)
27	c2nrjA_	 Alignment	not modelled	68.9	10	PDB header: toxin Chain: A; PDB Molecule: hbl b protein; PDBTitle: crystal structure of hemolysin binding component from2 bacillus cereus
28	c6h7nC_	 Alignment	not modelled	68.0	12	PDB header: viral protein Chain: C; PDB Molecule: spike protein;

28	c0b7nc	Alignment	not modelled	68.0	12	PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
29	d1ykb1	Alignment	not modelled	67.9	10	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
30	d1st6a4	Alignment	not modelled	66.7	14	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
31	c4iogD	Alignment	not modelled	66.2	19	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
32	c4abxB	Alignment	not modelled	65.9	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
33	c3euhB	Alignment	not modelled	64.4	12	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
34	c2ieqC	Alignment	not modelled	64.1	10	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
35	c2qihA	Alignment	not modelled	64.0	7	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
36	d1eq1a	Alignment	not modelled	63.9	10	Fold: Apolipoprotein III Superfamily: Apolipoprotein III Family: Apolipoprotein III
37	c6gajA	Alignment	not modelled	62.2	9	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)
38	c1kmiZ	Alignment	not modelled	62.1	16	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
39	c3gvmA	Alignment	not modelled	61.4	11	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
40	c2l81A	Alignment	not modelled	61.4	13	PDB header: cell adhesion Chain: A: PDB Molecule: enhancer of filamentation 1; PDBTitle: solution nmr structure of the serine-rich domain of hef1 (enhancer of filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
41	c3ojaB	Alignment	not modelled	60.3	11	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
42	c5wwlN	Alignment	not modelled	59.7	12	PDB header: cell cycle Chain: N: PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogony pombe kinetochore mis12c2 subcomplex
43	c1ei3E	Alignment	not modelled	59.6	8	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
44	c3ur1C	Alignment	not modelled	58.8	10	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.
45	c5szsC	Alignment	not modelled	58.2	11	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
46	c2p22A	Alignment	not modelled	56.7	16	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast escrt-i heterotetramer core
47	c6gy6Q	Alignment	not modelled	56.7	11	PDB header: toxin Chain: Q: PDB Molecule: xaxa; PDBTitle: xaxab pore complex from xenorhabdus nematophila
48	c4rh7A	Alignment	not modelled	55.8	3	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
49	c5zhyA	Alignment	not modelled	55.2	10	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
50	c3zbhC	Alignment	not modelled	55.0	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
51	c1degO	Alignment	not modelled	54.1	14	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
52	c2j9wB	Alignment	not modelled	53.7	13	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
53	d1st6a3	Alignment	not modelled	53.2	12	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
						PDB header: membrane protein

54	c6o7xa_	Alignment	not modelled	51.3	11	Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
55	c5lp5F_	Alignment	not modelled	50.7	13	PDB header: hydrolase/antibiotic Chain: F: PDB Molecule: rod shape-determining protein (mrec); PDBTitle: complex between penicillin-binding protein (pbp2) and mrec from2 helicobacter pylori
56	d2j9ua1	Alignment	not modelled	50.5	10	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like
57	c4lwsA_	Alignment	not modelled	48.8	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
58	c5y2gA_	Alignment	not modelled	48.2	13	PDB header: toxin Chain: A: PDB Molecule: maltose-binding periplasmic protein,protein b; PDBTitle: structure of mbp tagged gbs camp
59	d1h9ra2	Alignment	not modelled	46.8	16	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
60	d1quua1	Alignment	not modelled	46.7	12	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
61	c5j65A_	Alignment	not modelled	45.8	10	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
62	c5x5bB_	Alignment	not modelled	44.9	13	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
63	c6gapB_	Alignment	not modelled	44.3	10	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
64	c4lwsB_	Alignment	not modelled	44.1	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
65	c1ei3C_	Alignment	not modelled	43.6	9	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
66	c5i08A_	Alignment	not modelled	42.9	14	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
67	d1guta_	Alignment	not modelled	42.0	36	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
68	c5n76C_	Alignment	not modelled	41.0	28	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
69	d1h9ma2	Alignment	not modelled	40.7	28	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
70	c4nl6C_	Alignment	not modelled	40.4	7	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
71	c3j6vL_	Alignment	not modelled	39.7	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
72	c5zuvB_	Alignment	not modelled	38.8	10	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
73	c3c12A_	Alignment	not modelled	38.7	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
74	d2uubl1	Alignment	not modelled	38.4	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	c5xlrC_	Alignment	not modelled	38.4	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
76	c5tgvA_	Alignment	not modelled	38.2	16	PDB header: unknown function Chain: A: PDB Molecule: ps1; PDBTitle: nmr structure of holo-ps1
77	c3nwiC_	Alignment	not modelled	38.1	13	PDB header: transport protein Chain: C: PDB Molecule: zinc transport protein zntb; PDBTitle: the soluble domain structure of the zntb zn2+ efflux system
78	c6grjG_	Alignment	not modelled	37.9	7	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.
79	c1zn1L_	Alignment	not modelled	37.4	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-termination2 complex
80	c6cv0C_	Alignment	not modelled	37.2	7	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein;

