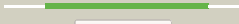

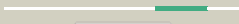
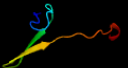
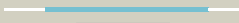
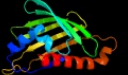



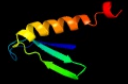





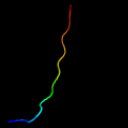

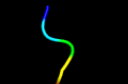



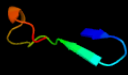


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2616 (-) _2945340_2945840
Date	Wed Aug 7 12:50:26 BST 2019
Unique Job ID	72dabf5932097cb0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ns9a1	 Alignment		55.4	13	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
2	c3kioB_	 Alignment		47.7	26	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: mouse rnase h2 complex
3	d2d4ra1	 Alignment		36.3	8	Fold: TBP-like Superfamily: Bet v1-like Family: oligoketide cyclase/dehydrase-like
4	d2pcsa1	 Alignment		28.0	5	Fold: TBP-like Superfamily: Bet v1-like Family: CoxG-like
5	c5vodD_	 Alignment		23.9	19	PDB header: viral protein/immune system Chain: D: PDB Molecule: envelope glycoprotein ul130; PDBTitle: crystal structure of hcmv pentamer in complex with neutralizing2 antibody 9i6
6	d2c9qa1	 Alignment		22.7	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
7	c2g0qA_	 Alignment		20.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: at5g39720.1 protein; PDBTitle: solution structure of at5g39720.1 from arabidopsis thaliana
8	d1ix2a_	 Alignment		20.1	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
9	d1xhsa_	 Alignment		18.9	67	Fold: Gamma-glutamyl cyclotransferase-like Superfamily: Gamma-glutamyl cyclotransferase-like Family: Gamma-glutamyl cyclotransferase-like
10	d1dfca3	 Alignment		18.0	21	Fold: beta-Trefoil Superfamily: Actin-crosslinking proteins Family: Fascin
11	d1jk8a2	 Alignment		17.1	30	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain

12	c6nfqC_	Alignment		16.7	36	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
13	d1es0a2	Alignment		16.7	35	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
14	d1s9va2	Alignment		16.7	30	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
15	d1iaka2	Alignment		16.5	30	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
16	d2p24a2	Alignment		16.3	25	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
17	c1ssfA_	Alignment		16.1	13	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
18	d1klua2	Alignment		16.1	25	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
19	d1vkba_	Alignment		16.0	83	Fold: Gamma-glutamyl cyclotransferase-like Superfamily: Gamma-glutamyl cyclotransferase-like Family: Gamma-glutamyl cyclotransferase-like
20	c3dlmA_	Alignment		15.9	19	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
21	d1muja2	Alignment	not modelled	15.8	30	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
22	c2jqvA_	Alignment	not modelled	15.4	31	PDB header: structural genomics Chain: A: PDB Molecule: aig2 protein-like; PDBTitle: solution structure at3g28950.1 from arabidopsis thaliana
23	c5icuA_	Alignment	not modelled	15.3	46	PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
24	d1v30a_	Alignment	not modelled	14.4	67	Fold: Gamma-glutamyl cyclotransferase-like Superfamily: Gamma-glutamyl cyclotransferase-like Family: Gamma-glutamyl cyclotransferase-like
25	d1fnqa2	Alignment	not modelled	14.1	20	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
26	c3jubA_	Alignment	not modelled	13.8	83	PDB header: transferase Chain: A: PDB Molecule: aig2-like domain-containing protein 1; PDBTitle: human gamma-glutamylamine cyclotransferase
27	d1uvqa2	Alignment	not modelled	13.7	25	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
28	c6amgA_	Alignment	not modelled	11.4	26	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cyt p460 of nitrosomonas sp. al212
						PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase

29	c6o3pA	Alignment	not modelled	11.2	26	nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
30	c3m51P	Alignment	not modelled	11.2	50	PDB header: protein binding Chain: P: PDB Molecule: n.plumbaginifolia h+-translocating atpase mrna; PDBTitle: structure of the 14-3-3/pma2 complex stabilized by pyrrolidone1
31	c5n1tM	Alignment	not modelled	10.5	31	PDB header: oxidoreductase Chain: M: PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
32	c3gqgD	Alignment	not modelled	10.2	31	PDB header: splicing Chain: D: PDB Molecule: protein unc-119 homolog a; PDBTitle: crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a
33	c4r7kA	Alignment	not modelled	10.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein jhp0584; PDBTitle: 1.88 angstrom resolution crystal structure of hypothetical protein2 jhp0584 from helicobacter pylori.
34	c4jmqA	Alignment	not modelled	9.9	30	PDB header: viral protein Chain: A: PDB Molecule: bacteriophage t5 distal tail protein; PDBTitle: crystal structure of pb9: the dit of bacteriophage t5.
35	d2g9ha2	Alignment	not modelled	9.7	25	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
36	d1ihra	Alignment	not modelled	9.5	17	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: TonB
37	d1sdda2	Alignment	not modelled	9.5	40	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
38	d2f0ca1	Alignment	not modelled	9.1	24	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Lactophage receptor-binding protein head domain
39	c2o1sC	Alignment	not modelled	8.9	42	PDB header: transferase Chain: C: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
40	c2grxC	Alignment	not modelled	8.9	17	PDB header: metal transport Chain: C: PDB Molecule: protein tonb; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
41	d1zrua1	Alignment	not modelled	8.6	24	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Lactophage receptor-binding protein head domain
42	c2o98P	Alignment	not modelled	8.4	63	PDB header: protein binding Chain: P: PDB Molecule: plasma membrane h+ atpase; PDBTitle: structure of the 14-3-3 / h+-atpase plant complex
43	c2mx4A	Alignment	not modelled	8.1	24	PDB header: translation,protein binding Chain: A: PDB Molecule: eukaryotic translation initiation factor 4e-binding protein PDBTitle: nmr structure of phosphorylated 4e-bp2
44	c2qikA	Alignment	not modelled	8.0	83	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0131 protein ykqa; PDBTitle: crystal structure of ykqa from bacillus subtilis. northeast structural2 genomics target sr631
45	d1f2ri	Alignment	not modelled	8.0	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
46	d2g3ra2	Alignment	not modelled	7.6	24	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
47	c2bsdC	Alignment	not modelled	7.6	23	PDB header: receptor Chain: C: PDB Molecule: receptor binding protein; PDBTitle: structure of lactococcal bacteriophage p2 receptor binding protein
48	c2k7mA	Alignment	not modelled	7.5	43	PDB header: membrane protein Chain: A: PDB Molecule: gap junction alpha-5 protein; PDBTitle: structure of the connexin40 carboxyl terminal domain
49	d2yt9a1	Alignment	not modelled	7.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	c2f0cC	Alignment	not modelled	7.3	24	PDB header: viral protein Chain: C: PDB Molecule: phage tp901-1 orf49 (bpp); PDBTitle: structure of the receptor binding protein (orf49, bpp) from lactophage2 tp901-1
51	c2r7fA	Alignment	not modelled	7.0	19	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease ii family protein; PDBTitle: crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
52	d1s6na	Alignment	not modelled	6.9	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
53	c1xx3A	Alignment	not modelled	6.8	18	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
54	d2r7da2	Alignment	not modelled	6.8	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNB domain-like
						PDB header: protein binding

55	c2ysgA_	Alignment	not modelled	6.7	31	Chain: A; PDB Molecule: syntaxin-binding protein 4; PDBTitle: solution structure of the ww domain from the human syntaxin-2 binding protein 4
56	d2vnud4	Alignment	not modelled	6.6	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: RNB domain-like
57	d1de3a_	Alignment	not modelled	6.5	33	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Ribotoxin
58	c3da0C_	Alignment	not modelled	6.4	24	PDB header: viral protein Chain: C; PDB Molecule: cleaved chimeric receptor binding protein from PDBTitle: crystal structure of a cleaved form of a chimeric receptor binding2 protein from lactococcal phages subspecies tp901-1 and p2
59	c2ysfA_	Alignment	not modelled	6.2	31	PDB header: protein binding Chain: A; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
60	d1x6ma_	Alignment	not modelled	6.1	36	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
61	c2aivA_	Alignment	not modelled	6.1	10	PDB header: transport protein Chain: A; PDB Molecule: fragment of nucleoporin nup116/nsp116; PDBTitle: multiple conformations in the ligand-binding site of the yeast nuclear2 pore targeting domain of nup116p
62	d1r9ja2	Alignment	not modelled	6.0	36	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
63	c3ke6A_	Alignment	not modelled	5.9	14	PDB header: unknown function Chain: A; PDB Molecule: protein rv1364c/mt1410; PDBTitle: the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
64	c3u6xF_	Alignment	not modelled	5.9	24	PDB header: viral protein Chain: F; PDB Molecule: bpp; PDBTitle: phage tp901-1 baseplate tripod
65	c3d8mA_	Alignment	not modelled	5.7	24	PDB header: virus/viral protein Chain: A; PDB Molecule: baseplate protein, receptor binding protein; PDBTitle: crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
66	d2gskb1	Alignment	not modelled	5.6	17	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
67	d1is3a_	Alignment	not modelled	5.5	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
68	c2ml7A_	Alignment	not modelled	5.3	83	PDB header: unknown function Chain: A; PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
69	c3r4zA_	Alignment	not modelled	5.3	13	PDB header: hydrolase Chain: A; PDB Molecule: glycosyl hydrolase family 32, n terminal; PDBTitle: crystal structure of alpha-neoagarobiose hydrolase (alpha-nabh) in2 complex with alpha-d-galactopyranose from saccharophagus degradans 2-3 40
70	c2jqmA_	Alignment	not modelled	5.2	24	PDB header: transferase Chain: A; PDB Molecule: envelope protein e; PDBTitle: yellow fever envelope protein domain iii nmr structure2 (s288-k398)
71	c2dmvA_	Alignment	not modelled	5.2	31	PDB header: ligase Chain: A; PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)