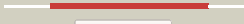

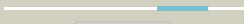
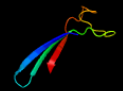



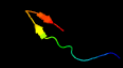



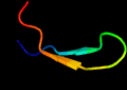
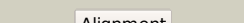






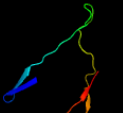


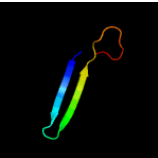
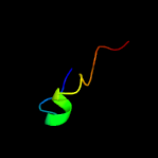


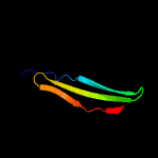

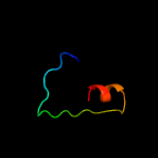

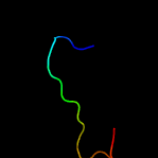


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2253 (-)_2527994_2528497
Date	Mon Aug 5 13:25:39 BST 2019
Unique Job ID	b450af5aeeb751c0


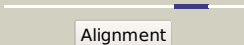
Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xlmB_	 Alignment		97.3	23	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase pknI; PDBTitle: monomer form of m.tuberculosis pknI sensor domain
2	c6hdvB_	 Alignment		38.9	23	PDB header: biotin binding protein Chain: B; PDB Molecule: afifavidin; PDBTitle: the crystal structure of intact afifavidin apo form
3	c2lboA_	 Alignment		37.8	11	PDB header: cell adhesion Chain: A; PDB Molecule: microneme protein 3; PDBTitle: eimeria tenella microneme protein 3 mar_b domain
4	d2p3pa1	 Alignment		37.3	33	Fold: PG1388-like Superfamily: PG1388-like Family: PG1388-like
5	c4ggzC_	 Alignment		30.4	23	PDB header: biotin binding protein Chain: C; PDB Molecule: bradavidin 2; PDBTitle: the structure of bradavidin2-biotin complex
6	c5oxwD_	 Alignment		24.5	38	PDB header: splicing Chain: D; PDB Molecule: neq068; PDBTitle: structure of neqn from nanoarchaeum equitans
7	c6ff43_	 Alignment		23.9	47	PDB header: splicing Chain: 3; PDB Molecule: bud13 homolog; PDBTitle: human bact spliceosome core structure
8	c2mkcC_	 Alignment		19.1	42	PDB header: splicing Chain: C; PDB Molecule: pre-mrna-splicing factor cwc26; PDBTitle: cooperative structure of the heterotrimeric pre-mrna retention and2 splicing complex
9	c5zwoY_	 Alignment		18.4	42	PDB header: splicing Chain: Y; PDB Molecule: pre-mrna-splicing factor cwc26; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
10	c6m9yD_	 Alignment		17.8	19	PDB header: fluorescent protein Chain: D; PDB Molecule: fluorescent protein lanfp6a; PDBTitle: x-ray structure of branchiostoma floridae fluorescent protein lanfp6a
11	d2o14a1	 Alignment		16.2	24	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: YxiM N-terminal domain-like

12	c4injA	Alignment		15.4	29	PDB header: protein binding Chain: A: PDB Molecule: streptavidin/rhizavidin hybrid; PDBTitle: structure based engineering of streptavidin monomer with a reduced2 biotin dissociation rate
13	c5xh9A	Alignment		13.6	23	PDB header: hydrolase Chain: A: PDB Molecule: extracellular invertase; PDBTitle: aspergillus kawachii beta-fructofuranosidase
14	c1qg9A	Alignment		13.6	50	PDB header: transmembrane channel Chain: A: PDB Molecule: protein (sodium channel protein, brain ii alpha PDBTitle: second repeat (is2mic) from voltage-gated sodium channel
15	d1kfw2	Alignment		13.0	44	Fold: FKBP-like Superfamily: Chitinase insertion domain Family: Chitinase insertion domain
16	c5mmjw	Alignment		12.1	17	PDB header: ribosome Chain: W: PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
17	c5gvyB	Alignment		11.8	28	PDB header: immune system Chain: B: PDB Molecule: beta-2-microglobulin; PDBTitle: crystal structure of duck mhc class i for 1.71 angstrom
18	c3rd5A	Alignment		11.7	33	PDB header: oxidoreductase Chain: A: PDB Molecule: mypaa.01249.c; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
19	d1fgpa	Alignment		11.5	22	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
20	c2j42A	Alignment		11.2	22	PDB header: toxin Chain: A: PDB Molecule: c2 toxin component-ii; PDBTitle: low quality crystal structure of the transport component c2-2 ii of the c2-toxin from clostridium botulinum
21	c5jk2I	Alignment	not modelled	11.1	57	PDB header: cell adhesion Chain: I: PDB Molecule: tp0751; PDBTitle: crystal structure of treponema pallidum tp0751 (pallilysin)
22	d1wioa4	Alignment	not modelled	10.9	63	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
23	d1vjha	Alignment	not modelled	10.6	11	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
24	d1swga	Alignment	not modelled	10.3	35	Fold: Streptavidin-like Superfamily: Avidin/streptavidin Family: Avidin/streptavidin
25	d1muja1	Alignment	not modelled	10.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
26	d1cida2	Alignment	not modelled	9.8	63	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
27	c1wcuA	Alignment	not modelled	9.5	38	PDB header: carbohydrate binding Chain: A: PDB Molecule: non-catalytic protein 1; PDBTitle: cbm29_1, a family 29 carbohydrate binding module from2 piromyces equi
28	d1gwma	Alignment	not modelled	9.1	50	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 29 carbohydrate binding module, CBM29
29	d1loxda	Alignment	not modelled	8.8	24	Fold: GFP-like Superfamily: GFP-like

					Family:Fluorescent proteins
30	c3rduA	Alignment	not modelled	8.7	23 PDB header: biotin binding protein Chain: A: PDB Molecule: streptavidin; PDBTitle: crystal structure of r7-2 streptavidin complexed with peg
31	c2xjqA	Alignment	not modelled	8.5	37 PDB header: cell adhesion Chain: A: PDB Molecule: flocculation protein flo5; PDBTitle: x-ray structure of the n-terminal domain of the flocculin2 flo5 from saccharomyces cerevisiae
32	c3ks7D	Alignment	not modelled	7.9	19 PDB header: hydrolase Chain: D: PDB Molecule: putative putative pngase f; PDBTitle: crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
33	c5uasA	Alignment	not modelled	7.9	50 PDB header: lyase Chain: A: PDB Molecule: ulvanlyase-pl25; PDBTitle: structure of a new family of polysaccharide lyase pl25-ulvanlyase2 bound to -[glca(1-4)rha3s]-
34	c6rrkC	Alignment	not modelled	7.8	44 PDB header: gene regulation Chain: C: PDB Molecule: double-strand-break repair protein rad21 homolog; PDBTitle: crystal structure of the central region of human cohesin subunit stag12 in complex with rad21 peptide
35	c3ew2A	Alignment	not modelled	7.8	14 PDB header: unknown function Chain: A: PDB Molecule: rhizavidin; PDBTitle: crystal structure of rhizavidin-biotin complex
36	c4he4A	Alignment	not modelled	7.6	14 PDB header: fluorescent protein Chain: A: PDB Molecule: yellow fluorescent protein; PDBTitle: crystal structure of the yellow fluorescent protein phiyfp (phialidium2 sp.)
37	c6f37B	Alignment	not modelled	7.5	36 PDB header: sugar binding protein Chain: B: PDB Molecule: nano3,fucose-binding lectin protein; PDBTitle: fusion protein of rsl and trimeric coiled coil
38	c5fk8B	Alignment	not modelled	7.4	28 PDB header: hydrolase Chain: B: PDB Molecule: beta-fructofuranosidase; PDBTitle: structure of d80a-fructofuranosidase from xanthophyllomyces2 dendrorhous complexed with neo-erlose
39	c4hzvA	Alignment	not modelled	7.4	33 PDB header: hydrolase Chain: A: PDB Molecule: neuraminidase; PDBTitle: the crystal structure of influenza a neuraminidase n3
40	d1uzma1	Alignment	not modelled	7.3	21 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
41	d1riea	Alignment	not modelled	7.3	18 Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
42	c5kgzA	Alignment	not modelled	7.1	57 PDB header: virulence factor Chain: A: PDB Molecule: modulin beta2; PDBTitle: phenol-soluble modulin beta2
43	c4dxbB	Alignment	not modelled	6.9	50 PDB header: structural protein Chain: B: PDB Molecule: nesprin-2; PDBTitle: human sun2-kash2 complex
44	c3kvoB	Alignment	not modelled	6.9	16 PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxysteroid dehydrogenase-like protein 2; PDBTitle: crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdI2)
45	c2rt4A	Alignment	not modelled	6.9	45 PDB header: de novo protein Chain: A: PDB Molecule: af.2a1; PDBTitle: nmr structure of designed protein, af.2a1, (ensembles)
46	c5y9hA	Alignment	not modelled	6.9	26 PDB header: cell adhesion Chain: A: PDB Molecule: safd,putative outer membrane protein,putative outer PDBTitle: crystal structure of safdaa-dsc complex
47	d1wwwv	Alignment	not modelled	6.7	27 Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin
48	c2rpsA	Alignment	not modelled	6.6	57 PDB header: immune system Chain: A: PDB Molecule: chemokine; PDBTitle: solution structure of a novel insect chemokine isolated from2 integument
49	c1vw4b	Alignment	not modelled	6.5	33 PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
50	c4h8pA	Alignment	not modelled	6.4	24 PDB header: heme-binding protein Chain: A: PDB Molecule: iron transport-associated domain protein; PDBTitle: neat5 domain of isdx2, a b. anthracis hemophore in complex with heme
51	c2n73B	Alignment	not modelled	6.2	29 PDB header: transferase/transferase regulator Chain: B: PDB Molecule: phosphatidylinositol 4-kinase beta; PDBTitle: solution structure of the acbd3:pi4kb complex
52	c1w0pA	Alignment	not modelled	6.2	24 PDB header: hydrolase Chain: A: PDB Molecule: sialidase; PDBTitle: vibrio cholerae sialidase with alpha-2,6-sialyllactose
53	c3qfhE	Alignment	not modelled	6.1	50 PDB header: hydrolase Chain: E: PDB Molecule: epidermin leader peptide processing serine protease epip; PDBTitle: 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
54	c4zelA	Alignment	not modelled	6.1	10 PDB header: oxidoreductase Chain: A: PDB Molecule: dopamine beta-hydroxylase; PDBTitle: human dopamine beta-hydroxylase