80	c0cvc_	Alignment	not modelled	37.2	7	PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
81	c1bf5A_	Alignment	not modelled	37.1	9	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
82	c5wrgB_	Alignment	not modelled	37.1	13	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
83	c1quuA_	Alignment	not modelled	36.8	11	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
84	c6o7ua_	Alignment	not modelled	35.3	10	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: crystal structure a talin rod fragment
85	c3dyjA_	Alignment	not modelled	35.3	9	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
86	d1h9ma1	Alignment	not modelled	34.4	24	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
87	c5x5fC_	Alignment	not modelled	33.5	12	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
88	c5cwsC_	Alignment	not modelled	32.9	7	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail and body
89	c6gaoC_	Alignment	not modelled	32.7	8	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrinin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
90	c6cs2A_	Alignment	not modelled	32.6	13	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
91	c6nzkB_	Alignment	not modelled	32.5	14	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
92	c1yvlB_	Alignment	not modelled	32.5	9	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
93	c5gasN_	Alignment	not modelled	31.9	9	PDB header: cell adhesion Chain: B: PDB Molecule: talin-1; PDBTitle: crystal structure of talin autoinhibition complex
94	c4f7gB_	Alignment	not modelled	31.7	14	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
95	d1k0ha_	Alignment	not modelled	31.6	22	PDB header: transferase Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 38; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
96	c5dfzA_	Alignment	not modelled	31.2	8	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
97	c3ghgl_	Alignment	not modelled	31.0	8	PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, PDBTitle: crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
98	c6iiuA_	Alignment	not modelled	30.7	13	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
99	c4n21E_	Alignment	not modelled	30.4	6	PDB header: lipid binding protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
100	c4jrbA_	Alignment	not modelled	30.2	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
101	d1wa8a1	Alignment	not modelled	30.1	8	Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Phosphorelay protein-like
102	d1yvia1	Alignment	not modelled	30.0	17	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
103	c3vkhA_	Alignment	not modelled	29.8	11	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
104	c2kg7B_	Alignment	not modelled	29.7	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
105	d2qall1	Alignment	not modelled	29.7	22	Fold: OB-fold

106	d1i94l_	Alignment	not modelled	29.2	32	Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
107	c3jclC_	Alignment	not modelled	29.1	9	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
108	c2dq3A_	Alignment	not modelled	29.1	9	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
109	d1hcia4	Alignment	not modelled	28.6	9	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
110	c2iakA_	Alignment	not modelled	27.7	7	PDB header: cell adhesion Chain: A: PDB Molecule: bullous pemphigoid antigen 1, isoform 5; PDBTitle: crystal structure of a protease resistant fragment of the plakin2 domain of bullous pemphigoid antigen1 (bpag1)
111	c6nb3B_	Alignment	not modelled	27.6	15	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
112	c2ql2B_	Alignment	not modelled	27.5	15	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
113	c6ezvX_	Alignment	not modelled	26.6	12	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
114	d1v5va1	Alignment	not modelled	26.6	20	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
115	c2mpnA_	Alignment	not modelled	26.3	17	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
116	c3ck6E_	Alignment	not modelled	26.2	8	PDB header: structural protein Chain: E: PDB Molecule: putative membrane transport protein; PDBTitle: crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
117	d2cu6a1	Alignment	not modelled	25.9	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
118	c5tvbB_	Alignment	not modelled	25.1	13	PDB header: transferase Chain: B: PDB Molecule: nucleoprotein tpr; PDBTitle: structure of the tpr oligomerization domain
119	c2odvA_	Alignment	not modelled	24.9	8	PDB header: structural protein Chain: A: PDB Molecule: plectin 1; PDBTitle: crystal structure of a fragment of the plakin domain of plectin, cys2 to ala mutant.
120	c1wncE_	Alignment	not modelled	24.1	13	PDB header: viral protein Chain: E: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of the sars-cov spike protein fusion core