



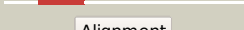

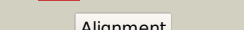









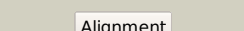
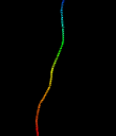
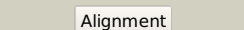
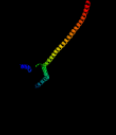

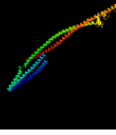
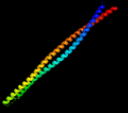
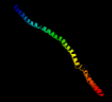






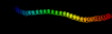


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2345 (-) _2623831_2625813
Date	Mon Aug 5 13:25:49 BST 2019
Unique Job ID	d015ef7b7bd3c17d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kptA_</a>	 Alignment		100.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a
2	<a href="#">c5anpB_</a>	 Alignment		99.9	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ba41; <b>PDBTitle:</b> crystal structure of the ba41 protein from bizionia argentinensis
3	<a href="#">c3ptjA_</a>	 Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0603 protein at1g54780, chloroplastic; <b>PDBTitle:</b> structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein attlp18.3
4	<a href="#">c2kw7A_</a>	 Alignment		99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
5	<a href="#">c2lt2A_</a>	 Alignment		99.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr structure of ba42 protein from the psychrophilic bacteria bizionia2 argentinensis sp. nov.
6	<a href="#">c6hwhT_</a>	 Alignment		99.7	13	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> uncharacterized protein msmeg_4692/msmej_4575; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
7	<a href="#">c5ew5C_</a>	 Alignment		97.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
8	<a href="#">c4cgkA_</a>	 Alignment		97.3	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> secreted 45 kda protein; <b>PDBTitle:</b> crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
9	<a href="#">c1c1gA_</a>	 Alignment		96.4	7	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> tropomyosin; <b>PDBTitle:</b> crystal structure of tropomyosin at 7 angstroms resolution in the2 spermine-induced crystal form
10	<a href="#">c3ojaB_</a>	 Alignment		96.4	9	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
11	<a href="#">c1ciiA_</a>	 Alignment		96.1	12	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia





















12	<a href="#">c6ewyA</a>	Alignment		95.0	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan endopeptidase ripa; <b>PDBTitle:</b> ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
13	<a href="#">c1deqO</a>	Alignment		94.9	9	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen (beta chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
14	<a href="#">c5jxfA</a>	Alignment		94.7	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
15	<a href="#">c6o7xa</a>	Alignment		94.6	7	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
16	<a href="#">c3ghgK</a>	Alignment		94.3	11	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
17	<a href="#">c1bg1A</a>	Alignment		94.1	5	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
18	<a href="#">c6gapB</a>	Alignment		94.0	15	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
19	<a href="#">c3wolB</a>	Alignment		93.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl aminopeptidase bii; <b>PDBTitle:</b> crystal structure of the dap bii dipeptide complex i
20	<a href="#">c1ei3E</a>	Alignment		93.9	6	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
21	<a href="#">c6gaoC</a>	Alignment	not modelled	93.8	6	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t11 reovirus sigma1 coiled coil tail and body
22	<a href="#">c1deqF</a>	Alignment	not modelled	93.7	6	<b>PDB header:</b> blood clotting <b>Chain:</b> F: <b>PDB Molecule:</b> fibrinogen (gamma chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
23	<a href="#">c1bf5A</a>	Alignment	not modelled	92.9	7	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
24	<a href="#">c2oevA</a>	Alignment	not modelled	92.2	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 6-interacting protein; <b>PDBTitle:</b> crystal structure of alix/aip1
25	<a href="#">c3vkqA</a>	Alignment	not modelled	91.9	11	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
26	<a href="#">c6f1tX</a>	Alignment	not modelled	91.6	10	<b>PDB header:</b> motor protein <b>Chain:</b> X: <b>PDB Molecule:</b> bicd family-like cargo adapter 1,bicd family-like cargo <b>PDBTitle:</b> cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
27	<a href="#">c3ghgI</a>	Alignment	not modelled	91.6	6	<b>PDB header:</b> blood clotting <b>Chain:</b> I: <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
28	<a href="#">c6f1tx</a>	Alignment	not modelled	91.5	10	<b>PDB header:</b> motor protein <b>Chain:</b> X: <b>PDB Molecule:</b> bicd family-like cargo adapter 1,bicd family-like cargo <b>PDBTitle:</b> cryo-em structure of two dynein tail domains bound to

