
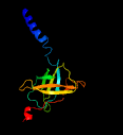



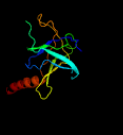

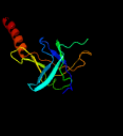

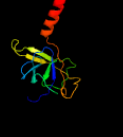

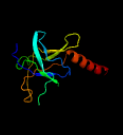





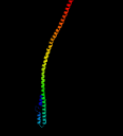

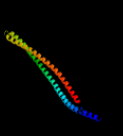

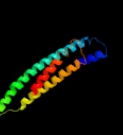


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0594_(mce2F)_693240_694790
 Date Fri Jul 26 01:50:15 BST 2019
 Unique Job ID 95ba8a2527f1f9bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	26	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	26	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	c5uvc_	 Alignment		99.4	20	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvcD_	 Alignment		99.4	20	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvcB_	 Alignment		99.4	20	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvcE_	 Alignment		99.4	20	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvcA_	 Alignment		99.4	20	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvcF_	 Alignment		99.4	20	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		96.1	12	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		94.0	11	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c3cwgA_	 Alignment		93.9	13	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment

12	c5xbjA_	Alignment		93.1	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) from <i>Campylobacter jejuni</i>
13	c4ut1A_	Alignment		91.7	13	PDB header: motor protein Chain: A; PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from <i>Burkholderia pseudomallei</i>
14	c3lnrA_	Alignment		90.1	16	PDB header: signaling protein Chain: A; PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the <i>P. aeruginosa</i> soluble2 receptor aer2
15	c5u0pU_	Alignment		88.8	8	PDB header: transcription Chain: U; PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
16	c3zx6A_	Alignment		88.7	9	PDB header: signaling Chain: A; PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
17	c2ch7A_	Alignment		88.2	13	PDB header: chemotaxis Chain: A; PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from <i>Thermotoga maritima</i>
18	c6e6aB_	Alignment		87.4	17	PDB header: protein binding Chain: B; PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
19	c1deqF_	Alignment		84.5	10	PDB header: blood clotting Chain: F; PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
20	c2ieqC_	Alignment		84.1	11	PDB header: viral protein Chain: C; PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus n163 spike2 glycoprotein
21	d1ykhb1	Alignment	not modelled	83.1	10	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
22	c2j5uB_	Alignment	not modelled	82.9	30	PDB header: cell shape regulation Chain: B; PDB Molecule: mreC protein; PDBTitle: mreC <i>listeria monocytogenes</i>
23	d1st6a4	Alignment	not modelled	80.3	16	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
24	c6b7nC_	Alignment	not modelled	80.3	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
25	c4abxB_	Alignment	not modelled	79.7	13	PDB header: dna binding protein Chain: B; PDB Molecule: dna repair protein recN; PDBTitle: crystal structure of <i>Deinococcus radiodurans</i> recN coiled-2 coil domain
26	c2d4yA_	Alignment	not modelled	79.3	11	PDB header: structural protein Chain: A; PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
27	c2qf4A_	Alignment	not modelled	76.6	19	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)
28	c2vs0B_	Alignment	not modelled	75.8	15	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxA; PDBTitle: structural analysis of homodimeric <i>Staphylococcus aureus</i> 2 virulence factor esxA

