

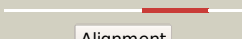

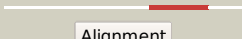

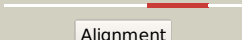

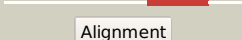



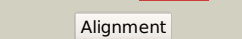

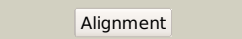

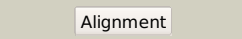

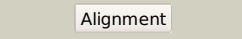

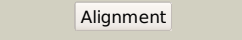



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1477_(-)_1666996_1668414
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	ebd05da4b24ac340

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xivA_	 Alignment		100.0	97	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
2	c3pbiA_	 Alignment		100.0	65	PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
3	c3gt2A_	 Alignment		100.0	59	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
4	c3i86A_	 Alignment		100.0	68	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
5	c6biqA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: clan ca, family c40, nlp/p60 superfamily cysteine PDBTitle: structure of nlp2 from trichomonas vaginalis
6	c2fg0B_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
7	c4fdyA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: similar to lipoprotein, nlp/p60 family; PDBTitle: crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
8	d2evra2	 Alignment		100.0	27	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
9	c3h41A_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
10	c3nfpB_	 Alignment		100.0	38	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
11	c4hpeA_	 Alignment		99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: putative cell wall hydrolase tn916-like,ctn1-orf17; PDBTitle: crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution

12	c6b8cA_	Alignment		99.9	39	PDB header: hydrolase Chain: A; PDB Molecule: nlp/p60; PDBTitle: crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga
13	c2k1gA_	Alignment		99.9	28	PDB header: lipoprotein Chain: A; PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
14	c4xcmB_	Alignment		99.9	24	PDB header: hydrolase Chain: B; PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlp/p60 d,l endopeptidase from t.2 thermophilus
15	c3m1uB_	Alignment		99.8	25	PDB header: hydrolase Chain: B; PDB Molecule: putative gamma-d-glutamyl-l-diamino acid endopeptidase; PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dву_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
16	c4cggA_	Alignment		99.5	15	PDB header: cell cycle Chain: A; PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
17	c2p1gA_	Alignment		99.2	29	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative xylanase; PDBTitle: crystal structure of a putative xylanase from bacteroides fragilis
18	c6ewyA_	Alignment		99.0	100	PDB header: structural protein Chain: A; PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
19	c5ew5C_	Alignment		98.2	13	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
20	c2kytA_	Alignment		97.9	26	PDB header: hydrolase Chain: A; PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
21	c2lktA_	Alignment	not modelled	97.6	29	PDB header: hydrolase Chain: A; PDB Molecule: retinoic acid receptor responder protein 3; PDBTitle: solution structure of n-terminal domain of human tig3 in 2 m urea
22	c6gaoC_	Alignment	not modelled	97.5	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
23	c3kw0D_	Alignment	not modelled	97.3	24	PDB header: hydrolase Chain: D; PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
24	c3ojaB_	Alignment	not modelled	97.1	12	PDB header: protein binding Chain: B; PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
25	c6o7xa_	Alignment	not modelled	97.1	10	PDB header: membrane protein Chain: A; PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
26	c2lrjA_	Alignment	not modelled	97.0	28	PDB header: biosynthetic protein Chain: A; PDB Molecule: staphyloxanthin biosynthesis protein, putative; PDBTitle: nmr solution structure of staphyloxanthin biosynthesis protein
27	c5xg2A_	Alignment	not modelled	96.9	13	PDB header: dna binding protein Chain: A; PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of a coiled-coil segment (residues 345-468 and 694-2 814) of pyrococcus yayanosii smc
28	c2i1kA_	Alignment	not modelled	96.9	12	PDB header: cell adhesion, membrane protein Chain: A; PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution

29	c6ogdB	Alignment	not modelled	96.9	10	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
30	c5cwsj	Alignment	not modelled	96.8	13	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
31	c2k3aA	Alignment	not modelled	96.8	31	PDB header: hydrolase Chain: A: PDB Molecule: chap domain protein; PDBTitle: nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
32	c3vkgA	Alignment	not modelled	96.8	6	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
33	c6gapB	Alignment	not modelled	96.6	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
34	c5wjbA	Alignment	not modelled	96.5	6	PDB header: actin/dna binding protein Chain: A: PDB Molecule: capsid assembly scaffolding protein,myosin-7; PDBTitle: crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
35	c6gajA	Alignment	not modelled	96.5	13	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)
36	c3ojaA	Alignment	not modelled	96.3	13	PDB header: protein binding Chain: A: PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/apl1c complex
37	c2efrB	Alignment	not modelled	96.2	10	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
38	c4olkB	Alignment	not modelled	96.2	12	PDB header: hydrolase Chain: B: PDB Molecule: endolysin; PDBTitle: the chap domain of lysgh15
39	d2if6a1	Alignment	not modelled	96.2	15	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Yiix-like
40	c3vkgB	Alignment	not modelled	96.2	9	PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
41	c5t1qB	Alignment	not modelled	96.1	24	PDB header: hydrolase Chain: B: PDB Molecule: n-acetylmuramoyl-l-alanine amidase domain-containing PDBTitle: 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus.
42	c5goxB	Alignment	not modelled	96.1	12	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad50; PDBTitle: eukaryotic rad50 functions as a rod-shaped dimer
43	c5udmA	Alignment	not modelled	96.1	26	PDB header: hydrolase Chain: A: PDB Molecule: phage-associated cell wall hydrolase; PDBTitle: phage-associated cell wall hydrolase plpy from streptococcus2 pyogenes, space group p6522
44	c1bg1A	Alignment	not modelled	96.1	7	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
45	c1bf5A	Alignment	not modelled	95.9	7	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
46	c4iloA	Alignment	not modelled	95.9	11	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
47	c3q8tB	Alignment	not modelled	95.9	9	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
48	c4hzbA	Alignment	not modelled	95.8	31	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
49	c6o7ua	Alignment	not modelled	95.8	8	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
50	c6f1tx	Alignment	not modelled	95.7	9	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1,bicd family-like cargo PDBTitle: cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
51	c6f1tX	Alignment	not modelled	95.6	9	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1,bicd family-like cargo PDBTitle: cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
52	c4i1bB	Alignment	not modelled	95.6	4	PDB header: signaling protein/transferase/inhibitor Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha complexed with nish2 of

						p85alpha
53	c4rh7A_	Alignment	not modelled	95.5	17	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
54	c5nmoA_	Alignment	not modelled	95.5	6	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
55	c3u59C_	Alignment	not modelled	95.3	9	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
56	c3na7A_	Alignment	not modelled	95.3	9	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
57	c6a9pD_	Alignment	not modelled	95.3	9	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
58	c1c1gA_	Alignment	not modelled	95.3	11	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
59	c1jchC_	Alignment	not modelled	95.2	11	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
60	c3ghgK_	Alignment	not modelled	95.1	10	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
61	c3cwgA_	Alignment	not modelled	95.1	7	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
62	c6e2jB_	Alignment	not modelled	95.0	6	PDB header: protein fibril Chain: B: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s233l mutation and wild-type human keratin 10 coil 1b
63	c1ei3C_	Alignment	not modelled	95.0	8	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
64	c2gl2B_	Alignment	not modelled	94.8	10	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
65	c2v71A_	Alignment	not modelled	94.8	11	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
66	c1ciiA_	Alignment	not modelled	94.8	12	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
67	c6djlE_	Alignment	not modelled	94.6	10	PDB header: signaling protein/protein transport Chain: E: PDB Molecule: sh3 domain-binding protein 5; PDBTitle: crystal structure of the rab11 gef sh3bp5 bound to nucleotide free2 rab11a
68	c5cwsC_	Alignment	not modelled	94.6	7	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
69	c3ghgl_	Alignment	not modelled	94.5	3	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
70	c5cwsE_	Alignment	not modelled	94.5	8	PDB header: protein transport Chain: E: PDB Molecule: nucleoporin nup57; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
71	c4gkwB_	Alignment	not modelled	94.4	11	PDB header: structural protein Chain: B: PDB Molecule: spindle assembly abnormal protein 6; PDBTitle: crystal structure of the coiled-coil domain of c. elegans sas-6
72	c6ec0A_	Alignment	not modelled	94.4	11	PDB header: protein fibril Chain: A: PDB Molecule: keratin 1; PDBTitle: crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10)
73	c2fxmB_	Alignment	not modelled	94.3	7	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
74	c1y4cA_	Alignment	not modelled	94.2	9	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
75	c2d3eD_	Alignment	not modelled	94.1	7	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
76	c4xa3A_	Alignment	not modelled	93.9	4	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

