


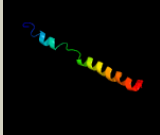

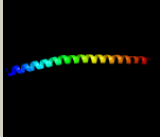

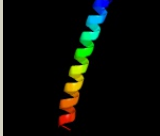

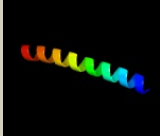

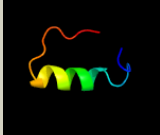
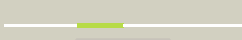
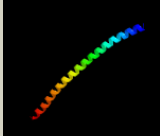

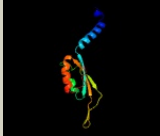






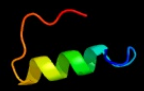

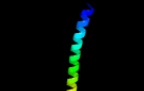

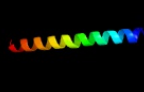


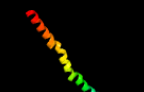
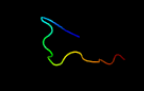


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1823 (-) _2069709_2070632
Date	Fri Aug 2 13:30:43 BST 2019
Unique Job ID	fe93e783060f7040

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gmgB_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein rv1825/mt1873; PDBTitle: crystal structure of an uncharacterized conserved protein from <i>Mycobacterium tuberculosis</i>
2	c3iynQ_	 Alignment		77.5	24	PDB header: virus Chain: Q; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
3	c5l5k_B_	 Alignment		75.5	20	PDB header: cell cycle Chain: B; PDB Molecule: polyamine-modulated factor 1; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
4	c5fv8B_	 Alignment		72.5	13	PDB header: structural protein Chain: B; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
5	c5fv8A_	 Alignment		72.4	13	PDB header: structural protein Chain: A; PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
6	d1nh8a2	 Alignment		70.5	29	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
7	c5ww1N_	 Alignment		69.0	10	PDB header: cell cycle Chain: N; PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogonosis pombe kinetochore mis12c2 subcomplex
8	c2vd3B_	 Alignment		66.3	18	PDB header: transferase Chain: B; PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from <i>Methanobacterium thermoautotrophicum</i>
9	c1junB_	 Alignment		65.6	21	PDB header: transcription regulation Chain: B; PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
10	c3iynR_	 Alignment		64.8	14	PDB header: virus Chain: R; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
11	c4yb5B_	 Alignment		64.0	21	PDB header: transferase Chain: B; PDB Molecule: atp phosphoribosyltransferase; PDBTitle: adenosine triphosphate phosphoribosyltransferase from <i>Campylobacter jejuni</i> in complex with the allosteric inhibitor histidine

12	c1nh7A_	Alignment		60.8	29	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
13	c2oqqB_	Alignment		58.7	25	PDB header: transcription Chain: B: PDB Molecule: transcription factor hy5; PDBTitle: crystal structure of hy5 leucine zipper homodimer from arabidopsis2 thaliana
14	c2xdjC_	Alignment		55.3	12	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein ybgf; PDBTitle: crystal structure of the n-terminal domain of e.coli ybgf
15	d1vioa2	Alignment		55.0	10	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
16	c3m9bk_	Alignment		54.4	20	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
17	c6czlA_	Alignment		54.2	12	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase catalytic subunit; PDBTitle: crystal structure of medicago truncatula atp-phosphoribosyltransferase2 in relaxed form
18	c4clvB_	Alignment		54.1	10	PDB header: metal binding protein Chain: B: PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
19	c3ghgK_	Alignment		51.4	12	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
20	d1qfha1	Alignment		50.2	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
21	c3n4xB_	Alignment	not modelled	49.0	10	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
22	c3cvfA_	Alignment	not modelled	48.7	16	PDB header: signaling protein Chain: A: PDB Molecule: homer protein homolog 3; PDBTitle: crystal structure of the carboxy terminus of homer3
23	c3u1aC_	Alignment	not modelled	47.8	9	PDB header: contractile protein Chain: C: PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
24	c5mg8B_	Alignment	not modelled	47.6	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
25	c4pxjB_	Alignment	not modelled	47.5	11	PDB header: protein binding Chain: B: PDB Molecule: c-jun-amino-terminal kinase-interacting protein 3; PDBTitle: crystallographic structure of the lzii fragment (anti-parallel2 orientation) from jip3
26	d1h3da2	Alignment	not modelled	46.8	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
27	c6e2jB_	Alignment	not modelled	44.1	15	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
28	c4cgkA_	Alignment	not modelled	43.8	19	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from

						streptococcus2 pneumoniae
29	c6a9pD_	Alignment	not modelled	43.5	15	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
30	c1ei3E_	Alignment	not modelled	42.1	14	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
31	c2w83C_	Alignment	not modelled	41.5	11	PDB header: protein transport Chain: C: PDB Molecule: c-jun-amino-terminal kinase-interacting protein PDBTitle: crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4
32	c2gl2B_	Alignment	not modelled	40.9	13	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
33	c1fosE_	Alignment	not modelled	39.6	12	PDB header: transcription/dna Chain: E: PDB Molecule: p55-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
34	c6e1rA_	Alignment	not modelled	39.2	35	PDB header: hydrolase Chain: A: PDB Molecule: tailspike protein; PDBTitle: crystal structure of the acinetobacter phage vb_apip_p1 tailspike2 protein
35	c1fosF_	Alignment	not modelled	38.9	23	PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
36	c2e43A_	Alignment	not modelled	38.8	18	PDB header: transcription/dna Chain: A: PDB Molecule: ccaat/enhancer-binding protein beta; PDBTitle: crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
37	c1degO_	Alignment	not modelled	38.6	13	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
38	c3ojaB_	Alignment	not modelled	38.0	16	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
39	c6ec0A_	Alignment	not modelled	37.9	11	PDB header: protein fibril Chain: A: PDB Molecule: keratin 1; PDBTitle: crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10)
40	c1cz7C_	Alignment	not modelled	37.1	14	PDB header: contractile protein Chain: C: PDB Molecule: microtubule motor protein ncd; PDBTitle: the crystal structure of a minus-end directed microtubule2 motor protein ncd reveals variable dimer conformations
41	c2o7hF_	Alignment	not modelled	37.0	19	PDB header: transcription Chain: F: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper
42	c1swiA_	Alignment	not modelled	36.3	19	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with benzene
43	c1rb6C_	Alignment	not modelled	36.3	19	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
44	c3swkB_	Alignment	not modelled	36.2	11	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
45	c3kinB_	Alignment	not modelled	35.9	9	PDB header: motor protein Chain: B: PDB Molecule: kinesin heavy chain; PDBTitle: kinesin (dimeric) from rattus norvegicus
46	c1ij3B_	Alignment	not modelled	35.8	15	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
47	c5xauC_	Alignment	not modelled	35.7	8	PDB header: cell adhesion Chain: C: PDB Molecule: laminin subunit gamma-1; PDBTitle: crystal structure of integrin binding fragment of laminin-511
48	c1ij2C_	Alignment	not modelled	33.5	18	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
49	c4u5tB_	Alignment	not modelled	33.4	19	PDB header: transcription/transcription inhibitor Chain: B: PDB Molecule: vbp leucine zipper; PDBTitle: crystal structure of vbp leucine zipper with bound arylstibonic acid
50	c3tnuA_	Alignment	not modelled	33.4	8	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)
51	c1rb1A_	Alignment	not modelled	33.3	21	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
52	c3k7zA_	Alignment	not modelled	33.3	21	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
53	c3k7zB_	Alignment	not modelled	33.3	21	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
						PDB header: dna binding protein

54	c1rb1B_	Alignment	not modelled	33.3	21	Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
55	c1ij3C_	Alignment	not modelled	32.8	18	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
56	c1t2kD_	Alignment	not modelled	32.5	15	PDB header: transcription/dna Chain: D: PDB Molecule: cyclic-amp-dependent transcription factor atf-2; PDBTitle: structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
57	c3o1A_	Alignment	not modelled	32.4	11	PDB header: structural protein Chain: A: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
58	c1ci6A_	Alignment	not modelled	32.2	12	PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
59	c2cqjA_	Alignment	not modelled	32.1	13	PDB header: rna binding protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
60	c5mg8A_	Alignment	not modelled	31.8	12	PDB header: recombination Chain: A: PDB Molecule: structural maintenance of chromosomes protein 5; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
61	c1debA_	Alignment	not modelled	30.8	10	PDB header: structural protein Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: crystal structure of the n-terminal coiled coil domain from apc
62	c1ij2B_	Alignment	not modelled	30.6	18	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
63	c4ug1A_	Alignment	not modelled	30.0	10	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
64	c3ra3D_	Alignment	not modelled	29.8	15	PDB header: de novo protein Chain: D: PDB Molecule: p2f; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
65	d1ryba_	Alignment	not modelled	29.8	15	Fold: Phosphorylase/hydrolase-like Superfamily: Peptidyl-tRNA hydrolase-like Family: Peptidyl-tRNA hydrolase-like
66	c5t58B_	Alignment	not modelled	29.8	5	PDB header: cell cycle Chain: B: PDB Molecule: klla0e05809p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
67	c1q1kA_	Alignment	not modelled	29.0	17	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: structure of atp-phosphoribosyltransferase from e. coli complexed with2 pr-atp
68	c3a5tB_	Alignment	not modelled	28.3	18	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
69	c1ztaA_	Alignment	not modelled	27.7	16	PDB header: dna-binding motif Chain: A: PDB Molecule: leucine zipper monomer; PDBTitle: the solution structure of a leucine-zipper motif peptide
70	c1ci6B_	Alignment	not modelled	26.9	16	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
71	c4w7yB_	Alignment	not modelled	26.7	10	PDB header: transport protein Chain: B: PDB Molecule: b-cell receptor-associated protein 29; PDBTitle: dimeric bap29 vded with disulfide bonds in crystal contacts
72	c6gajA_	Alignment	not modelled	25.1	14	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail (iodide)
73	c1kskA_	Alignment	not modelled	24.1	16	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
74	d1vc4a_	Alignment	not modelled	24.1	27	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
75	c1deqF_	Alignment	not modelled	24.0	10	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
76	c5w3dB_	Alignment	not modelled	23.9	13	PDB header: motor protein Chain: B: PDB Molecule: protein claret segregational; PDBTitle: the structure of kinesin-14 wild-type ncd-adp dimer
77	c6f1tX_	Alignment	not modelled	23.8	15	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
78	c6ewyA_	Alignment	not modelled	23.8	15	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
79	c2z5wA_	Alignment	not modelled	23.5	27	PDB header: structural protein Chain: A: PDB Molecule: bcla protein;

79	c2zwa	Alignment	not modelled	23.3	37	PDBTitle: tbcla, a recombinant spore surface protein from bacillus anthracis PDB header: de novo protein
80	c5j0kA	Alignment	not modelled	23.3	17	Chain: A: PDB Molecule: designed protein 2l4hc_23; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
81	d1f6ga	Alignment	not modelled	23.3	22	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
82	c1wckA	Alignment	not modelled	23.2	37	PDB header: structural protein Chain: A: PDB Molecule: bcla protein; PDBTitle: crystal structure of the c-terminal domain of bcla, the major antigen2 of the exosporium of the bacillus anthracis spore.
83	c3twiC	Alignment	not modelled	23.0	37	PDB header: immune system Chain: C: PDB Molecule: bcla protein; PDBTitle: variable lymphocyte receptor recognition of the immunodominant2 glycoprotein of bacillus anthracis spores
84	c6f1tx	Alignment	not modelled	22.8	15	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
85	c3ibpA	Alignment	not modelled	21.8	13	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
86	c2wt7B	Alignment	not modelled	21.7	18	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna
87	c2z2jA	Alignment	not modelled	21.5	22	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
88	c5bu8A	Alignment	not modelled	21.2	21	PDB header: viral protein Chain: A: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
89	d1h3fa2	Alignment	not modelled	21.1	8	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
90	c3ra3A	Alignment	not modelled	21.1	18	PDB header: de novo protein Chain: A: PDB Molecule: p1c; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
91	d1p9ka	Alignment	not modelled	20.9	14	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
92	c5dfzD	Alignment	not modelled	20.8	9	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
93	c5cj1B	Alignment	not modelled	20.4	11	PDB header: motor protein Chain: B: PDB Molecule: gp7-myh7-(1526-1571) chimera protein; PDBTitle: crystal structure of the coiled coil of myh7 residues 1526 to 15712 fused to gp7
94	d1k3ia1	Alignment	not modelled	20.4	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
95	c4xa3A	Alignment	not modelled	20.1	5	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
96	c6bl7A	Alignment	not modelled	19.7	11	PDB header: structural protein Chain: A: PDB Molecule: protein stu2; PDBTitle: s. cerevisiae stu2 coiled coil domain
97	c5yz0C	Alignment	not modelled	19.5	10	PDB header: cell cycle Chain: C: PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrip complex
98	c4aniA	Alignment	not modelled	19.2	14	PDB header: chaperone Chain: A: PDB Molecule: protein grpe; PDBTitle: structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426
99	d1gph11	Alignment	not modelled	18.9	45	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)