
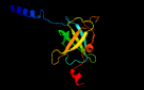



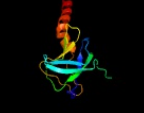











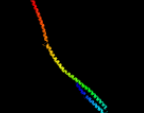

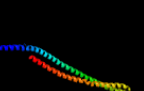

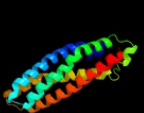
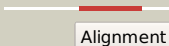
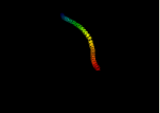



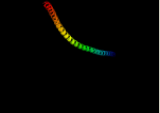


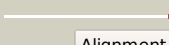
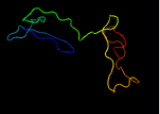

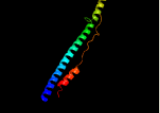



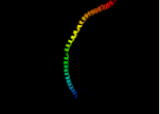


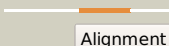

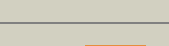
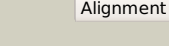
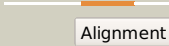
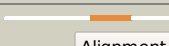




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0591_(mce2C)_689062_690507
 Date Fri Jul 26 01:50:15 BST 2019
 Unique Job ID 76fdbcfb7be78ac7

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		99.7	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	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
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	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
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		96.7	16	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		95.6	11	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c6e6aB_	 Alignment		95.5	15	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant

12	c6gajA_	 Alignment		94.4	17	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)
13	c2ch7A_	 Alignment		94.0	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
14	c2wpgA_	 Alignment		93.9	3	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)
15	c6gapB_	 Alignment		93.3	12	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
16	c4nl6C_	 Alignment		91.8	16	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
17	c1wyyB_	 Alignment		91.6	13	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
18	c2dq3A_	 Alignment		91.5	14	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
19	c1ei3C_	 Alignment		91.3	9	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
20	c1kmiZ_	 Alignment		90.8	11	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
21	c1degF_	 Alignment	not modelled	89.9	13	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
22	c5xbjA_	 Alignment	not modelled	89.9	9	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
23	c3zx6A_	 Alignment	not modelled	89.5	8	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
24	c3lnrA_	 Alignment	not modelled	89.4	10	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
25	c2ieqC_	 Alignment	not modelled	89.1	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
26	c6b7nC_	 Alignment	not modelled	88.2	20	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
27	c5u0pU_	 Alignment	not modelled	88.1	13	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
28	c3cwgA_	 Alignment	not modelled	88.1	10	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment

29	d1eq1a	Alignment	not modelled	87.9	12	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
30	c1deqO	Alignment	not modelled	87.4	15	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
31	c4rh7A	Alignment	not modelled	87.3	12	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	c5dfzA	Alignment	not modelled	87.0	13	PDB header: transferase Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 38; PDBTitle: structure of vps34 complex ii from <i>s. cerevisiae</i> .
33	c3ghgK	Alignment	not modelled	86.1	14	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
34	c1ei3E	Alignment	not modelled	85.0	16	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
35	c3ghgl	Alignment	not modelled	84.8	7	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
36	c4abxB	Alignment	not modelled	84.7	8	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
37	c2p22A	Alignment	not modelled	83.9	6	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast esct-i heterotetramer core
38	c5szsC	Alignment	not modelled	83.2	17	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
39	c3ojaB	Alignment	not modelled	82.0	12	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
40	d1st6a4	Alignment	not modelled	81.0	14	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
41	c4ut1A	Alignment	not modelled	81.0	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
42	c2qihA	Alignment	not modelled	81.0	11	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
43	d1ykhb1	Alignment	not modelled	81.0	9	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
44	c1quuA	Alignment	not modelled	80.8	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
45	c5j65A	Alignment	not modelled	80.4	8	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
46	c6ezvX	Alignment	not modelled	79.7	10	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
47	c2nrjA	Alignment	not modelled	79.1	13	PDB header: toxin Chain: A: PDB Molecule: hbl b protein; PDBTitle: crystal structure of hemolysin binding component from2 bacillus cereus
48	c3j99M	Alignment	not modelled	78.4	8	PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iiib)
49	c5lskD	Alignment	not modelled	77.1	14	PDB header: cell cycle Chain: D: PDB Molecule: kinetochore-associated protein dsn1 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
50	c2efrB	Alignment	not modelled	77.0	11	PDB header: contractile protein Chain: B: PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
51	d1g4us1	Alignment	not modelled	76.0	19	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
52	c6gaoC	Alignment	not modelled	75.5	12	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
53	c3vkhA	Alignment	not modelled	75.3	15	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
						PDB header: structural protein/hydrolase

54	c4a7fB_	Alignment	not modelled	74.8	8	Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
55	c6gy8B_	Alignment	not modelled	74.6	12	PDB header: toxin Chain: B: PDB Molecule: xaxa; PDBTitle: crystal structure of xaxa from xenorhabdus nematophila
56	c4ll7C_	Alignment	not modelled	73.7	17	PDB header: transport protein Chain: C: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: structure of she3p amino terminus.
57	c5x5bB_	Alignment	not modelled	72.9	17	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
58	c2gl2B_	Alignment	not modelled	71.6	16	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
59	c5nmoA_	Alignment	not modelled	70.2	12	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
60	c4wsrA_	Alignment	not modelled	70.0	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
61	c6grjG_	Alignment	not modelled	69.7	20	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.
62	c5xlrC_	Alignment	not modelled	69.5	17	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
63	c6nzkB_	Alignment	not modelled	68.3	18	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
64	c5cwsC_	Alignment	not modelled	67.8	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
65	c2d4yA_	Alignment	not modelled	66.7	11	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
66	c5i08A_	Alignment	not modelled	66.7	17	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
67	c5cwsJ_	Alignment	not modelled	66.5	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
68	c4n21E_	Alignment	not modelled	66.3	15	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
69	c6nb3B_	Alignment	not modelled	65.8	15	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
70	c2dq0A_	Alignment	not modelled	64.8	13	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
71	c5gasN_	Alignment	not modelled	64.5	14	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
72	c5wrgB_	Alignment	not modelled	63.8	17	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
73	c3jclC_	Alignment	not modelled	63.8	20	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
74	c2l81A_	Alignment	not modelled	63.5	15	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	c6cv0C_	Alignment	not modelled	63.4	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
76	c2j9wB_	Alignment	not modelled	62.5	12	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
77	c4lwsB_	Alignment	not modelled	61.8	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
78	c6cs2A_	Alignment	not modelled	61.6	16	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
79	c5mo8B_	Alignment	not modelled	61.6	15	PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes

79	c3imgbB_	Alignment	not modelled	61.8	13	protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
80	c3i9yA_	Alignment	not modelled	61.4	14	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the v. parahaemolyticus histidine kinase sensor2 tors sensor domain
81	c4fiuC_	Alignment	not modelled	61.3	12	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
82	d1hcia4	Alignment	not modelled	61.2	9	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
83	c2b9cA_	Alignment	not modelled	59.8	15	PDB header: contractile protein Chain: A: PDB Molecule: striated-muscle alpha tropomyosin; PDBTitle: structure of tropomyosin's mid-region: bending and binding sites for2 actin
84	c5lp5F_	Alignment	not modelled	59.4	33	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
85	c5yfpD_	Alignment	not modelled	58.4	19	PDB header: exocytosis Chain: D: PDB Molecule: exocyst complex component sec8; PDBTitle: cryo-em structure of the exocyst complex
86	c4e40A_	Alignment	not modelled	58.1	13	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
87	c2xzaA_	Alignment	not modelled	56.4	7	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
88	c5j9qH_	Alignment	not modelled	56.2	13	PDB header: transferase Chain: H: PDB Molecule: chromatin modification-related protein yng2; PDBTitle: crystal structure of the nua4 core complex
89	c4iogD_	Alignment	not modelled	56.2	8	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
90	d2j9ua1	Alignment	not modelled	56.1	14	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like
91	c2fxmB_	Alignment	not modelled	56.0	15	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
92	c3gvmA_	Alignment	not modelled	55.6	16	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
93	c2wr2B_	Alignment	not modelled	54.2	15	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
94	c3pe0B_	Alignment	not modelled	54.0	12	PDB header: structural protein Chain: B: PDB Molecule: plectin; PDBTitle: structure of the central region of the plakin domain of plectin
95	c1mg1A_	Alignment	not modelled	53.6	9	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
96	c6iiaA_	Alignment	not modelled	53.6	13	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
97	c2j5uB_	Alignment	not modelled	53.5	16	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
98	c6h9xA_	Alignment	not modelled	53.3	15	PDB header: ligase Chain: A: PDB Molecule: serine--trna ligase; PDBTitle: klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
99	c6gy6Q_	Alignment	not modelled	53.3	11	PDB header: toxin Chain: Q: PDB Molecule: xaxa; PDBTitle: xaxab pore complex from xenorhabdus nematophila
100	c3dtpA_	Alignment	not modelled	52.6	14	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain chimera of smooth and cardiac muscle; PDBTitle: tarantula heavy meromyosin obtained by flexible docking to tarantula2 muscle thick filament cryo-em 3d-map
101	c6j9rA_	Alignment	not modelled	52.6	10	PDB header: translation Chain: A: PDB Molecule: brain tumor protein; PDBTitle: coiled-coil domain of drosophila trim protein brat
102	c2dnxA_	Alignment	not modelled	52.5	16	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
103	c2ld3A_	Alignment	not modelled	51.5	17	PDB header: motor protein Chain: A: PDB Molecule: myosin vi; PDBTitle: solution structure of myosin vi lever arm extension
104	c2vs0B_	Alignment	not modelled	51.2	17	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
						PDB header: viral protein

105	c3bt6B_	Alignment	not modelled	50.7	5	Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
106	c5zhyA_	Alignment	not modelled	49.2	8	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
107	c3uunA_	Alignment	not modelled	49.0	14	PDB header: structural protein Chain: A: PDB Molecule: dystrophin; PDBTitle: crystal structure of n-terminal first spectrin repeat of dystrophin
108	c1u5pA_	Alignment	not modelled	48.9	10	PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: crystal structure of repeats 15 and 16 of chicken brain2 alpha spectrin
109	c4xa3A_	Alignment	not modelled	48.2	10	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
110	c3uulB_	Alignment	not modelled	48.0	13	PDB header: structural protein Chain: B: PDB Molecule: utrophin; PDBTitle: crystal structure of first n-terminal utrophin spectrin repeat
111	c4mc5C_	Alignment	not modelled	47.9	16	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of a subtype h18 hemagglutinin homologue from 2 a/flat-faced bat/peru/033/2010 (h18n11)
112	c2d3eD_	Alignment	not modelled	47.8	8	PDB header: contractile protein Chain: D: PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
113	c3lxbB_	Alignment	not modelled	47.4	19	PDB header: structural protein Chain: B: PDB Molecule: spectrin beta chain, erythrocyte; PDBTitle: crystal structure of the erythrocyte spectrin tetramerization domain2 complex
114	c3o4xF_	Alignment	not modelled	47.0	12	PDB header: protein binding Chain: F: PDB Molecule: protein diaphanous homolog 1; PDBTitle: crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
115	c3o4xE_	Alignment	not modelled	47.0	12	PDB header: protein binding Chain: E: PDB Molecule: protein diaphanous homolog 1; PDBTitle: crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
116	c6g7oA_	Alignment	not modelled	46.7	13	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
117	c3zbcC_	Alignment	not modelled	46.5	17	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
118	c2d3fD_	Alignment	not modelled	45.9	50	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
119	c1x1kC_	Alignment	not modelled	45.9	50	PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
120	c2d3ff_	Alignment	not modelled	45.9	50	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4