55	c2hpwA	Alignment	not modelled	6.0	13	PDB header: luminescent protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: green fluorescent protein from clytia gregaria
56	c5tpjA	Alignment	not modelled	6.0	38	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
57	c3c12A	Alignment	not modelled	6.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flagd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
58	c2naeA	Alignment	not modelled	6.0	40	PDB header: signaling protein Chain: A: PDB Molecule: t-cell-specific surface glycoprotein cd28; PDBTitle: membrane-bound mouse cd28 cytoplasmic tail
59	d3bkjh1	Alignment	not modelled	5.9	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
60	d1kp5a	Alignment	not modelled	5.8	24	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
61	c2z6zA	Alignment	not modelled	5.8	22	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent protein dropa; PDBTitle: crystal structure of a photoswitchable gfp-like protein2 dropa in the bright-state
62	c3imoC	Alignment	not modelled	5.7	18	PDB header: unknown function Chain: C: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of vibrio cholerae. integron2 cassette protein vch_cass14
63	c4k90B	Alignment	not modelled	5.7	14	PDB header: hydrolase Chain: B: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
64	c3szhB	Alignment	not modelled	5.6	25	PDB header: biotin-binding protein Chain: B: PDB Molecule: avidin/streptavidin; PDBTitle: crystal structure of apo shwanavidin (p1 form)
65	d2dk3a1	Alignment	not modelled	5.6	31	Fold: SH3-like barrel Superfamily: Mib/herc2 domain-like Family: Mib/herc2 domain
66	c4gqzB	Alignment	not modelled	5.6	32	PDB header: metal binding protein Chain: B: PDB Molecule: putative periplasmic or exported protein; PDBTitle: crystal structure of s.cuep
67	c4aivA	Alignment	not modelled	5.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nitrite reductase [nad(p)h] small subunit nird; PDBTitle: crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
68	c4dxrB	Alignment	not modelled	5.5	50	PDB header: structural protein Chain: B: PDB Molecule: nesprin-1; PDBTitle: human sun2-kash1 complex
69	d1c16a1	Alignment	not modelled	5.5	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
70	c3h6zA	Alignment	not modelled	5.5	50	PDB header: transcription Chain: A: PDB Molecule: polycomb protein sfmbt; PDBTitle: crystal structure of the four mbt repeats of drosophila melanogaster2 sfmbt in complex with peptide rhr (me)k vlr
71	c3dkmA	Alignment	not modelled	5.4	31	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hectd1; PDBTitle: crystal structure of the hectd1 cph domain
72	d2qamc2	Alignment	not modelled	5.4	50	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
73	c2e6pA	Alignment	not modelled	5.3	16	PDB header: structural protein Chain: A: PDB Molecule: obscurin-like protein 1; PDBTitle: solution structure of the ig-like domain (714-804) from2 human obscurin-like protein 1
74	c2x9aA	Alignment	not modelled	5.2	29	PDB header: viral protein Chain: A: PDB Molecule: attachment protein g3p; PDBTitle: crystal structure of g3p from phage if1 in complex with its2 coreceptor, the c-terminal domain of tola
75	d2cjta1	Alignment	not modelled	5.2	13	Fold: C2 domain-like Superfamily: C2 domain (Calcium/lipid-binding domain, CaLB) Family: PLC-like (P variant)
76	c3ij2B	Alignment	not modelled	5.2	25	PDB header: hormone/protein binding Chain: B: PDB Molecule: beta-nerve growth factor; PDBTitle: ligand-receptor structure
77	d2f01a1	Alignment	not modelled	5.1	37	Fold: Streptavidin-like Superfamily: Avidin/streptavidin Family: Avidin/streptavidin
78	d1c99a	Alignment	not modelled	5.1	50	Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C
79	d1cmca	Alignment	not modelled	5.1	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Met repressor, Metj (MetR)
80	c4uqtB	Alignment	not modelled	5.1	25	PDB header: translation Chain: B: PDB Molecule: pre-mrna-splicing factor cwc26; PDBTitle: rrm-peptide structure in res complex
81	d1b8mb	Alignment	not modelled	5.1	19	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin

82	c4b7qD_	 Alignment	not modelled	5.0	27	PDB header: hydrolase Chain: D: PDB Molecule: neuraminidase; PDBTitle: h1n1 2009 pandemic influenza virus: resistance of the i223r2 neuraminidase mutant explained by kinetic and structural analysis
83	c4bjjB_	 Alignment	not modelled	5.0	33	PDB header: transcription Chain: B: PDB Molecule: transcription factor tau subunit sfc7; PDBTitle: sfc1-sfc7 dimerization module