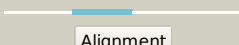
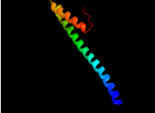

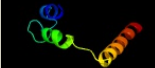


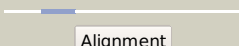

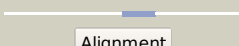

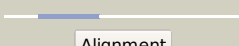
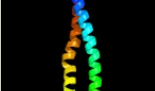
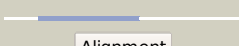

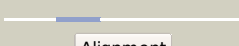
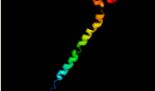


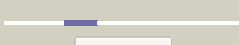
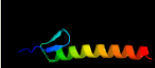




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3900c_(-)_4385551_4386486
Date	Sat Aug 10 22:05:08 BST 2019
Unique Job ID	1d7c6386f7c3d3bb3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xbjA_	 Alignment		31.6	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from <i>Campylobacter jejuni</i>
2	c1mg1A_	 Alignment		31.2	14	PDB header: viral protein Chain: A; PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose-binding protein) PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera
3	c2p58C_	 Alignment		26.2	28	PDB header: transport protein/chaperone Chain: C; PDB Molecule: putative type iii secretion protein yscg; PDBTitle: structure of the <i>Yersinia pestis</i> type iii secretion system needle2 protein yscf in complex with its chaperones ysce/yscg
4	c3hm5A_	 Alignment		25.6	30	PDB header: transcription Chain: A; PDB Molecule: dna methyltransferase 1-associated protein 1; PDBTitle: sant domain of human dna methyltransferase 1 associated protein 1
5	c2kngA_	 Alignment		24.3	62	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
6	c2vs0B_	 Alignment		23.5	14	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor exsa; PDBTitle: structural analysis of homodimeric <i>Staphylococcus aureus</i> virulence factor exsa
7	c4ut1A_	 Alignment		21.4	13	PDB header: motor protein Chain: A; PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from <i>Burkholderia pseudomallei</i>
8	c6odmK_	 Alignment		20.1	20	PDB header: viral protein Chain: K; PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
9	c4myyA_	 Alignment		19.1	50	PDB header: protein binding Chain: A; PDB Molecule: curg, curh fusion protein; PDBTitle: structure of a class 2 docking domain complex from modules curg and2 curh of the curacin a polyketide synthase
10	c2ynyC_	 Alignment		17.5	20	PDB header: membrane protein Chain: C; PDB Molecule: general control protein gcn4, putative inner membrane PDBTitle: salmonella enterica sada 255-302 fused to gcn4 adaptors (sadaK1)
11	d1r9da_	 Alignment		13.3	17	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: PFL-like

12	c3m91D_	Alignment		11.8	47	PDB header: hydrolase regulator Chain: D: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa
13	c3m91B_	Alignment		11.8	47	PDB header: hydrolase regulator Chain: B: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa
14	c2d4yA_	Alignment		11.6	15	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
15	c3pppA_	Alignment		11.4	2	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline-binding protein; PDBTitle: structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
16	d1nh2b_	Alignment		11.3	26	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
17	c1wwuA_	Alignment		10.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein flj21935; PDBTitle: solution structure of the sam_pnt domain of human protein2 flj21935
18	c4inmV_	Alignment		10.5	60	PDB header: structural protein/dna Chain: V: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle
19	c4x23V_	Alignment		10.5	60	PDB header: structural protein/dna Chain: V: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle
20	c4y6tD_	Alignment		10.2	52	PDB header: structural protein Chain: D: PDB Molecule: coat protein; PDBTitle: structure of tobacco streak virus coat protein dimer at 2.4 angstroms2 resolution
21	d1uptb_	Alignment	not modelled	9.5	46	Fold: GRIP domain Superfamily: GRIP domain Family: GRIP domain
22	c2e8mA_	Alignment	not modelled	9.4	25	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
23	d2dkya1	Alignment	not modelled	9.4	42	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
24	c5w54A_	Alignment	not modelled	9.3	67	PDB header: cytokine Chain: A: PDB Molecule: stress response peptide-2; PDBTitle: cytokine-like stress response peptide-2 in manduca sexta
25	c4n4jA_	Alignment	not modelled	9.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxylamine oxidoreductase; PDBTitle: kueningenia stuttgartiensis hydroxylamine oxidoreductase
26	d2h80a1	Alignment	not modelled	8.7	42	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
27	c4x23X_	Alignment	not modelled	8.4	60	PDB header: structural protein/dna Chain: X: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle
28	d1wa8a1	Alignment	not modelled	8.3	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
29	c5vtIA_	Alignment	not modelled	8.3	14	PDB header: unknown function Chain: A: PDB Molecule: tb427.07.360- putative uncharacterized metacyclic invariant PDBTitle: structure of metacyclic invariant surface protein ,

						tb427.07.360, from2 trypanosoma brucei.
30	c4inmX_	Alignment	not modelled	7.9	60	PDB header: structural protein/dna Chain: X: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle
31	c3ewqA_	Alignment	not modelled	7.6	20	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: hcov-229e nsp3 adrp domain
32	c5hudA_	Alignment	not modelled	7.5	30	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) PDBTitle: non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
33	c2bcwC_	Alignment	not modelled	7.1	22	PDB header: ribosome Chain: C: PDB Molecule: elongation factor g; PDBTitle: coordinates of the n-terminal domain of ribosomal protein l11,c-2 terminal domain of ribosomal protein l7/l12 and a portion of the g3 domain of elongation factor g, as fitted into cryo-em map of an4 escherichia coli 70s*ef-g*gdp*fusidic acid complex
34	c5azaA_	Alignment	not modelled	7.1	18	PDB header: sugar binding protein, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein,oligosaccharyl PDBTitle: crystal structure of mbp-saglb fusion protein with a 20-residue spacer2 in the connector helix
35	c2zs6B_	Alignment	not modelled	7.1	52	PDB header: toxin Chain: B: PDB Molecule: hemagglutinin components ha3; PDBTitle: ha3 subcomponent of botulinum type c progenitor toxin
36	c5t87D_	Alignment	not modelled	6.7	69	PDB header: toxin Chain: D: PDB Molecule: cdii immunity protein; PDBTitle: crystal structure of cdi complex from cupriavidus taiwanensis lmg2 19424
37	c3j47U_	Alignment	not modelled	6.6	16	PDB header: protein binding Chain: U: PDB Molecule: 26s proteasome regulatory subunit rpn8; PDBTitle: formation of an intricate helical bundle dictates the assembly of the2 26s proteasome lid
38	c2vriA_	Alignment	not modelled	6.4	23	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: structure of the nsp3 x-domain of human coronavirus nl63
39	d2b7oa1	Alignment	not modelled	6.2	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
40	c1rijA_	Alignment	not modelled	6.1	41	PDB header: de novo protein Chain: A: PDB Molecule: e6apn1 peptide; PDBTitle: e6-bind trp-cage (e6apn1)
41	c3zbhC_	Alignment	not modelled	6.0	24	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
42	c2csdB_	Alignment	not modelled	5.9	31	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
43	d1uxya2	Alignment	not modelled	5.8	32	Fold: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Superfamily: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
44	c5ydnA_	Alignment	not modelled	5.6	25	PDB header: viral protein Chain: A: PDB Molecule: gene product j; PDBTitle: mu pahge neck subunit
45	c3htrB_	Alignment	not modelled	5.5	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris
46	c1m1jA_	Alignment	not modelled	5.5	16	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
47	c5n2uC_	Alignment	not modelled	5.4	22	PDB header: viral protein Chain: C: PDB Molecule: nucleoprotein; PDBTitle: influenza d virus nucleoprotein
48	c3qflA_	Alignment	not modelled	5.4	18	PDB header: protein binding Chain: A: PDB Molecule: mla10; PDBTitle: coiled-coil domain-dependent homodimerization of intracellular mla2 immune receptors defines a minimal functional module for triggering3 cell death
49	c3a9kC_	Alignment	not modelled	5.3	38	PDB header: signaling protein/metal binding protein Chain: C: PDB Molecule: mitogen-activated protein kinase kinase kinase 7- PDBTitle: crystal structure of the mouse tab3-nzf in complex with2 lys63-linked di-ubiquitin
50	c3m9dQ_	Alignment	not modelled	5.2	47	PDB header: chaperone Chain: Q: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain
51	c3m9dP_	Alignment	not modelled	5.2	47	PDB header: chaperone Chain: P: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain
52	c3r6uA_	Alignment	not modelled	5.2	0	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein;

