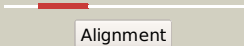
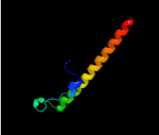
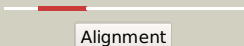
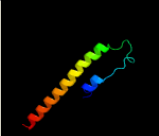
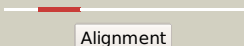

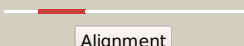
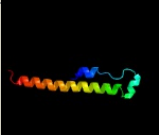
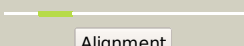
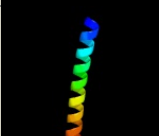
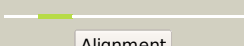
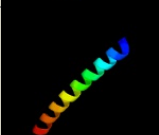
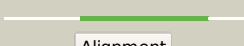
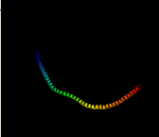



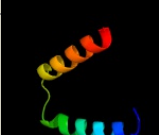



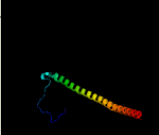


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2145c_wag31_2404624_2405406
 Date Mon Aug 5 13:25:26 BST 2019
 Unique Job ID 565c4c2e26ff3c3d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ug1A_	 Alignment		99.6	32	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
2	c6gqaD_	 Alignment		99.5	34	PDB header: cell cycle Chain: D: PDB Molecule: cell cycle protein gpsb; PDBTitle: cell division regulator s. pneumoniae gpsb
3	c4ug3C_	 Alignment		99.5	29	PDB header: cell cycle Chain: C: PDB Molecule: cell cycle protein gpsb; PDBTitle: b. subtilis gpsb n-terminal domain
4	c2wukD_	 Alignment		99.5	44	PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
5	c5fv8B_	 Alignment		65.8	34	PDB header: structural protein Chain: B: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
6	c5fv8A_	 Alignment		65.6	34	PDB header: structural protein Chain: A: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
7	c2zv4O_	 Alignment		57.1	12	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
8	c3a5tB_	 Alignment		52.2	19	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
9	c5tdyD_	 Alignment		43.8	14	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
10	c5gasN_	 Alignment		35.2	18	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
11	c5mqfl_	 Alignment		34.7	18	PDB header: splicing Chain: I: PDB Molecule: pre-mrna-processing factor 19; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of 2 splicing (c* complex)

12	d1dfoa_	Alignment		30.3	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
13	c2e43A_	Alignment		29.5	19	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
14	c2pl9F_	Alignment		28.6	45	PDB header: signaling protien Chain: F; PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
15	c2pl9E_	Alignment		28.6	45	PDB header: signaling protien Chain: E; PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
16	c2pl9D_	Alignment		28.5	45	PDB header: signaling protien Chain: D; PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
17	c1ci6A_	Alignment		27.8	20	PDB header: transcription Chain: A; PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
18	c5zk1A_	Alignment		26.7	19	PDB header: transcription/dna Chain: A; PDB Molecule: cyclic amp-responsive element-binding protein 1; PDBTitle: crystal structure of the crtc2(semet)-creb-cre complex
19	c1ysaD_	Alignment		26.0	15	PDB header: transcription/dna Chain: D; PDB Molecule: protein (gcn4); PDBTitle: the gcn4 basic region leucine zipper binds dna as a dimer2 of uninterrupted alpha helices: crystal structure of the3 protein-dna complex
20	c3qo8A_	Alignment		25.7	16	PDB header: ligase Chain: A; PDB Molecule: seryl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of seryl-trna synthetase from candida albicans
21	c1y4cA_	Alignment	not modelled	25.3	17	PDB header: de novo protein Chain: A; PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
22	c1gd2G_	Alignment	not modelled	24.8	17	PDB header: transcription/dna Chain: G; PDB Molecule: transcription factor pap1; PDBTitle: crystal structure of bzip transcription factor pap1 bound2 to dna
23	c2mxrA_	Alignment	not modelled	24.7	15	PDB header: signaling protein Chain: A; PDB Molecule: protein phosphatase 1 regulatory subunit 12a; PDBTitle: solution structure of coiled coil domain of myosin binding subunit of2 myosin light chain phosphatase
24	c1dh3A_	Alignment	not modelled	24.1	19	PDB header: transcription/dna Chain: A; PDB Molecule: transcription factor creb; PDBTitle: crystal structure of a creb bzip-cre complex reveals the2 basis for creb famly selective dimerization and dna3 binding
25	c4cr4Y_	Alignment	not modelled	23.9	39	PDB header: hydrolase Chain: Y; PDB Molecule: 26s proteasome complex subunit sem1; PDBTitle: deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
26	c5a5bY_	Alignment	not modelled	23.9	39	PDB header: hydrolase Chain: Y; PDB Molecule: 26s proteasome complex subunit sem1; PDBTitle: structure of the 26s proteasome-ubp6 complex
27	c4cr2Y_	Alignment	not modelled	23.9	39	PDB header: hydrolase Chain: Y; PDB Molecule: 26s proteasome complex subunit sem1; PDBTitle: deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
28	c4cr3Y_	Alignment	not modelled	23.9	39	PDB header: hydrolase Chain: Y; PDB Molecule: 26s proteasome complex subunit sem1; PDBTitle: deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome

29	c3iynQ	Alignment	not modelled	23.6	24	PDB header: virus Chain: Q; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
30	c1t2kD	Alignment	not modelled	23.5	18	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
31	c2rg8A	Alignment	not modelled	23.4	14	PDB header: apoptosis, translation Chain: A; PDB Molecule: programmed cell death protein 4; PDBTitle: crystal structure of programmed for cell death 4 middle ma3 domain
32	c1fosF	Alignment	not modelled	22.7	21	PDB header: transcription/dna Chain: F; PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
33	c1nfoA	Alignment	not modelled	21.9	19	PDB header: lipid transport Chain: A; PDB Molecule: apolipoprotein e2; PDBTitle: apolipoprotein e2 (apoe2, d154a mutation)
34	c2wt7B	Alignment	not modelled	21.3	26	PDB header: transcription Chain: B; PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna
35	c1fosE	Alignment	not modelled	20.4	23	PDB header: transcription/dna Chain: E; PDB Molecule: p53-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
36	c5jxfA	Alignment	not modelled	20.3	8	PDB header: hydrolase Chain: A; PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
37	d1nkpa	Alignment	not modelled	18.9	36	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
38	c3ecdC	Alignment	not modelled	17.8	15	PDB header: transferase Chain: C; PDB Molecule: serine hydroxymethyltransferase 2; PDBTitle: crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei
39	c5c9nB	Alignment	not modelled	17.1	41	PDB header: cell cycle Chain: B; PDB Molecule: geminin coiled-coil domain-containing protein 1; PDBTitle: crystal structure of gemc1 coiled-coil domain
40	c3n4xB	Alignment	not modelled	16.7	11	PDB header: replication Chain: B; PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
41	c4gegF	Alignment	not modelled	14.9	32	PDB header: cell cycle Chain: F; PDB Molecule: kinetochore-associated protein cnn1; PDBTitle: crystal structure of the spc24-spc25/cnn1 binding interface
42	c4cglA	Alignment	not modelled	14.7	15	PDB header: cell cycle Chain: A; PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
43	c5oi7A	Alignment	not modelled	14.6	15	PDB header: protein binding Chain: A; PDB Molecule: centrosomal protein of 85 kda; PDBTitle: human cep85 - coiled coil domain 4
44	c3q8tB	Alignment	not modelled	14.4	15	PDB header: apoptosis Chain: B; PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
45	c2dkjB	Alignment	not modelled	13.8	24	PDB header: transferase Chain: B; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
46	c2gl2B	Alignment	not modelled	13.6	6	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
47	d2oa5a1	Alignment	not modelled	12.6	32	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
48	c5wjba	Alignment	not modelled	12.3	12	PDB header: actin/dna binding protein Chain: A; PDB Molecule: capsid assembly scaffolding protein,myosin-7; PDBTitle: crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
49	c5j9qH	Alignment	not modelled	12.0	15	PDB header: transferase Chain: H; PDB Molecule: chromatin modification-related protein yng2; PDBTitle: crystal structure of the nua4 core complex
50	c5j0kA	Alignment	not modelled	12.0	31	PDB header: de novo protein Chain: A; PDB Molecule: designed protein 214hc2_23; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
51	c3iynR	Alignment	not modelled	11.9	22	PDB header: virus Chain: R; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
52	d1nlwa	Alignment	not modelled	11.4	12	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
53	c4c9yB	Alignment	not modelled	11.4	6	PDB header: cell cycle Chain: B; PDB Molecule: spindle and kinetochore-associated protein 1; PDBTitle: structural basis for the microtubule binding of the human2 kinetochore ska complex
54	c5ow5C	Alignment	not modelled	11.1	7	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9;

54	cJewJC_	Alignment	not modelled	11.1	7	PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9 PDB header: chaperone
55	c3m9bK_	Alignment	not modelled	11.0	22	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
56	d1nkpB_	Alignment	not modelled	10.3	19	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
57	c5d3aA_	Alignment	not modelled	10.3	16	PDB header: motor protein Chain: A; PDB Molecule: kinesin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
58	c2ke4A_	Alignment	not modelled	10.0	12	PDB header: membrane protein Chain: A; PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
59	c5w78B_	Alignment	not modelled	10.0	22	PDB header: hydrolase Chain: B; PDB Molecule: acyloxyacyl hydrolase; PDBTitle: human acyloxyacyl hydrolase (aoah), proteolytically processed
60	c2lycA_	Alignment	not modelled	10.0	12	PDB header: protein binding Chain: A; PDB Molecule: spindle and kinetochore-associated protein 1 homolog; PDBTitle: structure of c-terminal domain of ska1
61	c2n2tA_	Alignment	not modelled	9.9	40	PDB header: unknown function, structural genomics Chain: A; PDB Molecule: or303; PDBTitle: solution nmr structure of de novo designed protein (fda_60), northeast2 structural genomics consortium (nesg) target or303
62	c1avoA_	Alignment	not modelled	9.9	21	PDB header: proteasome activator Chain: A; PDB Molecule: 11s regulator; PDBTitle: proteasome activator reg(alpha)
63	c3oq3A_	Alignment	not modelled	9.5	23	PDB header: cytokine/viral protein Chain: A; PDB Molecule: interferon alpha-5; PDBTitle: structural basis of type-i interferon sequestration by a poxvirus2 decoy receptor
64	d2zjre1	Alignment	not modelled	9.4	21	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
65	c3seeA_	Alignment	not modelled	9.3	20	PDB header: sugar binding protein Chain: A; PDB Molecule: hypothetical sugar binding protein; PDBTitle: crystal structure of a putative sugar binding protein (bt_4411) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
66	d1wa8b1	Alignment	not modelled	9.3	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
67	d1nlwe_	Alignment	not modelled	9.1	13	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
68	d2fura1	Alignment	not modelled	9.0	27	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
69	c3n0lA_	Alignment	not modelled	8.9	17	PDB header: transferase Chain: A; PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
70	d1p7ba1	Alignment	not modelled	8.8	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
71	c4zryA_	Alignment	not modelled	8.8	16	PDB header: protein fibril Chain: A; PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
72	c4j2nB_	Alignment	not modelled	8.8	20	PDB header: viral protein Chain: B; PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
73	c5vr2A_	Alignment	not modelled	8.5	30	PDB header: signaling protein Chain: A; PDB Molecule: myocilin; PDBTitle: mouse myocilin leucine zipper c-terminal 7 heptad repeat
74	c4gokG_	Alignment	not modelled	8.3	44	PDB header: signaling protein Chain: G; PDB Molecule: protein unc-119 homolog a; PDBTitle: the crystal structure of arl2gppnhp in complex with unc119a
75	c5y4bA_	Alignment	not modelled	8.2	27	PDB header: electron transport Chain: A; PDB Molecule: bola-like protein 2; PDBTitle: solution structure of yeast fra2
76	c5yz0C_	Alignment	not modelled	8.1	14	PDB header: cell cycle Chain: C; PDB Molecule: atr-interacting protein; PDBTitle: cryo-em structure of human atr-atrip complex
77	d1l2pa_	Alignment	not modelled	8.1	17	Fold: Single transmembrane helix Superfamily: F1F0 ATP synthase subunit B, membrane domain Family: F1F0 ATP synthase subunit B, membrane domain
78	c4u8us_	Alignment	not modelled	8.1	19	PDB header: oxygen storage/transport Chain: S; PDB Molecule: globin d chain; PDBTitle: the crystallographic structure of the giant hemoglobin from2 glossoscolex paulistus at 3.2 a resolution.
79	d1wu3i_	Alignment	not modelled	7.8	26	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
						Fold: Ribosomal protein L6

80	d2qamg2	Alignment	not modelled	7.7	13	Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
81	c4j2nA	Alignment	not modelled	7.7	20	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
82	c1l8dB	Alignment	not modelled	7.5	26	PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: rad50 coiled-coil zn hook
83	c6e2jB	Alignment	not modelled	7.4	5	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
84	c2gd7B	Alignment	not modelled	7.4	35	PDB header: transcription Chain: B: PDB Molecule: hexim1 protein; PDBTitle: the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
85	d1r05a	Alignment	not modelled	7.3	21	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
86	c6dkuA	Alignment	not modelled	7.3	18	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
87	c4lwsB	Alignment	not modelled	7.3	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
88	c5jffD	Alignment	not modelled	7.3	17	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfict mutant g55r in complex with ecfca
89	d1gs9a	Alignment	not modelled	7.2	20	Fold: Four-helical up-and-down bundle Superfamily: Apolipoprotein Family: Apolipoprotein
90	c4y66D	Alignment	not modelled	7.1	22	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
91	c4wj3F	Alignment	not modelled	6.9	24	PDB header: ligase/rna Chain: F: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit c; PDBTitle: crystal structure of the asparagine transamidosome from pseudomonas aeruginosa
92	c5jy5A	Alignment	not modelled	6.8	31	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 1 from cryptococcus neoformans at 1.82 angstroms resolution
93	c4afiA	Alignment	not modelled	6.8	31	PDB header: cell cycle Chain: A: PDB Molecule: inhibitor of growth protein 4; PDBTitle: the crystal structure of the ing4 dimerization domain2 reveals the functional organization of the ing family of3 chromatin binding proteins.
94	c1ci6B	Alignment	not modelled	6.7	22	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
95	d1neja	Alignment	not modelled	6.6	29	Fold: Hypothetical protein YoaG Superfamily: Hypothetical protein YoaG Family: Hypothetical protein YoaG
96	d2gtsa1	Alignment	not modelled	6.5	26	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
97	c2xgjA	Alignment	not modelled	6.4	12	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
98	c4fmyE	Alignment	not modelled	6.4	10	PDB header: viral protein Chain: E: PDB Molecule: dna stabilization protein; PDBTitle: hk620 tail needle crystal form i
99	d1b5la	Alignment	not modelled	6.3	10	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)