

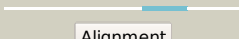

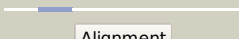


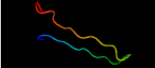

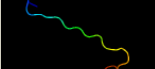

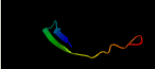

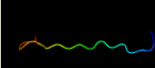


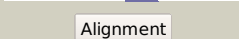
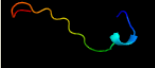

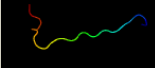
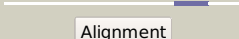
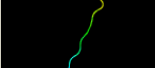


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3491 (-)_3910069_3910647
Date	Fri Aug 9 18:20:16 BST 2019
Unique Job ID	813cdfa347b7d5c2

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4r7vA_	 Alignment		43.3	17	PDB header: protein binding Chain: A; PDB Molecule: arrestin domain-containing protein 3; PDBTitle: crystal structure of n-lobe of human arrdc3(1-165)
2	c6czjA_	 Alignment		31.8	38	PDB header: de novo protein Chain: A; PDB Molecule: b10; PDBTitle: structure of a redesigned beta barrel, b10
3	d1hxmA2	 Alignment		27.6	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
4	c3qzrC_	 Alignment		22.3	20	PDB header: hormone receptor Chain: C; PDB Molecule: abscisic acid receptor pyl5; PDBTitle: crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
5	c1g4mA_	 Alignment		19.6	19	PDB header: signaling protein Chain: A; PDB Molecule: beta-arrestin1; PDBTitle: crystal structure of bovine beta-arrestin 1
6	c5icuA_	 Alignment		17.6	12	PDB header: chaperone Chain: A; PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylostinus trichosporium ob3b
7	c4gejD_	 Alignment		17.3	14	PDB header: protein binding Chain: D; PDB Molecule: thioredoxin-interacting protein; PDBTitle: n-terminal domain of vdup-1
8	c1suiA_	 Alignment		16.8	19	PDB header: signaling protein Chain: A; PDB Molecule: cone arrestin; PDBTitle: x-ray crystal structure of ambystoma tigrinum cone arrestin
9	c3n6yA_	 Alignment		16.7	23	PDB header: unknown function Chain: A; PDB Molecule: immunoglobulin-like protein; PDBTitle: crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
10	c1ayrA_	 Alignment		15.8	25	PDB header: sensory transduction Chain: A; PDB Molecule: arrestin; PDBTitle: arrestin from bovine rod outer segments
11	c1jsyA_	 Alignment		15.6	20	PDB header: signaling protein Chain: A; PDB Molecule: bovine arrestin-2 (full length); PDBTitle: crystal structure of bovine arrestin-2

12	c5djjA_	Alignment		14.5	25	PDB header: hydrolase Chain: A: PDB Molecule: 3'-phosphoadenosine 5'-phosphate phosphatase; PDBTitle: structure of m. tuberculosis cysq, a pap phosphatase with po4 and 2mg2 bound
13	c5x5sA_	Alignment		14.2	15	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: ligand induced structure of amyp-sbd
14	d2q9oa3	Alignment		12.3	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
15	d2hg6a1	Alignment		12.1	24	Fold: PA1123-like Superfamily: PA1123-like Family: PA1123-like
16	c1cf1B_	Alignment		11.6	25	PDB header: structural protein Chain: B: PDB Molecule: protein (arrestin); PDBTitle: arrestin from bovine rod outer segments
17	c3uc0B_	Alignment		9.7	25	PDB header: viral protein/immune system Chain: B: PDB Molecule: envelope protein; PDBTitle: crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
18	c3nr1B_	Alignment		9.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rumgna_01417; PDBTitle: crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
19	c6h7wC_	Alignment		9.1	5	PDB header: protein transport Chain: C: PDB Molecule: vacuolar protein sorting-associated protein 26-like PDBTitle: model of retromer-vps5 complex assembled on membrane.
20	c2rpsA_	Alignment		8.9	67	PDB header: immune system Chain: A: PDB Molecule: chemokine; PDBTitle: solution structure of a novel insect chemokine isolated from2 integument
21	c6b0nG_	Alignment	not modelled	8.7	27	PDB header: viral protein/immune system Chain: G: PDB Molecule: envelope glycoprotein gp140; PDBTitle: crystal structure of the cleavage-independent prefusion hiv env2 glycoprotein trimer of the clade a bg505 isolate (nfl construct) in3 complex with fabs pgt122 and pgv19 at 3.39 a
22	d1ypze2	Alignment	not modelled	8.7	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
23	c3fk4A_	Alignment	not modelled	8.7	14	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
24	d1lmia_	Alignment	not modelled	8.3	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Antigen MPT63/MPB63 (immunoprotective extracellular protein) Family: Antigen MPT63/MPB63 (immunoprotective extracellular protein)
25	d2j5la1	Alignment	not modelled	8.2	28	Fold: Apical membrane antigen 1 Superfamily: Apical membrane antigen 1 Family: Apical membrane antigen 1
26	c2j5IA_	Alignment	not modelled	8.2	28	PDB header: immune system Chain: A: PDB Molecule: apical membrane antigen 1; PDBTitle: structure of a plasmodium falciparum apical membrane antigen 1-fab f8.2 12.19 complex
27	d1usha1	Alignment	not modelled	8.2	11	Fold: 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain Superfamily: 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
28	c5hycC_	Alignment	not modelled	8.0	47	PDB header: unknown function Chain: C: PDB Molecule: cytoplasmic dynein 1 intermediate chain 2;

						PDBTitle: structure based function annotation of a hypothetical protein2 mgg_01005 related to the development of rice blast fungus
29	d1ykwa1	Alignment	not modelled	7.9	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
30	d1fcda2	Alignment	not modelled	7.7	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
31	d1lgbc_	Alignment	not modelled	7.5	31	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
32	d1qasa3	Alignment	not modelled	7.4	27	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
33	c6cp8B_	Alignment	not modelled	7.4	50	PDB header: toxin/antitoxin Chain: B; PDB Molecule: cdia; PDBTitle: contact-dependent growth inhibition toxin-immunity protein complex2 from from e. coli 3006
34	d2cpqa1	Alignment	not modelled	7.4	5	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
35	c4ufqB_	Alignment	not modelled	7.1	26	PDB header: hydrolase Chain: B; PDB Molecule: hyaluronidase; PDBTitle: structure of a novel hyaluronidase (hyal_sk) from streptomyces2 koganeiensis.
36	d1ka1a_	Alignment	not modelled	6.9	28	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
37	c5j6yA_	Alignment	not modelled	6.9	22	PDB header: cell adhesion Chain: A; PDB Molecule: antifreeze protein; PDBTitle: crystal structure of pa14 domain of mpafp antifreeze protein
38	c5fk0F_	Alignment	not modelled	6.5	9	PDB header: structural protein Chain: F; PDB Molecule: coatomer subunit delta; PDBTitle: yeast delta-cop-i mu-homology domain
39	d1svda1	Alignment	not modelled	6.4	24	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
40	c2djyB_	Alignment	not modelled	6.3	46	PDB header: ligase/signaling protein Chain: B; PDB Molecule: mothers against decapentaplegic homolog 7; PDBTitle: solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
41	c2kxqB_	Alignment	not modelled	6.3	46	PDB header: protein binding Chain: B; PDB Molecule: smad7 py motif containing peptide; PDBTitle: solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
42	c5yt6B_	Alignment	not modelled	6.0	17	PDB header: protein binding Chain: B; PDB Molecule: tax1-binding protein 1; PDBTitle: crystal structure of tax1bp1 ubz2 in complex with mono-ubiquitin
43	d1x4ka1	Alignment	not modelled	6.0	56	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
44	c2czhB_	Alignment	not modelled	5.9	25	PDB header: hydrolase Chain: B; PDB Molecule: inositol monophosphatase 2; PDBTitle: crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
45	c2n59A_	Alignment	not modelled	5.9	16	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein csgh; PDBTitle: solution structure of r. palustris csgh
46	c6hunA_	Alignment	not modelled	5.8	13	PDB header: photosynthesis Chain: A; PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
47	d1ej7I1	Alignment	not modelled	5.8	21	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
48	d1gv8a_	Alignment	not modelled	5.7	19	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Transferrin
49	c4nasD_	Alignment	not modelled	5.7	21	PDB header: lyase Chain: D; PDB Molecule: ribulose-bisphosphate carboxylase; PDBTitle: the crystal structure of a rubisco-like protein (mtnw) from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
50	d1cc3a_	Alignment	not modelled	5.5	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
51	d2fmra_	Alignment	not modelled	5.5	6	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
52	d1w7ca2	Alignment	not modelled	5.5	38	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
53	c5swkC_	Alignment	not modelled	5.4	13	PDB header: de novo protein Chain: C; PDB Molecule: de novo protein based on the inhibitor amoebiasin-1; PDBTitle: crystal structure of p53 epitope-scaffold based on a inhibitor of2 cysteine proteases in complex with human mdm2
54	c1m1jA_	Alignment	not modelled	5.3	38	PDB header: blood clotting Chain: A; PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two

					different2 bound ligands
55	c4gdgA_	Alignment	not modelled	5.2	21 PDB header: hydrolase Chain: A: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase1 from entamoeba histolytica
56	c3nwrA_	Alignment	not modelled	5.2	17 PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
57	d1nwpa_	Alignment	not modelled	5.2	13 Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
58	c5muyB_	Alignment	not modelled	5.1	38 PDB header: viral protein Chain: B: PDB Molecule: l protein; PDBTitle: structure of a c-terminal domain of a reptarenavirus I protein with2 m7gtp
59	c4h69A_	Alignment	not modelled	5.1	33 PDB header: isomerase Chain: A: PDB Molecule: allene oxide cyclase; PDBTitle: crystal structure of the allene oxide cyclase 2 from physcomitrella2 patens complexed with substrate analog
60	c4s3lA_	Alignment	not modelled	5.1	13 PDB header: cell adhesion Chain: A: PDB Molecule: major pilin protein; PDBTitle: crystal structure of major pilin protein pitb from type ii pilus of2 streptococcus pneumoniae
61	c5lc5A_	Alignment	not modelled	5.1	38 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-ubiquinone oxidoreductase chain 3; PDBTitle: structure of mammalian respiratory complex i, class2