29	c1bf5A	Alignment	not modelled	75.5	9	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
30	c4e40A	Alignment	not modelled	75.1	7	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
31	d1eq1a	Alignment	not modelled	74.6	10	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
32	c6gy6Q	Alignment	not modelled	74.0	9	PDB header: toxin Chain: Q: PDB Molecule: xaxa; PDBTitle: xaxab pore complex from xenorhabdus nematophila
33	c2kbbA	Alignment	not modelled	74.0	15	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
34	c1ei3C	Alignment	not modelled	73.1	9	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
35	c2yfaA	Alignment	not modelled	73.0	16	PDB header: receptor Chain: A: PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
36	c2qihA	Alignment	not modelled	72.5	11	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
37	c2wpgA	Alignment	not modelled	71.8	9	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)
38	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/ap1c complex
39	c5wwlN	Alignment	not modelled	70.8	15	PDB header: cell cycle Chain: N: PDB Molecule: kinetochore protein nfn1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
40	c1ei3E	Alignment	not modelled	67.4	5	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
41	c1bg1A	Alignment	not modelled	67.3	14	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
42	c3euhB	Alignment	not modelled	65.9	8	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
43	c6grjG	Alignment	not modelled	65.5	9	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.
44	c5szsC	Alignment	not modelled	65.4	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
45	d1st6a3	Alignment	not modelled	64.7	11	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
46	c6gaoC	Alignment	not modelled	63.5	7	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
47	c1deqO	Alignment	not modelled	63.1	7	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
48	c2nrjA	Alignment	not modelled	63.1	8	PDB header: toxin Chain: A: PDB Molecule: hbl b protein; PDBTitle: crystal structure of hemolysin binding component from2 bacillus cereus
49	c5zhyA	Alignment	not modelled	62.7	12	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
50	d1st6a5	Alignment	not modelled	62.6	11	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
51	c6ezvX	Alignment	not modelled	61.7	11	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component l1; PDBTitle: the cytotoxin maka from vibrio cholerae
52	c1wywB	Alignment	not modelled	61.6	7	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
53	c6gapB	Alignment	not modelled	61.5	11	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
54	c2dnxA	Alignment	not modelled	61.1	11	PDB header: transport protein Chain: A: PDB Molecule: syntaxin-12; PDBTitle: solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
						PDB header: signaling protein

55	c1kmiZ_	Alignment	not modelled	59.5	13	Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
56	c4iogD_	Alignment	not modelled	59.3	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
57	c5n76C_	Alignment	not modelled	59.1	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
58	c3vkhA_	Alignment	not modelled	58.7	6	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
59	d1szia_	Alignment	not modelled	58.5	10	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
60	c2j9wB_	Alignment	not modelled	56.5	12	PDB header: protein transport Chain: B: PDB Molecule: vps28-prov protein; PDBTitle: structural insight into the escrt-ii link and its role in mvb2 trafficking
61	d2j9ua1	Alignment	not modelled	56.3	10	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like
62	c5lp5F_	Alignment	not modelled	55.9	16	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
63	c3ghgl_	Alignment	not modelled	52.6	10	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
64	c5c3lC_	Alignment	not modelled	52.5	10	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup62; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
65	c5dfzA_	Alignment	not modelled	51.9	9	PDB header: transferase Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 38; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
66	c6o7ua_	Alignment	not modelled	51.7	11	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
67	c3ur1C_	Alignment	not modelled	51.6	6	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.
68	c5x5bB_	Alignment	not modelled	51.6	14	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
69	c6nzkB_	Alignment	not modelled	51.5	14	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
70	d1h9ra2	Alignment	not modelled	51.2	19	Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
71	c6gajA_	Alignment	not modelled	50.9	5	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail (iodide)
72	c3gvmA_	Alignment	not modelled	50.7	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
73	c5i08A_	Alignment	not modelled	50.6	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
74	c2l81A_	Alignment	not modelled	50.5	11	PDB header: cell adhesion Chain: A: PDB Molecule: enhancer of filamentation 1; PDBTitle: solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
75	d1quua1	Alignment	not modelled	50.3	12	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
76	c3zbcC_	Alignment	not modelled	50.0	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
77	d1t98a2	Alignment	not modelled	49.6	15	Fold: STAT-like Superfamily: MukF C-terminal domain-like Family: MukF C-terminal domain-like
78	c1yv1B_	Alignment	not modelled	49.1	9	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
79	c2dq3A_	Alignment	not modelled	49.0	10	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
80	c5xlrC_	Alignment	not modelled	47.4	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein

81	c5x5fC	Alignment	not modelled	47.4	10	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
82	c2ql2B	Alignment	not modelled	47.3	17	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
83	c6o7xa	Alignment	not modelled	45.7	14	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
84	c6nb3B	Alignment	not modelled	45.4	14	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
85	c3dyjA	Alignment	not modelled	45.0	11	PDB header: structural protein Chain: A: PDB Molecule: stalin-1; PDBTitle: crystal structure a talin rod fragment
86	c5cwsj	Alignment	not modelled	44.8	8	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
87	c6cs2A	Alignment	not modelled	44.8	14	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
88	c6gy8B	Alignment	not modelled	44.5	6	PDB header: toxin Chain: B: PDB Molecule: xaxa; PDBTitle: crystal structure of xaxa from xenorhabdus nematophila
89	c6cv0C	Alignment	not modelled	44.3	7	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
90	d2cp6a1	Alignment	not modelled	43.9	17	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
91	c5cwsC	Alignment	not modelled	43.7	6	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
92	c1quuA	Alignment	not modelled	43.3	12	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
93	c3ghgK	Alignment	not modelled	42.3	6	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
94	c3jclC	Alignment	not modelled	42.3	9	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
95	c4fiuC	Alignment	not modelled	42.0	12	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
96	c5t58B	Alignment	not modelled	41.7	13	PDB header: cell cycle Chain: B: PDB Molecule: kla0e05809p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
97	c5j65A	Alignment	not modelled	41.6	12	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
98	c4rh7A	Alignment	not modelled	41.5	2	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
99	d1guta	Alignment	not modelled	38.7	32	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
100	d1h9ma2	Alignment	not modelled	38.4	28	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
101	c5gasN	Alignment	not modelled	38.3	7	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
102	c6ewyA	Alignment	not modelled	38.3	14	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
103	c4f7gB	Alignment	not modelled	37.9	14	PDB header: cell adhesion Chain: B: PDB Molecule: stalin-1; PDBTitle: crystal structure of talin autoinhibition complex
104	c2q13A	Alignment	not modelled	37.7	10	PDB header: protein transport Chain: A: PDB Molecule: dcc-interacting protein 13 alpha; PDBTitle: crystal structure of bar-ph domain of appl1
105	c5wrgB	Alignment	not modelled	37.3	9	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
106	c4lwsA	Alignment	not modelled	36.9	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora

						curvata
107	c5jxpA_	Alignment	not modelled	36.8	8	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
108	c6flnE_	Alignment	not modelled	36.5	7	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspry domains
109	c1mg1A_	Alignment	not modelled	36.0	17	PDB header: viral protein Chain: A: PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose-binding protein PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera
110	c3nwiC_	Alignment	not modelled	35.8	13	PDB header: transport protein Chain: C: PDB Molecule: zinc transport protein zntb; PDBTitle: the soluble domain structure of the zntb zn2+ efflux system
111	c5y2gA_	Alignment	not modelled	35.5	15	PDB header: toxin Chain: A: PDB Molecule: maltose-binding periplasmic protein,protein b; PDBTitle: structure of mbp tagged gbs camp
112	c1t98B_	Alignment	not modelled	34.9	8	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of mukf(1-287)
113	d2uubl1	Alignment	not modelled	34.5	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
114	c3j6vL_	Alignment	not modelled	34.5	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
115	c3bt6B_	Alignment	not modelled	33.2	5	PDB header: viral protein Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
116	c2wr2B_	Alignment	not modelled	33.2	7	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
117	c4xa3A_	Alignment	not modelled	32.8	8	PDB header: motor protein Chain: A: PDB Molecule: gp7-myh7(1361-1425)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 2 of myh7
118	d1u5pa1	Alignment	not modelled	32.1	8	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
119	c2iakA_	Alignment	not modelled	32.0	9	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)
120	c1zn1L_	Alignment	not modelled	31.9	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-termination2 complex