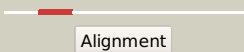

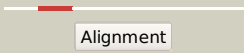
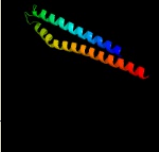

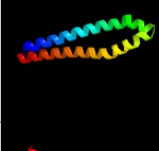
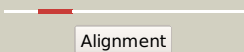

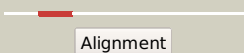
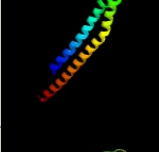
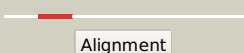


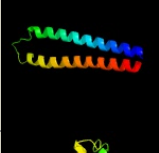
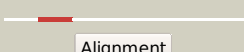
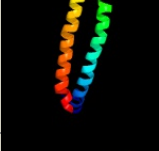
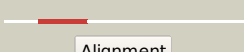
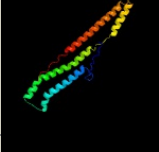
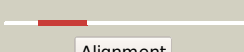
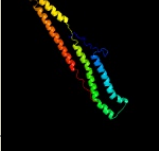
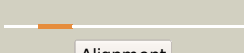
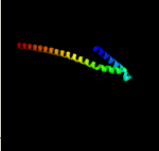
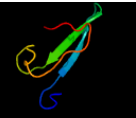
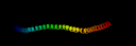

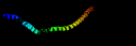

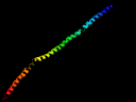
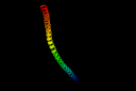

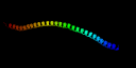


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3879c_(-)_4357771_4359960
Date	Sat Aug 10 22:05:06 BST 2019
Unique Job ID	b8773fd6f02dcd2d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4iogD_	 Alignment		96.8	11	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
2	c3gvmA_	 Alignment		96.8	21	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
3	c2vs0B_	 Alignment		96.7	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
4	c4lwsA_	 Alignment		96.7	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
5	c3zbhC_	 Alignment		96.6	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
6	d1wa8a1	 Alignment		95.6	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
7	c4lwsB_	 Alignment		94.6	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	d1wa8b1	 Alignment		93.4	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	d2g38b1	 Alignment		91.0	14	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
10	c2g38B_	 Alignment		91.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppa protein complex from mycobacterium tuberculosis
11	c3f1iH_	 Alignment		87.5	14	PDB header: protein binding Chain: H: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: human escrt-0 core complex

12	c5imuA	Alignment		86.6	22	PDB header: signaling protein Chain: A: PDB Molecule: tat (twin-arginine translocation) pathway signal sequence PDBTitle: a fragment of conserved hypothetical protein rv3899c (residues 184-2 410) from mycobacterium tuberculosis
13	c1ei3E	Alignment		84.7	12	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
14	c2p0pA	Alignment		80.6	47	PDB header: metal binding protein Chain: A: PDB Molecule: alr1010 protein; PDBTitle: calcium binding protein in the free form
15	c1deqF	Alignment		79.8	9	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
16	c2kq7B	Alignment		79.7	6	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
17	c1deqO	Alignment		72.3	10	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
18	c6e2jB	Alignment		72.1	10	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
19	c2gl2B	Alignment		69.0	18	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
20	c6ec0A	Alignment		67.3	8	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)
21	c3ghgI	Alignment	not modelled	63.3	8	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
22	c5xfsB	Alignment	not modelled	61.2	12	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
23	c1ei3C	Alignment	not modelled	60.4	13	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
24	c6a9pD	Alignment	not modelled	59.7	11	PDB header: structural protein Chain: D: PDB Molecule: glial fibrillary acidic protein; PDBTitle: crystal structure of the human glial fibrillary acidic protein 1b2 domain
25	c3ojaB	Alignment	not modelled	59.1	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
26	c4i0xA	Alignment	not modelled	59.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
27	c3ghgK	Alignment	not modelled	58.9	10	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
28	c3ol1A	Alignment	not modelled	57.6	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
						PDB header: hydrolase

29	c5ew5C_	Alignment	not modelled	49.7	7	Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
30	c4l6rA_	Alignment	not modelled	49.6	7	PDB header: membrane protein Chain: A; PDB Molecule: soluble cytochrome b562 and glucagon receptor chimera; PDBTitle: structure of the class b human glucagon g protein coupled receptor
31	c4wj2A_	Alignment	not modelled	48.9	12	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
32	c4piuB_	Alignment	not modelled	48.8	37	PDB header: cell cycle Chain: B; PDB Molecule: double-strand-break repair protein rad21 homolog; PDBTitle: crystal structure of human stromal antigen 2 (sa2) in complex with2 sister chromatid cohesion protein 1 (scc1)
33	c4yiiA_	Alignment	not modelled	47.7	36	PDB header: ligase/cell cycle Chain: A; PDB Molecule: anaphase-promoting complex subunit 2; PDBTitle: structure of an apc2-ubch10 complex reveals distinctive cullin-ring2 ligase mechanism for anaphase-promoting complex/cyclosome
34	c6gajA_	Alignment	not modelled	47.5	7	PDB header: viral protein Chain: A; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
35	c3terA_	Alignment	not modelled	45.6	5	PDB header: metal binding protein Chain: A; PDB Molecule: mammalian stromal interaction molecule-1; PDBTitle: crystal structure of soar domain with inhibition helix from c. elegans
36	c3g67A_	Alignment	not modelled	45.2	10	PDB header: signaling protein Chain: A; PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
37	d1dda_	Alignment	not modelled	45.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: SCF ubiquitin ligase complex WHB domain
38	c4kkpA_	Alignment	not modelled	40.2	38	PDB header: structural protein Chain: A; PDB Molecule: rbma protein; PDBTitle: crystal structure of vibrio cholerae rbma (crystal form 2)
39	c1bf5A_	Alignment	not modelled	40.1	7	PDB header: gene regulation/dna Chain: A; PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
40	c4rh7A_	Alignment	not modelled	40.1	12	PDB header: motor protein Chain: A; PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
41	c3ceyA_	Alignment	not modelled	39.6	20	PDB header: transcription regulator Chain: A; PDB Molecule: lethal(3)malignant brain tumor-like 2 protein; PDBTitle: crystal structure of l3mbtl2
42	c4ll8E_	Alignment	not modelled	38.6	7	PDB header: motor protein/transport protein Chain: E; PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: complex of carboxy terminal domain of myo4p and she3p middle fragment
43	c3q8tB_	Alignment	not modelled	35.8	9	PDB header: apoptosis Chain: B; PDB Molecule: beclin-1; PDBTitle: crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
44	c4cg4D_	Alignment	not modelled	35.6	5	PDB header: actin-binding protein Chain: D; PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
45	c6gapB_	Alignment	not modelled	35.0	11	PDB header: viral protein Chain: B; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
46	c5d3aA_	Alignment	not modelled	31.7	8	PDB header: motor protein Chain: A; PDB Molecule: kinesin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
47	d1qb5d_	Alignment	not modelled	30.4	33	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
48	c6ogdB_	Alignment	not modelled	29.3	7	PDB header: toxin Chain: B; PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepore state
49	c4ll7C_	Alignment	not modelled	28.8	10	PDB header: transport protein Chain: C; PDB Molecule: swi5-dependent ho expression protein 3; PDBTitle: structure of she3p amino terminus.
50	c6hk5A_	Alignment	not modelled	28.0	31	PDB header: metal binding protein Chain: A; PDB Molecule: cooj; PDBTitle: x-ray structure of a truncated mutant of the metallochaperone cooj2 with a high-affinity nickel-binding site
51	c3vkhA_	Alignment	not modelled	26.7	7	PDB header: motor protein Chain: A; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
52	d2qtsa1	Alignment	not modelled	25.2	7	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
53	c5ed8A_	Alignment	not modelled	25.0	15	PDB header: transport protein Chain: A; PDB Molecule: mkiaa0668 protein; PDBTitle: crystal structure of cc2-sun of mouse sun2
						PDB header: contractile protein Chain: A; PDB Molecule: myosin-7;

54	c5tbyA_	Alignment	not modelled	23.5	8	PDBTitle: human beta cardiac heavy meromyosin interacting-heads motif obtained2 by homology modeling (using swiss-model) of human sequence from3 aphonopelma homology model (pdb-3jhb), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
55	c3teqB_	Alignment	not modelled	22.2	9	PDB header: signaling protein Chain: B: PDB Molecule: stromal interaction molecule 1; PDBTitle: crystal structure of soar domain
56	c3s4rB_	Alignment	not modelled	21.9	11	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
57	c5cqVb_	Alignment	not modelled	21.8	8	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein q8dvw2 from streptococcus2 agalactiae
58	c3vkhB_	Alignment	not modelled	20.6	9	PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
59	d1m0wa1	Alignment	not modelled	20.6	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Eukaryotic glutathione synthetase, substrate-binding domain
60	c6gaoC_	Alignment	not modelled	20.5	11	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail and body
61	c3jcuO_	Alignment	not modelled	20.2	21	PDB header: membrane protein Chain: O: PDB Molecule: oxygen-evolving enhancer protein 1, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
62	c3a6mB_	Alignment	not modelled	19.4	7	PDB header: chaperone Chain: B: PDB Molecule: protein grpe; PDBTitle: crystal structure of grpe from thermus thermophilus hb8
63	d1vp5a_	Alignment	not modelled	19.2	9	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
64	c1dkgB_	Alignment	not modelled	19.2	20	PDB header: complex (hsp24/hsp70) Chain: B: PDB Molecule: nucleotide exchange factor grpe; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
65	c6o7xa_	Alignment	not modelled	18.8	11	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
66	d1kqfb2	Alignment	not modelled	18.8	33	Fold: Single transmembrane helix Superfamily: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor Family: Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
67	d2gu2a1	Alignment	not modelled	18.8	15	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
68	c5cofA_	Alignment	not modelled	18.6	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
69	c5jxfA_	Alignment	not modelled	18.4	9	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
70	c5wwlN_	Alignment	not modelled	18.0	10	PDB header: cell cycle Chain: N: PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
71	c5ywwA_	Alignment	not modelled	17.6	12	PDB header: nuclear protein Chain: A: PDB Molecule: sun domain-containing protein 1; PDBTitle: aid-sun tandem of sun1
72	c3ibpA_	Alignment	not modelled	17.0	5	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
73	c2j8pA_	Alignment	not modelled	16.0	23	PDB header: nuclear protein Chain: A: PDB Molecule: cleavage stimulation factor 64 kda subunit; PDBTitle: nmr structure of c-terminal domain of human cstf-64
74	c3okqA_	Alignment	not modelled	16.0	14	PDB header: protein binding Chain: A: PDB Molecule: bud site selection protein 6; PDBTitle: crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
75	c5yfpE_	Alignment	not modelled	15.6	9	PDB header: exocytosis Chain: E: PDB Molecule: exocyst complex component sec10; PDBTitle: cryo-em structure of the exocyst complex
76	c5j9qH_	Alignment	not modelled	15.3	14	PDB header: transferase Chain: H: PDB Molecule: chromatin modification-related protein yng2; PDBTitle: crystal structure of the nua4 core complex
77	d1rmja_	Alignment	not modelled	15.2	22	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
78	c2fuqA_	Alignment	not modelled	15.1	17	PDB header: sugar binding protein Chain: A: PDB Molecule: heparinase ii protein; PDBTitle: crystal structure of heparinase ii
79	c2ch7A_	Alignment	not modelled	15.0	7	PDB header: chemotaxis Chain: A: PDB Molecule: methyl-accepting chemotaxis protein;

79	c2c17A	Alignment	not modelled	13.9	7	PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima PDB header: transcription Chain: A; PDB Molecule: nf-kb essential modulator,nf-kappa-b essential modulator, PDBTitle: structure of nemo(51-112) with n- and c-terminal coiled-coil adaptors.
80	c6mi3A	Alignment	not modelled	14.9	12	PDB header: splicing Chain: K; PDB Molecule: pre-mrna-splicing factor spf27; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
81	c5mqfK	Alignment	not modelled	14.9	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
82	d2ez9a3	Alignment	not modelled	14.8	22	PDB header: transferase Chain: B; PDB Molecule: non-lee encoded effector protein nleb; PDBTitle: structure of transferase mutant-c23s,c199s
83	c5h5yB	Alignment	not modelled	14.6	30	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
84	d1qnta2	Alignment	not modelled	14.6	27	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
85	d1lvfa	Alignment	not modelled	14.5	11	PDB header: ligase Chain: A; PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
86	c3lssA	Alignment	not modelled	14.3	5	PDB header: protein binding Chain: A; PDB Molecule: effector protein avr3a; PDBTitle: solution structure of avr3a_60-147 from phytophthora infestans
87	c2narA	Alignment	not modelled	14.3	33	PDB header: immune system Chain: A; PDB Molecule: m protein, serotype 2.1; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m23 protein
88	c5hyuA	Alignment	not modelled	14.1	14	Fold: PH domain-like barrel Superfamily: PH domain-like Family: VPS36 N-terminal domain-like
89	d2hthb1	Alignment	not modelled	14.1	17	PDB header: contractile protein Chain: D; PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
90	c2d3eD	Alignment	not modelled	14.0	7	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
91	d1gija1	Alignment	not modelled	13.8	37	PDB header: hydrolase Chain: B; PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
92	c5voxb	Alignment	not modelled	13.8	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
93	d1tifa	Alignment	not modelled	13.7	29	Fold: Regulator of G-protein signaling, RGS Superfamily: Regulator of G-protein signaling, RGS Family: Regulator of G-protein signaling, RGS
94	d1iapa	Alignment	not modelled	13.4	44	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
95	d3buxb3	Alignment	not modelled	13.1	30	PDB header: hydrolase/unknown function Chain: C; PDB Molecule: uncharacterized protein pf2011; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
96	c3enoC	Alignment	not modelled	12.9	32	PDB header: contractile protein Chain: C; PDB Molecule: smooth muscle tropomyosin alpha; PDBTitle: n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
97	c3u1aC	Alignment	not modelled	12.7	11	PDB header: immune system Chain: A; PDB Molecule: ring-infected erythrocyte surface antigen; PDBTitle: shifting the polarity of some critical residues in malarial peptides2 binding to host cells is a key factor in breaking conserved antigens
98	c2muaA	Alignment	not modelled	12.6	57	PDB header: signaling protein Chain: F; PDB Molecule: kiaa0380; PDBTitle: structure of the rgs-like domain from pdz-rhogef
99	c1htjF	Alignment	not modelled	12.5	56	