77	c2im9A	Alignment	not modelled	93.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
78	d2im9a1	Alignment	not modelled	93.9	22	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Lpg0564-like
79	c5voxb	Alignment	not modelled	93.7	7	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
80	c4h4jA	Alignment	not modelled	93.6	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a n-acetylmuramoyl-l-alanine amidase2 (bacuni_02947) from bacteroides uniformis atcc 8492 at 1.15 a3 resolution
81	c3o11A	Alignment	not modelled	93.4	11	PDB header: structural protein Chain: A: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
82	c4f4mA	Alignment	not modelled	93.3	20	PDB header: hydrolase regulator Chain: A: PDB Molecule: papain peptidoglycan amidase effector tse1; PDBTitle: structure of the type vi peptidoglycan amidase effector tse1 (c30a)2 from pseudomonas aeruginosa
83	c1yv1B	Alignment	not modelled	93.3	7	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
84	c1ei3E	Alignment	not modelled	93.2	12	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
85	c3hnwB	Alignment	not modelled	93.1	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
86	c3swkB	Alignment	not modelled	93.1	12	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
87	c5y06A	Alignment	not modelled	93.0	12	PDB header: unknown function Chain: A: PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
88	c4f0wA	Alignment	not modelled	92.8	20	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of type effector tse1 c30a mutant from pseudomonas2 aeruginosa
89	c5nenB	Alignment	not modelled	92.8	10	PDB header: hydrolase Chain: B: PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
90	d2io8a2	Alignment	not modelled	92.8	16	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: CHAP domain
91	c3o0zD	Alignment	not modelled	92.8	10	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
92	c4xa1D	Alignment	not modelled	92.7	12	PDB header: motor protein Chain: D: PDB Molecule: gp7-myh7(1173-1238)-eb1 chimera protein; PDBTitle: crystal structure of the coiled-coil surrounding skip 1 of myh7
93	c4a7fB	Alignment	not modelled	92.5	8	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
94	c5bu8A	Alignment	not modelled	92.4	8	PDB header: viral protein Chain: A: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystalized at ph 7.5 and derivatized with xenon
95	c4ll8E	Alignment	not modelled	91.6	9	PDB header: motor protein/transport protein Chain: E: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: complex of carboxy terminal domain of myo4p and she3p middle fragment
96	c5gasN	Alignment	not modelled	91.6	9	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
97	c5jxfA	Alignment	not modelled	91.4	6	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
98	c2ocyB	Alignment	not modelled	90.9	15	PDB header: endocytosis/exocytosis Chain: B: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: complex of the guanine exchange factor sec2p and the rab gtpase sec4p
99	c3ipkA	Alignment	not modelled	90.7	16	PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
100	c5ijnT	Alignment	not modelled	90.5	5	PDB header: transport protein Chain: T: PDB Molecule: nuclear pore glycoprotein p62; PDBTitle: composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
101	c4fmyE	Alignment	not modelled	90.5	11	PDB header: viral protein Chain: E: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystal form i

102	c4zryA_	Alignment	not modelled	90.3	15	PDB header: protein fibril Chain: A: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of 2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
103	c4rfxA_	Alignment	not modelled	90.1	14	PDB header: protein transport Chain: A: PDB Molecule: dynactin subunit 1; PDBTitle: crystal structure of the dynactin dctn1 fragment involved in dynein2 interaction
104	c1deqO_	Alignment	not modelled	90.1	4	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
105	c4eyzB_	Alignment	not modelled	90.1	50	PDB header: hydrolase Chain: B: PDB Molecule: cellulosome-related protein module from ruminococcus PDBTitle: crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases
106	c3tnuB_	Alignment	not modelled	90.1	10	PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
107	c2qjhA_	Alignment	not modelled	89.9	15	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
108	c5mg8B_	Alignment	not modelled	89.8	9	PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
109	c6flnE_	Alignment	not modelled	89.6	6	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspy domains
110	c4rsiB_	Alignment	not modelled	89.3	8	PDB header: cell cycle Chain: B: PDB Molecule: structural maintenance of chromosomes protein 4; PDBTitle: yeast smc2-smc4 hinge domain with extended coiled coils
111	c3vkhD_	Alignment	not modelled	88.9	10	PDB header: motor protein Chain: D: PDB Molecule: PDBTitle: x-ray structure of a functional full-length dynein motor domain
112	c4pa5A_	Alignment	not modelled	88.7	19	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: tgl - a bacterial spore coat transglutaminase - cystamine complex
113	c1deqF_	Alignment	not modelled	88.7	7	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
114	c5j1iA_	Alignment	not modelled	88.2	10	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: structure of the spectrin repeats 7, 8, and 9 of the plakin domain of 2 plectin
115	c3g67A_	Alignment	not modelled	88.1	9	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
116	c5dfzD_	Alignment	not modelled	88.1	7	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
117	c5tvbB_	Alignment	not modelled	88.1	9	PDB header: transferase Chain: B: PDB Molecule: nucleoprotein tpr; PDBTitle: structure of the tpr oligomerization domain
118	c3woiB_	Alignment	not modelled	87.9	8	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
119	c3dtpA_	Alignment	not modelled	87.8	7	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
120	c2zv4O_	Alignment	not modelled	87.1	13	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution