

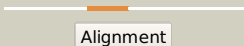
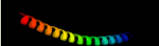
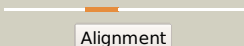


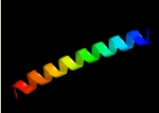

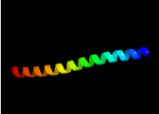
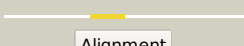

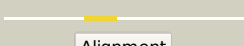


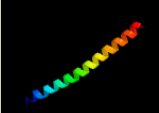

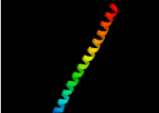




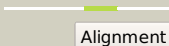

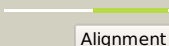
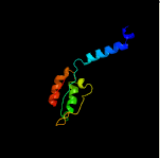

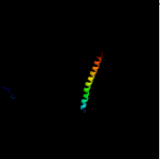

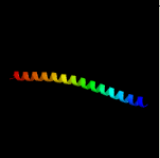

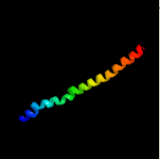

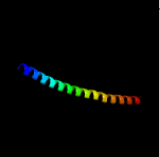

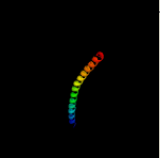

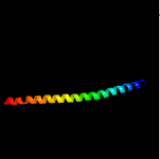

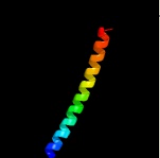
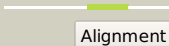
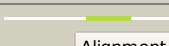

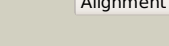
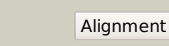
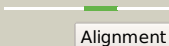
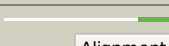



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1825 (- )_2071043_2071921
Date	Fri Aug 2 13:30:43 BST 2019
Unique Job ID	af22aaacbfaf9dd6

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gmgB_</a>	 Alignment		100.0	100	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein rv1825/mt1873; <b>PDBTitle:</b> crystal structure of an uncharacterized conserved protein from <i>Mycobacterium tuberculosis</i>
2	<a href="#">c3u1aC_</a>	 Alignment		87.3	15	<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
3	<a href="#">c5fv8A_</a>	 Alignment		86.3	32	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
4	<a href="#">c5fv8B_</a>	 Alignment		85.8	32	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
5	<a href="#">c4pxjB_</a>	 Alignment		83.1	18	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> c-jun-amino-terminal kinase-interacting protein 3; <b>PDBTitle:</b> crystallographic structure of the lzii fragment (anti-parallel2 orientation) from jip3
6	<a href="#">c1debA_</a>	 Alignment		79.6	23	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenomatous polyposis coli protein; <b>PDBTitle:</b> crystal structure of the n-terminal coiled coil domain from apc
7	<a href="#">c2w83C_</a>	 Alignment		79.3	21	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> c-jun-amino-terminal kinase-interacting protein <b>PDBTitle:</b> crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4
8	<a href="#">c3cvfA_</a>	 Alignment		74.2	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> homer protein homolog 3; <b>PDBTitle:</b> crystal structure of the carboxy terminus of homer3
9	<a href="#">c3swkB_</a>	 Alignment		71.9	19	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin coil1b fragment
10	<a href="#">c2oqqB_</a>	 Alignment		69.3	22	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> transcription factor hy5; <b>PDBTitle:</b> crystal structure of hy5 leucine zipper homodimer from <i>Arabidopsis thaliana</i>
11	<a href="#">c6e2jB_</a>	 Alignment		69.1	15	<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 s2331 mutation and wild-type human keratin 10 coil 1b

12	<a href="#">c1junB_</a>	 Alignment		68.2	20	<b>PDB header:</b> transcription regulation <b>Chain:</b> B: <b>PDB Molecule:</b> c-jun homodimer; <b>PDBTitle:</b> nmr study of c-jun homodimer
13	<a href="#">c2vd3B_</a>	 Alignment		65.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
14	<a href="#">c3iynR_</a>	 Alignment		65.5	25	<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
15	<a href="#">c6a9pD_</a>	 Alignment		64.5	25	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> glial fibrillary acidic protein; <b>PDBTitle:</b> crystal structure of the human glial fibrillary acidic protein 1b2 domain
16	<a href="#">c3ghgK_</a>	 Alignment		63.8	9	<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="#">c6ec0A_</a>	 Alignment		63.7	13	<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) and3 keratin 10 (krt10)
18	<a href="#">c3ol1A_</a>	 Alignment		62.5	19	<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
19	<a href="#">c5lskB_</a>	 Alignment		62.3	14	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> polyamine-modulated factor 1; <b>PDBTitle:</b> crystal structure of the human kinetochore mis12-cenp-c complex
20	<a href="#">c1ci6B_</a>	 Alignment		61.8	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor c/ebp beta; <b>PDBTitle:</b> transcription factor atf4-c/ebp beta bzip heterodimer
21	<a href="#">c1ic2B_</a>	 Alignment	not modelled	61.1	21	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> tropomyosin alpha chain, skeletal muscle; <b>PDBTitle:</b> deciphering the design of the tropomyosin molecule
22	<a href="#">c1deqO_</a>	 Alignment	not modelled	60.8	14	<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)
23	<a href="#">c3m9bK_</a>	 Alignment	not modelled	59.7	27	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
24	<a href="#">c3iynQ_</a>	 Alignment	not modelled	58.8	30	<b>PDB header:</b> virus <b>Chain:</b> Q: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
25	<a href="#">c1fosF_</a>	 Alignment	not modelled	57.9	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> F: <b>PDB Molecule:</b> c-jun proto-oncogene protein; <b>PDBTitle:</b> two human c-fos:c-jun:dna complexes
26	<a href="#">d1nh8a2</a>	 Alignment	not modelled	57.8	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
27	<a href="#">c3qqiB_</a>	 Alignment	not modelled	55.7	11	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> crystal structure of the ha1 receptor binding domain of h22 hemagglutinin
28	<a href="#">c2pnvA_</a>	 Alignment	not modelled	55.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> small conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the leucine zipper domain of small-2

						conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
29	<a href="#">c5xauC_</a>	Alignment	not modelled	55.6	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> laminin subunit gamma-1; <b>PDBTitle:</b> crystal structure of integrin binding fragment of laminin-511
30	<a href="#">c2pfuA_</a>	Alignment	not modelled	55.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biopolymer transport exbd protein; <b>PDBTitle:</b> nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
31	<a href="#">c4cgkA_</a>	Alignment	not modelled	53.9	16	<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
32	<a href="#">c6f1tx_</a>	Alignment	not modelled	52.9	21	<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
33	<a href="#">c6f1tX_</a>	Alignment	not modelled	52.3	21	<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
34	<a href="#">c5wwlN_</a>	Alignment	not modelled	51.9	10	<b>PDB header:</b> cell cycle <b>Chain:</b> N: <b>PDB Molecule:</b> kinetochore protein nnf1; <b>PDBTitle:</b> crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
35	<a href="#">c3n4xB_</a>	Alignment	not modelled	51.8	15	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> monopolin complex subunit csm1; <b>PDBTitle:</b> structure of csm1 full-length
36	<a href="#">c2e43A_</a>	Alignment	not modelled	50.5	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ccaat/enhancer-binding protein beta; <b>PDBTitle:</b> crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
37	<a href="#">c6e1rA_</a>	Alignment	not modelled	48.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tailspike protein; <b>PDBTitle:</b> crystal structure of the acinetobacter phage vb_apip_p1 tailspike2 protein
38	<a href="#">c1fosE_</a>	Alignment	not modelled	48.5	19	<b>PDB header:</b> transcription/dna <b>Chain:</b> E: <b>PDB Molecule:</b> p53-c-fos proto-oncogene protein; <b>PDBTitle:</b> two human c-fos:c-jun:dna complexes
39	<a href="#">c3kinB_</a>	Alignment	not modelled	47.9	12	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin heavy chain; <b>PDBTitle:</b> kinesin (dimeric) from rattus norvegicus
40	<a href="#">c1ei3E_</a>	Alignment	not modelled	47.8	14	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
41	<a href="#">c5mg8B_</a>	Alignment	not modelled	47.8	14	<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
42	<a href="#">c4clvB_</a>	Alignment	not modelled	47.2	18	<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
43	<a href="#">c5mg8A_</a>	Alignment	not modelled	47.1	19	<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
44	<a href="#">c4yb5B_</a>	Alignment	not modelled	46.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> adenosine triphosphate phosphoribosyltransferase from campylobacter2 jejuni in complex with the allosteric inhibitor histidine
45	<a href="#">d1r05a_</a>	Alignment	not modelled	46.7	23	<b>Fold:</b> HLH-like <b>Superfamily:</b> HLH, helix-loop-helix DNA-binding domain <b>Family:</b> HLH, helix-loop-helix DNA-binding domain
46	<a href="#">c2l5gB_</a>	Alignment	not modelled	46.6	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ncor2; <b>PDBTitle:</b> co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
47	<a href="#">c6cfzC_</a>	Alignment	not modelled	46.4	23	<b>PDB header:</b> nuclear protein <b>Chain:</b> C: <b>PDB Molecule:</b> dad2; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
48	<a href="#">c6czlA_</a>	Alignment	not modelled	45.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase catalytic subunit; <b>PDBTitle:</b> crystal structure of medicago truncatula atp-phosphoribosyltransferase2 in relaxed form
49	<a href="#">c2gl2B_</a>	Alignment	not modelled	45.3	19	<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
50	<a href="#">c1t2kD_</a>	Alignment	not modelled	45.2	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> cyclic-amp-dependent transcription factor atf-2; <b>PDBTitle:</b> structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
51	<a href="#">d1vioa2</a>	Alignment	not modelled	44.8	14	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Pseudouridine synthase RsuA N-terminal domain
52	<a href="#">c5by4A_</a>	Alignment	not modelled	44.7	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein tolr; <b>PDBTitle:</b> structure and function of the escherichia coli tol-pal stator protein2 tolr

53	<a href="#">c6bl7A_</a>	Alignment	not modelled	44.2	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein stu2; <b>PDBTitle:</b> s. cerevisiae stu2 coiled coil domain
54	<a href="#">c4cyzC_</a>	Alignment	not modelled	43.0	18	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> structure of the a_mallard_sweden_51_2002 h10 avian2 haemagglutinin in complex with avian receptor analog Ista
55	<a href="#">c3ojaB_</a>	Alignment	not modelled	42.3	14	<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 Irim1/apl1c complex
56	<a href="#">c3ra3D_</a>	Alignment	not modelled	42.0	30	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> p2f; <b>PDBTitle:</b> crystal structure of a section of a de novo design gigadalton protein2 fibre
57	<a href="#">c1nh7A_</a>	Alignment	not modelled	41.9	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp phosphoribosyltransferase; <b>PDBTitle:</b> atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
58	<a href="#">c2jeeA_</a>	Alignment	not modelled	40.8	25	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein zapb; <b>PDBTitle:</b> xray structure of e. coli yiuu
59	<a href="#">d1qfha1</a>	Alignment	not modelled	40.6	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
60	<a href="#">c5cj1B_</a>	Alignment	not modelled	40.5	19	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp7-myh7-(1526-1571) chimera protein; <b>PDBTitle:</b> crystal structure of the coiled coil of myh7 residues 1526 to 15712 fused to gp7
61	<a href="#">d1p88a_</a>	Alignment	not modelled	40.4	18	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
62	<a href="#">c1ci6A_</a>	Alignment	not modelled	39.6	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor atf-4; <b>PDBTitle:</b> transcription factor atf4-c/ebp beta bzip heterodimer
63	<a href="#">c3a5tB_</a>	Alignment	not modelled	37.6	22	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor mafg; <b>PDBTitle:</b> crystal structure of mafg-dna complex
64	<a href="#">c6gajA_</a>	Alignment	not modelled	35.9	14	<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)
65	<a href="#">c1ztaA_</a>	Alignment	not modelled	34.8	23	<b>PDB header:</b> dna-binding motif <b>Chain:</b> A: <b>PDB Molecule:</b> leucine zipper monomer; <b>PDBTitle:</b> the solution structure of a leucine-zipper motif peptide
66	<a href="#">c1ij2C_</a>	Alignment	not modelled	34.4	23	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
67	<a href="#">c5dudA_</a>	Alignment	not modelled	34.2	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ybgk; <b>PDBTitle:</b> crystal structure of e. coli ybgjk
68	<a href="#">c1ij3B_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvs1 coiled-coil trimer with serine at the a(16)2 position
69	<a href="#">c1ij3C_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvs1 coiled-coil trimer with serine at the a(16)2 position
70	<a href="#">c5wjba_</a>	Alignment	not modelled	34.0	16	<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
71	<a href="#">c1deqF_</a>	Alignment	not modelled	34.0	11	<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)
72	<a href="#">c3k7zA_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
73	<a href="#">c1rb1B_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
74	<a href="#">c3k7zB_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
75	<a href="#">c1rb1A_</a>	Alignment	not modelled	34.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
76	<a href="#">d1ejda_</a>	Alignment	not modelled	33.6	16	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> Enolpyruvate transferase, EPT
77	<a href="#">c4f15D_</a>	Alignment	not modelled	33.1	16	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> molecular basis of infectivity of 2009 pandemic h1n1 influenza a2 viruses
78	<a href="#">c2o7hf_</a>	Alignment	not modelled	32.5	21	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> crystal structure of trimeric coiled coil gcn4 leucine zipper
						<b>PDB header:</b> protein binding

79	<a href="#">c3p8cD_</a>	Alignment	not modelled	32.1	21	<b>Chain:</b> D: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein family member 1; <b>PDBTitle:</b> structure and control of the actin regulatory wave complex
80	<a href="#">c1ij2B_</a>	Alignment	not modelled	31.7	23	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvt1 coiled-coil trimer with threonine at the a(16)2 position
81	<a href="#">c3tnuA_</a>	Alignment	not modelled	31.5	12	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 14; <b>PDBTitle:</b> heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
82	<a href="#">c1swiA_</a>	Alignment	not modelled	31.3	25	<b>PDB header:</b> leucine zipper <b>Chain:</b> A: <b>PDB Molecule:</b> gcn4p1; <b>PDBTitle:</b> gcn4-leucine zipper core mutant as n16a complexed with benzene
83	<a href="#">c1rb6C_</a>	Alignment	not modelled	31.3	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
84	<a href="#">c4rfxA_</a>	Alignment	not modelled	31.0	19	<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
85	<a href="#">c6o7xa_</a>	Alignment	not modelled	30.6	15	<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
86	<a href="#">d1h3da2</a>	Alignment	not modelled	29.9	22	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
87	<a href="#">d2azeb1</a>	Alignment	not modelled	29.6	19	<b>Fold:</b> E2F-DP heterodimerization region <b>Superfamily:</b> E2F-DP heterodimerization region <b>Family:</b> E2F dimerization segment
88	<a href="#">c4xa1D_</a>	Alignment	not modelled	29.5	15	<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
89	<a href="#">c1cz7C_</a>	Alignment	not modelled	29.5	16	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> microtubule motor protein ncd; <b>PDBTitle:</b> the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
90	<a href="#">c3s4rB_</a>	Alignment	not modelled	29.4	21	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
91	<a href="#">c2cqjA_</a>	Alignment	not modelled	28.4	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein <b>PDBTitle:</b> solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
92	<a href="#">c3ssuB_</a>	Alignment	not modelled	28.3	22	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin coil1a/1b fragment
93	<a href="#">c4w7yB_</a>	Alignment	not modelled	28.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> b-cell receptor-associated protein 29; <b>PDBTitle:</b> dimeric bap29 vded with disulfide bonds in crystal contacts
94	<a href="#">c5oi7A_</a>	Alignment	not modelled	27.8	13	<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
95	<a href="#">c2wt7B_</a>	Alignment	not modelled	27.5	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor mafb; <b>PDBTitle:</b> crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna
96	<a href="#">c6ckoD_</a>	Alignment	not modelled	26.7	14	<b>PDB header:</b> dna binding protein/transferase <b>Chain:</b> D: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 specific; <b>PDBTitle:</b> crystal structure of an af10 fragment
97	<a href="#">c6ckoC_</a>	Alignment	not modelled	26.7	14	<b>PDB header:</b> dna binding protein/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-79 specific; <b>PDBTitle:</b> crystal structure of an af10 fragment
98	<a href="#">d1ti8a1</a>	Alignment	not modelled	26.6	13	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
99	<a href="#">c3mmlE_</a>	Alignment	not modelled	26.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> allophanate hydrolase subunit 2; <b>PDBTitle:</b> allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
100	<a href="#">c5dfzD_</a>	Alignment	not modelled	26.0	9	<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.
101	<a href="#">c1jccC_</a>	Alignment	not modelled	25.7	23	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> major outer membrane lipoprotein; <b>PDBTitle:</b> crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
102	<a href="#">c2yy0D_</a>	Alignment	not modelled	25.7	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> c-myc-binding protein; <b>PDBTitle:</b> crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
103	<a href="#">c2efrB_</a>	Alignment	not modelled	25.0	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- and2 c-terminal extensions of the leucine zipper at 1.8

						angstroms3 resolution
104	<a href="#">c3layF_</a>	Alignment	not modelled	24.9	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> zinc resistance-associated protein; <b>PDBTitle:</b> alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
105	<a href="#">c6n6sB_</a>	Alignment	not modelled	24.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tnfaip3-interacting protein 1; <b>PDBTitle:</b> crystal structure of abin-1 uban
106	<a href="#">c1ysaD_</a>	Alignment	not modelled	24.5	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> protein (gcn4); <b>PDBTitle:</b> the gcn4 basic region leucine zipper binds dna as a dimer2 of uninterrupted alpha helices: crystal structure of the3 protein-dna complex
107	<a href="#">c5bu8A_</a>	Alignment	not modelled	24.3	11	<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
108	<a href="#">c6ewyA_</a>	Alignment	not modelled	24.2	23	<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
109	<a href="#">c2xdjF_</a>	Alignment	not modelled	24.2	16	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein ybgf; <b>PDBTitle:</b> crystal structure of the n-terminal domain of e.coli ybgf
110	<a href="#">d1vqza2</a>	Alignment	not modelled	23.9	18	<b>Fold:</b> Class II aaRS and biotin synthetases <b>Superfamily:</b> Class II aaRS and biotin synthetases <b>Family:</b> LplA-like
111	<a href="#">c2z5wA_</a>	Alignment	not modelled	23.9	34	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> tbcla protein; <b>PDBTitle:</b> tbcla, a recombinant spore surface protein from bacillus anthracis
112	<a href="#">c1flla_</a>	Alignment	not modelled	23.8	15	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor associated factor 3; <b>PDBTitle:</b> molecular basis for cd40 signaling mediated by traf3
113	<a href="#">c3a7pB_</a>	Alignment	not modelled	23.8	21	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> autophagy protein 16; <b>PDBTitle:</b> the crystal structure of saccharomyces cerevisiae atg16
114	<a href="#">c6cknA_</a>	Alignment	not modelled	23.8	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein af-10; <b>PDBTitle:</b> crystal structure of an af10 fragment
115	<a href="#">d1jsda_</a>	Alignment	not modelled	23.7	24	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Influenza hemagglutinin headpiece
116	<a href="#">c3zwhQ_</a>	Alignment	not modelled	23.6	30	<b>PDB header:</b> ca-binding protein/motor protein <b>Chain:</b> Q: <b>PDB Molecule:</b> myosin-9; <b>PDBTitle:</b> ca2+-bound s100a4 c3s, c81s, c86s and f45w mutant complexed2 with myosin iia
117	<a href="#">c1wckA_</a>	Alignment	not modelled	23.6	34	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcla protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of bcla, the major antigen2 of the exosporium of the bacillus anthracis spore.
118	<a href="#">c5yz0C_</a>	Alignment	not modelled	23.3	10	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> atr-interacting protein; <b>PDBTitle:</b> cryo-em structure of human atr-atrip complex
119	<a href="#">c3twiC_</a>	Alignment	not modelled	23.2	34	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> bcla protein; <b>PDBTitle:</b> variable lymphocyte receptor recognition of the immunodominant2 glycoprotein of bacillus anthracis spores
120	<a href="#">c3r07A_</a>	Alignment	not modelled	23.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoate-protein ligase a subunit 1; <b>PDBTitle:</b> structural analysis of an archaeal lipoylation system. a bi-partite2 lipoate protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum