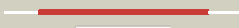
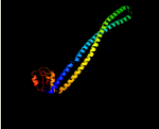







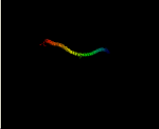

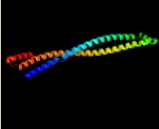
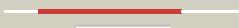
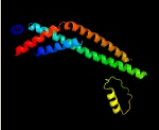
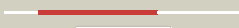
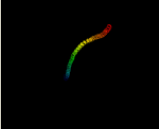



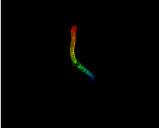

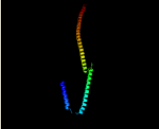


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2229c_(-)_2502743_2503480
Date	Mon Aug 5 13:25:36 BST 2019
Unique Job ID	185f4d98f92c5fae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5y06A_	 Alignment		100.0	60	PDB header: unknown function Chain: A; PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
2	c4iloA_	 Alignment		100.0	18	PDB header: unknown function Chain: A; PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
3	c3na7A_	 Alignment		100.0	16	PDB header: gene regulation, chaperone Chain: A; PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
4	c6gapB_	 Alignment		97.8	14	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
5	c6gaoC_	 Alignment		97.6	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
6	c4cglA_	 Alignment		97.3	12	PDB header: cell cycle Chain: A; PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
7	c6o7xa_	 Alignment		97.2	15	PDB header: membrane protein Chain: A; PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
8	c6gajA_	 Alignment		97.2	12	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)
9	c4l1bB_	 Alignment		97.2	14	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
10	c2d3eD_	 Alignment		97.1	17	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
11	c3ojaA_	 Alignment		97.1	13	PDB header: protein binding Chain: A; PDB Molecule: leucine-rich immune molecule 1; PDBTitle: crystal structure of lrim1/ap1c complex

12	c2efrB_	Alignment		96.9	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- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
13	c5ew5C_	Alignment		96.9	10	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
14	c3o0zD_	Alignment		96.6	13	PDB header: transferase Chain: D: PDB Molecule: rho-associated protein kinase 1; PDBTitle: crystal structure of a coiled-coil domain from human rock i
15	c4gkwB_	Alignment		96.5	14	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
16	c4a7fB_	Alignment		96.5	14	PDB header: structural protein/hydrolase Chain: B: PDB Molecule: tropomyosin 1 alpha; PDBTitle: structure of the actin-tropomyosin-myosin complex (rigor atm 3)
17	c3ojaB_	Alignment		96.3	13	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
18	c1bf5A_	Alignment		96.2	9	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
19	c5cwsJ_	Alignment		96.1	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
20	c5xg2A_	Alignment		95.8	11	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
21	c5gasN_	Alignment	not modelled	95.6	20	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
22	c2fxmB_	Alignment	not modelled	95.5	13	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, cardiac muscle beta isoform; PDBTitle: structure of the human beta-myosin s2 fragment
23	c5nmoA_	Alignment	not modelled	95.5	10	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
24	c5ijnF_	Alignment	not modelled	95.3	11	PDB header: transport protein Chain: F: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
25	c4a55B_	Alignment	not modelled	95.0	15	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
26	c3vkgA_	Alignment	not modelled	94.9	11	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
27	c2y3aB_	Alignment	not modelled	94.6	12	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit beta; PDBTitle: crystal structure of p110beta in complex with icsh2 of p85beta and the2 drug gdc-0941
						PDB header: actin/dna binding protein Chain: A: PDB Molecule: capsid assembly scaffolding

28	c5wjba_	Alignment	not modelled	94.6	10	protein,myosin-7; PDBTitle: crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
29	c4xa3A_	Alignment	not modelled	94.3	15	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
30	c1jchC_	Alignment	not modelled	94.2	9	PDB header: ribosome inhibitor, hydrolase Chain: C: PDB Molecule: colicin e3; PDBTitle: crystal structure of colicin e3 in complex with its immunity protein
31	c6ewyA_	Alignment	not modelled	94.1	16	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
32	c1bg1A_	Alignment	not modelled	94.0	11	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
33	c6e2jB_	Alignment	not modelled	93.9	10	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
34	c6a9pD_	Alignment	not modelled	93.8	14	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
35	c5cwsC_	Alignment	not modelled	93.8	13	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
36	c3hizB_	Alignment	not modelled	93.7	13	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: crystal structure of p110alpha h1047r mutant in complex with nish2 of2 p85alpha
37	c4zryA_	Alignment	not modelled	93.5	13	PDB header: protein fibril Chain: A: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
38	c1degF_	Alignment	not modelled	93.5	9	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
39	c3vkgB_	Alignment	not modelled	93.5	10	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
40	c2b9cA_	Alignment	not modelled	93.3	8	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
41	c1c1gA_	Alignment	not modelled	93.3	16	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
42	c6o7ua_	Alignment	not modelled	93.2	7	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
43	c3cwgA_	Alignment	not modelled	93.1	12	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
44	c6mi3A_	Alignment	not modelled	92.8	11	PDB header: transcription Chain: A: PDB Molecule: nf-kb essential modulator,nf-kappa-b essential modulator, PDBTitle: structure of nemo(51-112) with n- and c-terminal coiled-coil adaptors.
45	c5ijnT_	Alignment	not modelled	92.8	9	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)
46	c2v1yB_	Alignment	not modelled	92.6	14	PDB header: transferase Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
47	c3dtpA_	Alignment	not modelled	92.6	15	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
48	c5nenB_	Alignment	not modelled	92.5	15	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
49	c3u59C_	Alignment	not modelled	92.2	14	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
50	c3ol1A_	Alignment	not modelled	92.0	13	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
						PDB header: protein fibril Chain: A: PDB Molecule: keratin 1;

51	c6ec0A_	Alignment	not modelled	91.9	12	PDBTitle: crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10) 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 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
52	c5cwsE_	Alignment	not modelled	91.2	13	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear distribution protein nude-like 1; PDBTitle: coiled-coil region of nudel
53	c4ll8E_	Alignment	not modelled	91.2	7	PDB header: cell cycle Chain: B: PDB Molecule: structural maintenance of chromosomes protein 4; PDBTitle: yeast smc2-smc4 hinge domain with extended coiled coils PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
54	c2v71A_	Alignment	not modelled	91.0	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
55	c4rsiB_	Alignment	not modelled	90.9	12	PDB header: cytosolic protein Chain: A: PDB Molecule: intraflagellar transport protein 74; PDBTitle: t. brucei ift22/74/81 gtp-bound crystal structure
56	c5fywW_	Alignment	not modelled	90.9	20	PDB header: apoptosis Chain: B: PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
57	c2ocyB_	Alignment	not modelled	90.8	12	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
58	c6ianA_	Alignment	not modelled	90.7	11	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
59	c3q8tB_	Alignment	not modelled	90.6	13	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
60	c5iy9Q_	Alignment	not modelled	90.2	20	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
61	c5dfzD_	Alignment	not modelled	89.8	12	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
62	c1degO_	Alignment	not modelled	89.7	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
63	c3ghgl_	Alignment	not modelled	89.6	3	PDB header: transferase/oncoprotein Chain: B: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha; PDBTitle: structure of a human p110alpha/p85alpha complex
64	c1ciiA_	Alignment	not modelled	89.6	15	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: structure of the spectrin repeats 7, 8, and 9 of the plakin domain of2 plectin
65	c2gl2B_	Alignment	not modelled	89.3	15	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup62; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
66	c2rd0B_	Alignment	not modelled	89.2	12	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
67	c5jliA_	Alignment	not modelled	88.5	11	PDB header: transcription Chain: W: PDB Molecule: transcription factor tfiie subunit; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
68	c5c3lC_	Alignment	not modelled	88.4	12	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
69	c1y4cA_	Alignment	not modelled	87.9	14	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
70	c5oqmW_	Alignment	not modelled	87.3	20	PDB header: transcription Chain: R: PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
71	c1ei3E_	Alignment	not modelled	87.2	10	PDB header: signaling protein Chain: A: PDB Molecule: phage shock protein a; PDBTitle: crystal structure of e. coli phage shock protein a (pspa 1-144)
72	c5oqjW_	Alignment	not modelled	87.1	20	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
73	c5fmfR_	Alignment	not modelled	86.2	20	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
74	c4wheA_	Alignment	not modelled	86.1	13	PDB header: cell adhesion, membrane protein
75	c6f1tX_	Alignment	not modelled	86.1	11	

76	c2i1kA	Alignment	not modelled	85.7	11	Chain: A: PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
77	c5goxB	Alignment	not modelled	85.6	13	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad50; PDBTitle: eukaryotic rad50 functions as a rod-shaped dimer
78	c3jhbA	Alignment	not modelled	85.6	14	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain striated muscle; PDBTitle: two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
79	c5xonV	Alignment	not modelled	85.5	29	PDB header: transcription/rna Chain: V: PDB Molecule: transcription elongation factor spt4; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tffis
80	c5voxb	Alignment	not modelled	85.5	8	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)
81	c1yvlB	Alignment	not modelled	85.3	6	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
82	c3swkB	Alignment	not modelled	85.2	17	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
83	c2qa7C	Alignment	not modelled	84.6	10	PDB header: actin binding Chain: C: PDB Molecule: huntingtin-interacting protein 1; PDBTitle: crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
84	c5bu8A	Alignment	not modelled	84.5	17	PDB header: viral protein Chain: A: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
85	c5ol0B	Alignment	not modelled	84.3	24	PDB header: hydrolase Chain: B: PDB Molecule: putative silent information regulator 2,putative silent PDBTitle: structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
86	c5tvbB	Alignment	not modelled	84.3	15	PDB header: transferase Chain: B: PDB Molecule: nucleoprotein tpr; PDBTitle: structure of the tpr oligomerization domain
87	c3ghgK	Alignment	not modelled	84.2	11	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
88	c6gymW	Alignment	not modelled	84.1	20	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha, PDBTitle: structure of a yeast closed complex with distorted dna (ccd1st)
89	d1q1aa	Alignment	not modelled	84.0	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
90	c4rfxA	Alignment	not modelled	83.5	14	PDB header: protein transport Chain: A: PDB Molecule: dyactin subunit 1; PDBTitle: crystal structure of the dyactin dctn1 fragment involved in dynein2 interaction
91	c2lcqA	Alignment	not modelled	82.8	23	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
92	c5mg8B	Alignment	not modelled	82.4	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
93	c6g5iy	Alignment	not modelled	81.8	38	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
94	c2d9kA	Alignment	not modelled	81.1	20	PDB header: immune system Chain: A: PDB Molecule: fln29 gene product; PDBTitle: solution structure of the zf-traf domain of fln29 gene2 product
95	c1ei3C	Alignment	not modelled	80.4	12	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
96	c5flmL	Alignment	not modelled	80.3	36	PDB header: transcription Chain: L: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc4; PDBTitle: structure of transcribing mammalian rna polymerase ii
97	c3glsC	Alignment	not modelled	80.2	30	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
98	c2fwtA	Alignment	not modelled	79.6	31	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
99	c6h2xA	Alignment	not modelled	79.6	11	PDB header: dna binding protein Chain: A: PDB Molecule: chromosome partition protein mukb,chromosome partition PDBTitle: mukb coiled-coil elbow from e. coli
100	c2e7sM	Alignment	not modelled	79.4	14	PDB header: endocytosis/exocytosis Chain: M: PDB Molecule: rab guanine nucleotide exchange factor sec2; PDBTitle: crystal structure of the yeast sec2p gef domain PDB header: contractile protein

101	c4pd3B_	Alignment	not modelled	79.3	10	Chain: B: PDB Molecule: nonmuscle myosin heavy chain b, alpha-actinin a chimera PDBTitle: crystal structure of rigor-like human nonmuscle myosin-2b
102	c3u99A_	Alignment	not modelled	79.0	31	PDB header: electron transport Chain: A: PDB Molecule: diheme cytochrome c; PDBTitle: the experimental x-ray structure of the new diheme cytochrome type c2 from shewanella baltica os155 sb-dhc
103	c3h7hA_	Alignment	not modelled	78.7	22	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
104	c2y0fD_	Alignment	not modelled	78.2	46	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
105	c4xa1D_	Alignment	not modelled	77.9	16	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
106	c1q14A_	Alignment	not modelled	77.6	20	PDB header: hydrolase Chain: A: PDB Molecule: hst2 protein; PDBTitle: structure and autoregulation of the yeast hst2 homolog of sir2
107	c2lo2A_	Alignment	not modelled	77.4	25	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 11; PDBTitle: solution structure of sgf11(63-99) zinc finger domain
108	c3vkhA_	Alignment	not modelled	77.2	11	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
109	c5tbyA_	Alignment	not modelled	76.2	12	PDB header: contractile protein Chain: A: PDB Molecule: myosin-7; PDBTitle: human beta cardiac heavy meromyosin interacting-heads motif obtained2 by homology modeling (using swiss-model) of human sequence from3 aphonopelma homology model (pdb-3jhb), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
110	d1yc5a1	Alignment	not modelled	76.0	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
111	d2cona1	Alignment	not modelled	75.5	38	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
112	c3tnuB_	Alignment	not modelled	75.4	13	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)
113	c4ll7C_	Alignment	not modelled	75.2	15	PDB header: transport protein Chain: C: PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: structure of she3p amino terminus.
114	c5oj7A_	Alignment	not modelled	74.7	31	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacylase; PDBTitle: sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
115	c5yz0C_	Alignment	not modelled	73.3	11	PDB header: cell cycle Chain: C: PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrip complex
116	d1vd4a_	Alignment	not modelled	72.9	20	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
117	c2eodA_	Alignment	not modelled	72.5	18	PDB header: signaling protein Chain: A: PDB Molecule: tnf receptor-associated factor 4; PDBTitle: solution structure of traf-type zinc finger domains (190-2 248) from human tnf receptor-associated factor 4
118	c4fmyE_	Alignment	not modelled	71.9	19	PDB header: viral protein Chain: E: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystal form i
119	c3tnuA_	Alignment	not modelled	71.2	19	PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
120	c5oi7A_	Alignment	not modelled	71.2	10	PDB header: protein binding Chain: A: PDB Molecule: centrosomal protein of 85 kda; PDBTitle: human cep85 - coiled coil domain 4