						dynactin and2 bicdr1
29	<a href="#">c6ogdB_</a>	Alignment	not modelled	91.4	10	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> toxin subunit yena2; <b>PDBTitle:</b> cryo-em structure of yentca in its prepore state
30	<a href="#">c5jxpA_</a>	Alignment	not modelled	91.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
31	<a href="#">c3cwgA_</a>	Alignment	not modelled	90.5	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
32	<a href="#">c6gajA_</a>	Alignment	not modelled	90.2	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
33	<a href="#">c4iloA_</a>	Alignment	not modelled	89.7	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ct398; <b>PDBTitle:</b> 2.12a resolution structure of ct398 from chlamydia trachomatis
34	<a href="#">c6mi3A_</a>	Alignment	not modelled	89.1	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kb essential modulator,nf-kappa-b essential modulator, <b>PDBTitle:</b> structure of nemo(51-112) with n- and c-terminal coiled-coil adaptors.
35	<a href="#">c3na7A_</a>	Alignment	not modelled	88.9	8	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hp0958; <b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
36	<a href="#">c41lbB_</a>	Alignment	not modelled	88.7	4	<b>PDB header:</b> signaling protein/transferase/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha complexed with nish2 of p85alpha
37	<a href="#">c5wjbA_</a>	Alignment	not modelled	88.5	14	<b>PDB header:</b> actin/dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7; <b>PDBTitle:</b> crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
38	<a href="#">c1yvlB_</a>	Alignment	not modelled	88.0	8	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
39	<a href="#">c6o7ua_</a>	Alignment	not modelled	87.0	7	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
40	<a href="#">c1y4cA_</a>	Alignment	not modelled	86.5	17	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed <b>PDBTitle:</b> designed helical protein fusion mbp
41	<a href="#">c3wuqA_</a>	Alignment	not modelled	86.0	10	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic dynein 1 heavy chain 1; <b>PDBTitle:</b> structure of the entire stalk region of the dynein motor domain
42	<a href="#">c5goxB_</a>	Alignment	not modelled	86.0	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rad50; <b>PDBTitle:</b> eukaryotic rad50 functions as a rod-shaped dimer
43	<a href="#">c5dfzD_</a>	Alignment	not modelled	85.7	8	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
44	<a href="#">c4zryA_</a>	Alignment	not modelled	85.3	9	<b>PDB header:</b> protein fibril <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 10; <b>PDBTitle:</b> crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
45	<a href="#">c5cwsJ_</a>	Alignment	not modelled	83.6	6	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> nucleoporin nup49; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
46	<a href="#">c3ojaA_</a>	Alignment	not modelled	82.8	4	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich immune molecule 1; <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
47	<a href="#">c4xa3A_</a>	Alignment	not modelled	82.6	13	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp7-myh7(1361-1425)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 2 of myh7
48	<a href="#">c5ijnF_</a>	Alignment	not modelled	82.5	11	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
49	<a href="#">c2fxmB_</a>	Alignment	not modelled	81.7	8	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin heavy chain, cardiac muscle beta isoform; <b>PDBTitle:</b> structure of the human beta-myosin s2 fragment
50	<a href="#">c2v66C_</a>	Alignment	not modelled	80.8	10	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear distribution protein nude-like 1; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of ndel1 (a.a.258 to 169)c
51	<a href="#">c1deqD_</a>	Alignment	not modelled	79.9	14	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> fibrinogen (alpha chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
52	<a href="#">c6e2jB_</a>	Alignment	not modelled	79.6	10	<b>PDB header:</b> protein fibril <b>Chain:</b> B: <b>PDB Molecule:</b> keratin, type i cytoskeletal 10; <b>PDBTitle:</b> crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s233l mutation and wild-type human keratin 10 coil 1b

53	<a href="#">c3jbhA</a>	Alignment	not modelled	79.5	14	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into 2 tarantula thick filament 3d-map allows in depth study of intra- and 3 intermolecular interactions
54	<a href="#">c1ei3C</a>	Alignment	not modelled	79.5	10	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
55	<a href="#">c5xg2A</a>	Alignment	not modelled	78.6	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of a coiled-coil segment (residues 345-468 and 694-2 814) of pyrococcus yayanosii smc
56	<a href="#">c3u59C</a>	Alignment	not modelled	78.4	13	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> tropomyosin beta chain; <b>PDBTitle:</b> n-terminal 98-aa fragment of smooth muscle tropomyosin beta
57	<a href="#">c5tbyA</a>	Alignment	not modelled	78.0	17	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-7; <b>PDBTitle:</b> human beta cardiac heavy meromyosin interacting-heads motif obtained 2 by homology modeling (using swiss-model) of human sequence from 3 aphonopelma homology model (pdb-3jbh), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
58	<a href="#">c2zv4O</a>	Alignment	not modelled	77.0	10	<b>PDB header:</b> structural protein <b>Chain:</b> O: <b>PDB Molecule:</b> major vault protein; <b>PDBTitle:</b> the structure of rat liver vault at 3.5 angstrom resolution
59	<a href="#">c4xa1D</a>	Alignment	not modelled	75.8	12	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> gp7-myh7(1173-1238)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 1 of myh7
60	<a href="#">c3tnuB</a>	Alignment	not modelled	75.6	12	<b>PDB header:</b> cytosolic protein <b>Chain:</b> B: <b>PDB Molecule:</b> keratin, type ii cytoskeletal 5; <b>PDBTitle:</b> heterocomplex of coil 2b domains of human intermediate filament 2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
61	<a href="#">c5voxb</a>	Alignment	not modelled	75.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type proton atpase subunit b; <b>PDBTitle:</b> yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
62	<a href="#">c2v71A</a>	Alignment	not modelled	75.2	15	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear distribution protein nude-like 1; <b>PDBTitle:</b> coiled-coil region of nudel
63	<a href="#">c4a7fB</a>	Alignment	not modelled	74.7	12	<b>PDB header:</b> structural protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tropomyosin 1 alpha; <b>PDBTitle:</b> structure of the actin-tropomyosin-myosin complex (rigor atm 3)
64	<a href="#">c2no2A</a>	Alignment	not modelled	74.6	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> huntingtin-interacting protein 1; <b>PDBTitle:</b> crystal structure of the dllrk-containing coiled-coil 2 domain of huntingtin-interacting protein 1
65	<a href="#">c3dtpA</a>	Alignment	not modelled	74.3	9	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and cardiac muscle; <b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to tarantula 2 muscle thick filament cryo-em 3d-map
66	<a href="#">c3ipkA</a>	Alignment	not modelled	73.9	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> agi/ii; <b>PDBTitle:</b> crystal structure of a3vp1 of agi/ii of streptococcus mutans
67	<a href="#">c6ec0A</a>	Alignment	not modelled	73.2	12	<b>PDB header:</b> protein fibril <b>Chain:</b> A: <b>PDB Molecule:</b> keratin 1; <b>PDBTitle:</b> crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and 3 keratin 10 (krt10)
68	<a href="#">c5mg8B</a>	Alignment	not modelled	72.8	12	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 6; <b>PDBTitle:</b> crystal structure of the s.pombe smc5/6 hinge domain
69	<a href="#">c4rh7A</a>	Alignment	not modelled	72.6	10	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein/cytoplasmic dynein 2 heavy chain <b>PDBTitle:</b> crystal structure of human cytoplasmic dynein 2 motor domain in 2 complex with adp.vi
70	<a href="#">c5nugB</a>	Alignment	not modelled	72.6	12	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> cytoplasmic dynein 1 heavy chain 1; <b>PDBTitle:</b> motor domains from human cytoplasmic dynein-1 in the phi-particle 2 conformation
71	<a href="#">c2efrB</a>	Alignment	not modelled	72.1	15	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal tropomyosin fragment with n- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms 3 resolution
72	<a href="#">c1jchC</a>	Alignment	not modelled	71.6	10	<b>PDB header:</b> ribosome inhibitor, hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin e3; <b>PDBTitle:</b> crystal structure of colicin e3 in complex with its immunity protein
73	<a href="#">c5nenB</a>	Alignment	not modelled	71.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase c; <b>PDBTitle:</b> crystal structure of the soluble domain of lipc, a membrane fusion 2 protein of a type i secretion system
74	<a href="#">c4gkwB</a>	Alignment	not modelled	70.5	7	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> spindle assembly abnormal protein 6; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of c. elegans sas-6
75	<a href="#">c5oi7A</a>	Alignment	not modelled	70.2	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 85 kda; <b>PDBTitle:</b> human cep85 - coiled coil domain 4
76	<a href="#">c6a9nD</a>	Alignment	not modelled	69.8	12	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> glial fibrillary acidic protein;

76	<a href="#">c6a2pD</a>	Alignment	not modelled	65.8	12	<b>PDBTitle:</b> crystal structure of the human glial fibrillary acidic protein 1b2 domain <b>PDB header:</b> apoptosis
77	<a href="#">c3q8tB</a>	Alignment	not modelled	66.9	9	<b>Chain:</b> B; <b>PDB Molecule:</b> beclin-1; <b>PDBTitle:</b> crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
78	<a href="#">c3o1A</a>	Alignment	not modelled	66.6	11	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
79	<a href="#">c2d3eD</a>	Alignment	not modelled	66.6	13	<b>PDB header:</b> contractile protein <b>Chain:</b> D; <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
80	<a href="#">c3vkgB</a>	Alignment	not modelled	66.5	7	<b>PDB header:</b> motor protein <b>Chain:</b> B; <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
81	<a href="#">c4rfxA</a>	Alignment	not modelled	66.3	10	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> dynactin subunit 1; <b>PDBTitle:</b> crystal structure of the dynactin dctn1 fragment involved in dynein2 interaction
82	<a href="#">c5tvbB</a>	Alignment	not modelled	65.9	10	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> nucleoprotein tpr; <b>PDBTitle:</b> structure of the tpr oligomerization domain
83	<a href="#">c2y3aB</a>	Alignment	not modelled	65.7	8	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit beta; <b>PDBTitle:</b> crystal structure of p110beta in complex with icsh2 of p85beta and the2 drug gdc-0941
84	<a href="#">c5cwsC</a>	Alignment	not modelled	65.4	11	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> nucleoporin nsp1; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
85	<a href="#">c2ch7A</a>	Alignment	not modelled	65.3	13	<b>PDB header:</b> chemotaxis <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
86	<a href="#">c4a55B</a>	Alignment	not modelled	64.8	4	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
87	<a href="#">c4wheA</a>	Alignment	not modelled	62.8	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> phage shock protein a; <b>PDBTitle:</b> crystal structure of e. coli phage shock protein a (pspa 1-144)
88	<a href="#">c3g67A</a>	Alignment	not modelled	61.2	7	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of a soluble chemoreceptor from thermotoga2 maritima
89	<a href="#">c1g8xB</a>	Alignment	not modelled	59.7	10	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> myosin ii heavy chain fused to alpha-actinin 3; <b>PDBTitle:</b> structure of a genetically engineered molecular motor
90	<a href="#">c1s1jB</a>	Alignment	not modelled	58.4	6	<b>PDB header:</b> contractile protein <b>Chain:</b> B; <b>PDB Molecule:</b> actinin; <b>PDBTitle:</b> cryo-em structure of chicken gizzard smooth muscle alpha-actinin
91	<a href="#">c5j1iA</a>	Alignment	not modelled	58.4	10	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the spectrin repeats 7, 8, and 9 of the plakin domain of2 plectin
92	<a href="#">c4fmyE</a>	Alignment	not modelled	58.0	10	<b>PDB header:</b> viral protein <b>Chain:</b> E; <b>PDB Molecule:</b> dna stabilization protein; <b>PDBTitle:</b> hk620 tail needle crystal form i
93	<a href="#">c3hnwB</a>	Alignment	not modelled	57.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
94	<a href="#">c2b9cA</a>	Alignment	not modelled	56.6	12	<b>PDB header:</b> contractile protein <b>Chain:</b> A; <b>PDB Molecule:</b> striated-muscle alpha tropomyosin; <b>PDBTitle:</b> structure of tropomyosin's mid-region: bending and binding sites for2 actin
95	<a href="#">c3o0zD</a>	Alignment	not modelled	56.1	9	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> rho-associated protein kinase 1; <b>PDBTitle:</b> crystal structure of a coiled-coil domain from human rock i
96	<a href="#">c6flnE</a>	Alignment	not modelled	56.0	8	<b>PDB header:</b> protein binding <b>Chain:</b> E; <b>PDB Molecule:</b> e3 ubiquitin/isc15 ligase trim25; <b>PDBTitle:</b> crystal structure of the human trim25 coiled-coil and pryspry domains
97	<a href="#">c5nenA</a>	Alignment	not modelled	55.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase c; <b>PDBTitle:</b> crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
98	<a href="#">c5bu8A</a>	Alignment	not modelled	53.9	9	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna stabilization protein; <b>PDBTitle:</b> hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
99	<a href="#">c2qa7C</a>	Alignment	not modelled	51.5	13	<b>PDB header:</b> actin binding <b>Chain:</b> C; <b>PDB Molecule:</b> huntingtin-interacting protein 1; <b>PDBTitle:</b> crystal structure of huntingtin-interacting protein 12 (hip1) coiled-coil domain with a basic surface suitable3 for hip-protein interactor (hippi)
100	<a href="#">c3u1aC</a>	Alignment	not modelled	51.1	10	<b>PDB header:</b> contractile protein <b>Chain:</b> C; <b>PDB Molecule:</b> smooth muscle tropomyosin alpha; <b>PDBTitle:</b> n-terminal 81-aa fragment of smooth muscle tropomyosin alpha



101	<a href="#">c4clvB_</a>	 Alignment	not modelled	50.9	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
102	<a href="#">c1f5nA_</a>	 Alignment	not modelled	50.7	7	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced guanylate-binding protein 1; <b>PDBTitle:</b> human guanylate binding protein-1 in complex with the gtp analogue,2 gmppnp.
103	<a href="#">c4u5pA_</a>	 Alignment	not modelled	47.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rhcc; <b>PDBTitle:</b> crystal structure of native rhcc (yp_702633.1) from rhodococcus jostii2 rha1 at 1.78 angstrom
104	<a href="#">c2i1kA_</a>	 Alignment	not modelled	45.9	11	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
105	<a href="#">c5mg8A_</a>	 Alignment	not modelled	45.7	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 5; <b>PDBTitle:</b> crystal structure of the s.pombe smc5/6 hinge domain
106	<a href="#">c6h2xA_</a>	 Alignment	not modelled	43.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein mukb,chromosome partition <b>PDBTitle:</b> mukb coiled-coil elbow from e. coli
107	<a href="#">c3ajwA_</a>	 Alignment	not modelled	43.7	6	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar fljij protein; <b>PDBTitle:</b> structure of fljij, a soluble component of flagellar type iii export2 apparatus
108	<a href="#">c3c6vB_</a>	 Alignment	not modelled	43.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> probable tautomerase/dehalogenase au4130; <b>PDBTitle:</b> crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
109	<a href="#">c3woaA_</a>	 Alignment	not modelled	41.9	11	<b>PDB header:</b> dna binding protein, sugar binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein ci, maltose-binding periplasmic protein; <b>PDBTitle:</b> crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
110	<a href="#">c6djlE_</a>	 Alignment	not modelled	41.8	12	<b>PDB header:</b> signaling protein/protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> sh3 domain-binding protein 5; <b>PDBTitle:</b> crystal structure of the rab11 gef sh3bp5 bound to nucleotide free2 rab11a
111	<a href="#">c2gl2B_</a>	 Alignment	not modelled	41.4	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
112	<a href="#">c4cg4D_</a>	 Alignment	not modelled	41.2	7	<b>PDB header:</b> actin-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pyrin; <b>PDBTitle:</b> crystal structure of the chs-b30.2 domains of trim20
113	<a href="#">c6fkip_</a>	 Alignment	not modelled	40.0	8	<b>PDB header:</b> membrane protein <b>Chain:</b> P: <b>PDB Molecule:</b> atp synthase subunit c, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3
114	<a href="#">c5y06A_</a>	 Alignment	not modelled	39.6	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> msmeg_4306; <b>PDBTitle:</b> structural characterization of msmeg_4306 from mycobacterium smegmatis
115	<a href="#">c3iynR_</a>	 Alignment	not modelled	39.5	20	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
116	<a href="#">c5cwsE_</a>	 Alignment	not modelled	39.4	10	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> nucleoporin nup57; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
117	<a href="#">c5ijnT_</a>	 Alignment	not modelled	39.2	7	<b>PDB header:</b> transport protein <b>Chain:</b> T: <b>PDB Molecule:</b> nuclear pore glycoprotein p62; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
118	<a href="#">c1quuA_</a>	 Alignment	not modelled	35.5	10	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> human skeletal muscle alpha-actinin 2; <b>PDBTitle:</b> crystal structure of two central spectrin-like repeats from alpha-2 actinin
119	<a href="#">c5lm2B_</a>	 Alignment	not modelled	34.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 23; <b>PDBTitle:</b> crystal structure of hd-ptp phosphatase
120	<a href="#">c3vkhD_</a>	 Alignment	not modelled	33.1	15	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain