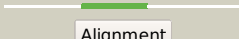
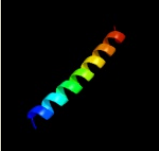
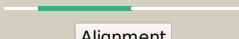
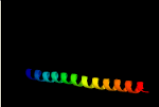
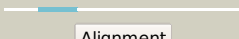


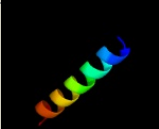

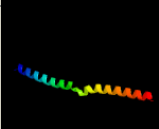

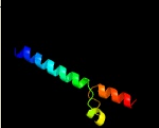

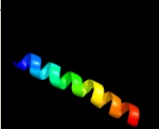


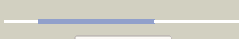
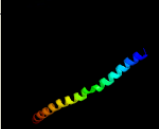
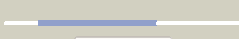
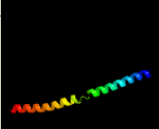




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0250c_(-)_301735_302028
Date	Tue Jul 23 14:50:31 BST 2019
Unique Job ID	66d971248cfd8aa3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3he4A_	 Alignment		52.8	25	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
2	c2n64B_	 Alignment		40.1	20	PDB header: signaling protein Chain: B: PDB Molecule: sh3 domain-containing kinase-binding protein 1; PDBTitle: nmr structure of the c-terminal coiled-coil domain of cin85
3	c4cvoA_	 Alignment		35.8	28	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-6; PDBTitle: crystal structure of the n-terminal coiled-coil domain of human dna2 excision repair protein ercc-6
4	c1mofA_	 Alignment		30.9	24	PDB header: viral protein Chain: A: PDB Molecule: moloney murine leukemia virus p15; PDBTitle: coat protein
5	c6a9pD_	 Alignment		30.1	13	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
6	c3ssuB_	 Alignment		29.4	25	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment
7	c3kltB_	 Alignment		26.0	33	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
8	c6h9mA_	 Alignment		24.0	15	PDB header: membrane protein Chain: A: PDB Molecule: coiled-coil domain-containing protein 90b, mitochondrial, PDBTitle: coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
9	c2n9bB_	 Alignment		23.9	15	PDB header: motor protein/transcription Chain: B: PDB Molecule: unconventional myosin-x, general control protein gcn4 PDBTitle: solution nmr structure of antiparallel myosin-10:gcn4 tandem coiled-2 coil
10	c6e2jB_	 Alignment		22.3	11	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
11	d1hywa_	 Alignment		19.4	15	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW

12	c3o11A_	Alignment		17.4	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
13	c3pp5A_	Alignment		17.2	37	PDB header: structural protein Chain: A; PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1
14	d1st6a5	Alignment		17.1	28	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
15	c2z5dA_	Alignment		16.4	22	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-conjugating enzyme e2 h; PDBTitle: human ubiquitin-conjugating enzyme e2 h
16	c3p8cE_	Alignment		15.4	30	PDB header: protein binding Chain: E; PDB Molecule: probable protein brick1; PDBTitle: structure and control of the actin regulatory wave complex
17	c3h0gK_	Alignment		15.4	13	PDB header: transcription Chain: K; PDB Molecule: dna-directed rna polymerase ii subunit rpb11; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
18	c3hroA_	Alignment		15.3	14	PDB header: transport protein Chain: A; PDB Molecule: transient receptor potential (trp) channel subfamily p PDBTitle: crystal structure of a c-terminal coiled coil domain of transient2 receptor potential (trp) channel subfamily p member 2 (trpp2,3 polycystic kidney disease 2)
19	c6b12B_	Alignment		12.6	38	PDB header: antimicrobial protein Chain: B; PDB Molecule: tni2; PDBTitle: structure of the tne2 in complex with tni2
20	c3iynQ_	Alignment		12.3	13	PDB header: virus Chain: Q; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
21	c4jrbA_	Alignment	not modelled	12.2	17	PDB header: lipid binding protein Chain: A; PDB Molecule: green fluorescent protein; PDBTitle: structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
22	d1wjta_	Alignment	not modelled	12.1	14	Fold: N-cbl like Superfamily: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70 Family: Conserved domain common to transcription factors TFIIIS, elongin A, CRSP70
23	c5apzA_	Alignment	not modelled	12.1	13	PDB header: dna binding protein Chain: A; PDB Molecule: general control protein gcn4, nor1 tcar0761, general PDBTitle: thermosinus carboxydivorans nor1 tcar0761 residues 68-101 and 191-2112 fused to gcn4 adaptors
24	c6dk9I_	Alignment	not modelled	12.1	22	PDB header: lyase Chain: I; PDB Molecule: dna damage-inducible protein; PDBTitle: yeast ddi2 cyanamide hydratase
25	c3iynR_	Alignment	not modelled	12.0	16	PDB header: virus Chain: R; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
26	c6gajA_	Alignment	not modelled	11.4	12	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)
27	c1s94A_	Alignment	not modelled	11.4	11	PDB header: endocytosis/exocytosis Chain: A; PDB Molecule: s-syntaxin; PDBTitle: crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
28	d1s94a_	Alignment	not modelled	11.4	11	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins

29	d2gfqa1	Alignment	not modelled	11.2	57	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
30	d1yqea1	Alignment	not modelled	10.9	71	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
31	c1y4mC_	Alignment	not modelled	10.9	10	PDB header: membrane protein Chain: C: PDB Molecule: herv-frd_6p24.1 provirus ancestral env polyprotein; PDBTitle: crystal structure of human endogenous retrovirus herv-frd envelope2 protein (syncitin-2)
32	c4jvyA_	Alignment	not modelled	10.5	19	PDB header: rna binding protein Chain: A: PDB Molecule: female germline-specific tumor suppressor gld-1; PDBTitle: structure of the star (signal transduction and activation of rna)2 domain of gld-1 bound to rna
33	c2gfqC_	Alignment	not modelled	10.5	57	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: upf0204 protein ph0006; PDBTitle: structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
34	c4bwdA_	Alignment	not modelled	10.0	29	PDB header: structural protein Chain: A: PDB Molecule: short coiled-coil protein; PDBTitle: human short coiled coil protein
35	c4wjgY_	Alignment	not modelled	9.3	18	PDB header: endocytosis Chain: Y: PDB Molecule: haptoglobin-hemoglobin receptor; PDBTitle: structure of t. brucei haptoglobin-hemoglobin receptor binding to2 human haptoglobin-hemoglobin
36	c5j0hA_	Alignment	not modelled	9.1	17	PDB header: de novo protein Chain: A: PDB Molecule: design construct 216hc3_13; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
37	c5u0pU_	Alignment	not modelled	8.7	17	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
38	c4jgsI_	Alignment	not modelled	8.4	25	PDB header: viral protein Chain: I: PDB Molecule: mlv-related proviral env polyprotein; PDBTitle: crystal structure of the xmrv tm retroviral fusion core
39	c2lf0A_	Alignment	not modelled	8.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yibI; PDBTitle: solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
40	c3hrnA_	Alignment	not modelled	8.3	14	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential (trp) channel subfamily p PDBTitle: crystal structure of a c-terminal coiled coil domain of transient2 receptor potential (trp) channel subfamily p member 2 (trpp2,3 polycystic kidney disease 2)
41	c2wayB_	Alignment	not modelled	8.2	71	PDB header: hydrolase Chain: B: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: structure of the human ddx6 c-terminal domain in complex2 with an edc3-fdf peptide
42	d1wmib1	Alignment	not modelled	8.2	13	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: RelB-like Family: RelB-like
43	d2it9a1	Alignment	not modelled	8.1	19	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
44	c2waxD_	Alignment	not modelled	7.9	71	PDB header: hydrolase Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: structure of the human ddx6 c-terminal domain in complex2 with an edc3-fdf peptide
45	c6dlcA_	Alignment	not modelled	7.9	22	PDB header: de novo protein Chain: A: PDB Molecule: designed protein dhd1:234_a; PDBTitle: designed protein dhd1:234_a, designed protein dhd1:234_b
46	c2waxB_	Alignment	not modelled	7.8	71	PDB header: hydrolase Chain: B: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: structure of the human ddx6 c-terminal domain in complex2 with an edc3-fdf peptide
47	c6cfzD_	Alignment	not modelled	7.7	17	PDB header: nuclear protein Chain: D: PDB Molecule: duo1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
48	c3sk7B_	Alignment	not modelled	7.6	57	PDB header: replication inhibitor Chain: B: PDB Molecule: protein seqa; PDBTitle: crystal structure of v. cholerae seqa
49	c6nuwF_	Alignment	not modelled	7.6	33	PDB header: cell cycle Chain: F: PDB Molecule: inner kinetochore subunit okp1; PDBTitle: yeast ctf19 complex
50	c3qh9A_	Alignment	not modelled	7.4	26	PDB header: structural protein Chain: A: PDB Molecule: liprin-beta-2; PDBTitle: human liprin-beta2 coiled-coil
51	c4jf3A_	Alignment	not modelled	7.3	13	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: crystal structure of the mpmv tm retroviral fusion core
52	c4yliA_	Alignment	not modelled	7.0	19	PDB header: sugar binding protein Chain: A: PDB Molecule: collectin-11; PDBTitle: cl-k1 trimer
53	c1ljzB_	Alignment	not modelled	6.9	80	PDB header: receptor, toxin Chain: B: PDB Molecule: acetylcholine receptor protein; PDBTitle: nmr structure of anachr-peptide (torpedo californica, alpha-subunit2 residues 182-202) in complex with alpha-bungarotoxin

54	d1rp3a1	Alignment	not modelled	6.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
55	d2cuqa1	Alignment	not modelled	6.7	11	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
56	d1yh6a1	Alignment	not modelled	6.7	22	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
57	c4b86H_	Alignment	not modelled	6.5	20	PDB header: gene regulation Chain: H: PDB Molecule: male-specific lethal 2 homolog; PDBTitle: crystal structure of the msl1-msl2 complex (3.5a)
58	d1st6a4	Alignment	not modelled	6.4	15	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
59	c5lskB_	Alignment	not modelled	6.4	9	PDB header: cell cycle Chain: B: PDB Molecule: polyamine-modulated factor 1; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
60	d1st6a3	Alignment	not modelled	6.3	15	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
61	c1qoyA_	Alignment	not modelled	6.2	5	PDB header: toxin Chain: A: PDB Molecule: hemolysin e; PDBTitle: e.coli hemolysin e (hlye, clya, shea)
62	c1jccC_	Alignment	not modelled	6.0	15	PDB header: membrane protein Chain: C: PDB Molecule: major outer membrane lipoprotein; PDBTitle: crystal structure of a novel alanine-zipper trimer at 1.7 a2 resolution, v13a,l16a,v20a,l23a,v27a,m30a,v34a mutations
63	c3oa7A_	Alignment	not modelled	5.9	15	PDB header: structural protein Chain: A: PDB Molecule: head morphogenesis protein, chaotic nuclear migration PDBTitle: structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
64	c4o7kA_	Alignment	not modelled	5.8	33	PDB header: antitumor protein Chain: A: PDB Molecule: protein osa; PDBTitle: crystal structure of oncogenic suppression activity protein - a2 plasmid fertility inhibition factor
65	c6hs5A_	Alignment	not modelled	5.7	25	PDB header: transport protein Chain: A: PDB Molecule: tssa; PDBTitle: n-terminal domain including the conserved impa_n region of the tssa2 component of the type vi secretion system from burkholderia3 cenocepacia
66	c3u24A_	Alignment	not modelled	5.5	18	PDB header: lipid binding protein Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: the structure of a putative lipoprotein of unknown function from2 shewanella oneidensis.
67	c3m9bK_	Alignment	not modelled	5.5	16	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
68	c5k9xA_	Alignment	not modelled	5.4	8	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
69	c6cfzE_	Alignment	not modelled	5.4	19	PDB header: nuclear protein Chain: E: PDB Molecule: dad4; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
70	d2qtsa1	Alignment	not modelled	5.3	17	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
71	d1j3ea_	Alignment	not modelled	5.3	43	Fold: Replication modulator SeqA, C-terminal DNA-binding domain Superfamily: Replication modulator SeqA, C-terminal DNA-binding domain Family: Replication modulator SeqA, C-terminal DNA-binding domain
72	c3swkB_	Alignment	not modelled	5.2	11	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1b fragment
73	c5wd9A_	Alignment	not modelled	5.2	25	PDB header: protein binding Chain: A: PDB Molecule: lem22; PDBTitle: crystal structure of legionella pneumophila effector lpg2328