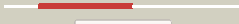
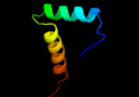










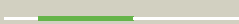








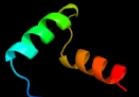


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2601A (-) _2930080_2930367
Date	Wed Aug 7 12:50:24 BST 2019
Unique Job ID	11a84d385bea1788

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bsqe1	 Alignment		91.9	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
2	c2h1oH	 Alignment		90.9	21	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
3	c5x3tA	 Alignment		88.5	41	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapb26; PDBTitle: vapbc from mycobacterium tuberculosis
4	c2an7A	 Alignment		66.4	35	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
5	d1p94a	 Alignment		58.5	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	c2k5jB	 Alignment		57.4	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
7	d1mnta	 Alignment		50.1	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
8	c2ca9B	 Alignment		45.0	18	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
9	d2hzab1	 Alignment		44.6	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	d2hzaa1	 Alignment		39.8	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
11	d2bj7a1	 Alignment		38.7	13	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

12	c2bj3D_	Alignment		34.4	13	PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
13	c1q5vB_	Alignment		30.6	24	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
14	c2kj1A_	Alignment		27.2	23	PDB header: transport protein Chain: A; PDB Molecule: bm2 protein; PDBTitle: cytoplasmic domain structure of bm2 proton channel from2 influenza b virus
15	c3j9eD_	Alignment		21.5	40	PDB header: viral protein Chain: D; PDB Molecule: vp5; PDBTitle: atomic structure of a non-enveloped virus reveals ph sensors for a2 coordinated process of cell entry
16	c3qoqC_	Alignment		20.8	23	PDB header: transcription/dna Chain: C; PDB Molecule: alginate and motility regulator z; PDBTitle: crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
17	c1rijA_	Alignment		16.5	29	PDB header: de novo protein Chain: A; PDB Molecule: e6apn1 peptide; PDBTitle: e6-bind trp-cage (e6apn1)
18	d1ujpa_	Alignment		15.7	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
19	c5tchG_	Alignment		14.1	14	PDB header: lyase Chain: G; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
20	d1hw1a1	Alignment		12.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
21	c1u9pA_	Alignment	not modelled	10.4	15	PDB header: unknown function Chain: A; PDB Molecule: parc; PDBTitle: permuted single-chain arc
22	c5sxpG_	Alignment	not modelled	9.1	70	PDB header: signaling protein/ligase Chain: G; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
23	c5sxpF_	Alignment	not modelled	9.0	70	PDB header: signaling protein/ligase Chain: F; PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: structural basis for the interaction between itch prr and beta-pix
24	c5k9xA_	Alignment	not modelled	9.0	20	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
25	c6g1nB_	Alignment	not modelled	8.2	11	PDB header: antitoxin Chain: B; PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
26	c6cmxA_	Alignment	not modelled	8.1	13	PDB header: membrane protein Chain: A; PDB Molecule: teneurin-2; PDBTitle: human teneurin 2 extra-cellular region
27	c2xa0A_	Alignment	not modelled	7.6	29	PDB header: apoptosis Chain: A; PDB Molecule: apoptosis regulator bcl-2; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
28	c6f1eA_	Alignment	not modelled	6.8	7	PDB header: immune system Chain: A; PDB Molecule: interferon gamma; PDBTitle: crystal structure of olive flounder [paralichthys olivaceus]2 interferon gamma at 2.3 angstrom resolution PDB header: ligase

29	c3fshC_	Alignment	not modelled	6.3	33	Chain: C; PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78
30	c5j10A_	Alignment	not modelled	5.7	46	PDB header: de novo protein Chain: A; PDB Molecule: peptide design 2l4hc2_24; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
31	c4drvA_	Alignment	not modelled	5.6	27	PDB header: viral protein Chain: A; PDB Molecule: outer capsid protein vp4; PDBTitle: cell attachment protein vp8* of a human rotavirus specifically2 interacts with a-type histo-blood group antigen
32	d1j09a1	Alignment	not modelled	5.4	24	Fold: An anticodon-binding domain of class I aminoacyl-tRNA synthetases Superfamily: An anticodon-binding domain of class I aminoacyl-tRNA synthetases Family: C-terminal domain of glutamyl-tRNA synthetase (GluRS)
33	c5gj6B_	Alignment	not modelled	5.4	36	PDB header: viral protein Chain: B; PDB Molecule: outer capsid protein vp4; PDBTitle: functional and structural characterization of p[19] rotavirus vp8*2 interaction with histo-blood group antigens
34	c2lxpB_	Alignment	not modelled	5.4	33	PDB header: ligase Chain: B; PDB Molecule: e3 ubiquitin-protein ligase amfr; PDBTitle: nmr structure of two domains in ubiquitin ligase gp78, ring and g2br,2 bound to its conjugating enzyme ube2g
35	c6a7vU_	Alignment	not modelled	5.3	28	PDB header: toxin/antitoxin Chain: U; PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
36	c3h8kB_	Alignment	not modelled	5.3	33	PDB header: ligase Chain: B; PDB Molecule: autocrine motility factor receptor, isoform 2; PDBTitle: crystal structure of ube2g2 complexed with the g2br domain of gp78 at2 1.8-a resolution
37	c3pmdA_	Alignment	not modelled	5.3	20	PDB header: lipid binding protein Chain: A; PDB Molecule: conserved domain protein; PDBTitle: crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
38	c5ey5A_	Alignment	not modelled	5.2	17	PDB header: lyase Chain: A; PDB Molecule: lbcats-a; PDBTitle: lbcats
39	c3navB_	Alignment	not modelled	5.1	9	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961