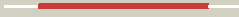





















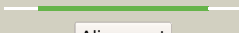




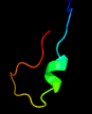





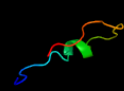






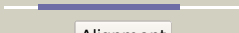
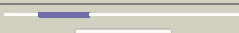
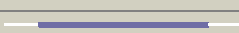

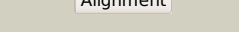
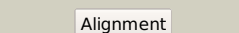




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3098A_(RVBD3098A)_3467603_3467923
 Date Thu Aug 8 16:20:27 BST 2019
 Unique Job ID 6f4bba0c72561dca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1m1fa_	 Alignment		100.0	23	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
2	c4mzpC_	 Alignment		100.0	28	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
3	d1ne8a_	 Alignment		99.9	31	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
4	c5hjaz_	 Alignment		99.9	27	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
5	d1ub4a_	 Alignment		99.9	23	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
6	c5xe3B_	 Alignment		99.9	27	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
7	c5hk3B_	 Alignment		99.9	24	PDB header: hydrolase/dna Chain: B: PDB Molecule: endoribonuclease mazf6; PDBTitle: crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna
8	c5wygC_	 Alignment		99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
9	c5ccaA_	 Alignment		99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	c3jrzA_	 Alignment		97.2	13	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvi-formii-ph5.6
11	d3vuba_	 Alignment		94.7	14	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB

12	c2l89A_	 Alignment		52.7	9	PDB header: protein binding Chain: A; PDB Molecule: pwwp domain-containing protein 1; PDBTitle: solution structure of pdp1 pwwp domain reveals its unique binding2 sites for methylated h4k20 and dna
13	c5ikjA_	 Alignment		38.0	17	PDB header: transcription Chain: A; PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
14	c3mxuA_	 Alignment		30.6	21	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
15	c6n1bA_	 Alignment		27.4	14	PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate-binding protein; PDBTitle: crystal structure of an n-acetylgalactosamine deacetylase from f.2 plautii in complex with blood group b trisaccharide
16	c2edgA_	 Alignment		22.9	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
17	d1onla_	 Alignment		21.9	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
18	c3a8jF_	 Alignment		20.3	21	PDB header: transferase/transport protein Chain: F; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
19	d1h3za_	 Alignment		17.9	8	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
20	c2yewB_	 Alignment		17.7	45	PDB header: virus Chain: B; PDB Molecule: e1 envelope glycoprotein; PDBTitle: modeling barmah forest virus structural proteins
21	d2daqal	 Alignment	not modelled	16.7	12	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
22	d1hpca_	 Alignment	not modelled	16.6	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
23	c4rmoA_	 Alignment	not modelled	16.5	14	PDB header: toxin/rna Chain: A; PDB Molecule: cptn toxin; PDBTitle: crystal structure of the cptn type iii toxin-antitoxin system from2 eubacterium rectale
24	c6nk6B_	 Alignment	not modelled	15.3	36	PDB header: virus like particle/signaling protein Chain: B; PDB Molecule: e1 glycoprotein; PDBTitle: electron cryo-microscopy of chikungunya vlp in complex with mouse2 mxra8 receptor
25	c3iftA_	 Alignment	not modelled	15.1	17	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
26	c2alaA_	 Alignment	not modelled	14.8	41	PDB header: viral protein Chain: A; PDB Molecule: structural polyprotein (p130); PDBTitle: crystal structure of the semliki forest virus envelope protein e1 in2 its monomeric conformation.
27	c2xfcD_	 Alignment	not modelled	14.6	36	PDB header: virus Chain: D; PDB Molecule: e1 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the semliki forest virus cryo-em map
28	c2xfbF_	 Alignment	not modelled	14.6	36	PDB header: virus Chain: F; PDB Molecule: e1 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map

29	c3n42F_	Alignment	not modelled	14.5	36	PDB header: viral protein Chain: F; PDB Molecule: e1 envelope glycoprotein; PDBTitle: crystal structures of the mature envelope glycoprotein complex (furin2 cleavage) of chikungunya virus.
30	c1ld4O_	Alignment	not modelled	14.1	41	PDB header: virus Chain: O; PDB Molecule: spike glycoprotein e1; PDBTitle: placement of the structural proteins in sindbis virus
31	d2alaa2	Alignment	not modelled	13.2	41	Fold: Viral glycoprotein, central and dimerisation domains Superfamily: Viral glycoprotein, central and dimerisation domains Family: Viral glycoprotein, central and dimerisation domains
32	c5vc8B_	Alignment	not modelled	13.1	8	PDB header: dna binding protein Chain: B; PDB Molecule: histone-lysine n-methyltransferase nsd2; PDBTitle: crystal structure of the whsc1 pwwp1 domain
33	c2jysA_	Alignment	not modelled	12.2	30	PDB header: hydrolase Chain: A; PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
34	c3j0cG_	Alignment	not modelled	11.1	36	PDB header: virus Chain: G; PDB Molecule: e1 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
35	c1z8yE_	Alignment	not modelled	11.1	41	PDB header: virus Chain: E; PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
36	c3muwE_	Alignment	not modelled	10.6	41	PDB header: virus Chain: E; PDB Molecule: structural polyprotein; PDBTitle: pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
37	c3pfsA_	Alignment	not modelled	10.6	10	PDB header: protein binding Chain: A; PDB Molecule: bromodomain and phd finger-containing protein 3; PDBTitle: pwwp domain of human bromodomain and phd finger-containing protein 3
38	c3j0fG_	Alignment	not modelled	10.5	41	PDB header: virus Chain: G; PDB Molecule: e1 envelope glycoprotein; PDBTitle: sindbis virion
39	c5cuzA_	Alignment	not modelled	10.5	45	PDB header: chaperone Chain: A; PDB Molecule: methylmalonic aciduria and homocystinuria type d protein, PDBTitle: crystal structure of semet-substituted n-terminal truncated human b12-2 chaperone cbld (108-296)
40	c6mx4J_	Alignment	not modelled	10.3	36	PDB header: virus Chain: J; PDB Molecule: e1; PDBTitle: cryoem structure of chimeric eastern equine encephalitis virus
41	c4p7xA_	Alignment	not modelled	9.9	21	PDB header: oxidoreductase Chain: A; PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
42	c3jb4A_	Alignment	not modelled	9.8	20	PDB header: virus Chain: A; PDB Molecule: vp1; PDBTitle: structure of ljunjan virus: insight into picornavirus packaging
43	c1l1kA_	Alignment	not modelled	9.4	36	PDB header: protein binding Chain: A; PDB Molecule: barstar; PDBTitle: nmr identification and characterization of the flexible2 regions in the 160 kd molten globule-like aggregate of3 barstar at low ph
44	c3muuA_	Alignment	not modelled	9.1	41	PDB header: viral protein Chain: A; PDB Molecule: structural polyprotein; PDBTitle: crystal structure of the sindbis virus e2-e1 heterodimer at low ph
45	c3efyB_	Alignment	not modelled	8.7	29	PDB header: cell cycle Chain: B; PDB Molecule: cif (cell cycle inhibiting factor); PDBTitle: structure of the cyclomodulin cif from pathogenic2 escherichia coli
46	d2nlua1	Alignment	not modelled	8.4	9	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
47	c4ld6A_	Alignment	not modelled	7.7	7	PDB header: unknown function Chain: A; PDB Molecule: pwwp domain-containing protein 2b; PDBTitle: pwwp domain of human pwwp domain-containing protein 2b
48	d1e5ra_	Alignment	not modelled	7.6	10	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
49	d1n27a_	Alignment	not modelled	7.5	9	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
50	c3llrA_	Alignment	not modelled	7.3	11	PDB header: transferase Chain: A; PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the pwwp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
51	d1ex0a1	Alignment	not modelled	7.2	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
52	c1ssfA_	Alignment	not modelled	6.7	23	PDB header: cell cycle Chain: A; PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
53	c1e9yB_	Alignment	not modelled	6.7	23	PDB header: hydrolase Chain: B; PDB Molecule: urease subunit beta; PDBTitle: crystal structure of helicobacter pylori urease in complex with2 aceto-hydroxamic acid
						PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein;

54	c2v1IA_	Alignment	not modelled	6.2	20	PDBTitle: structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
55	c3d55A_	Alignment	not modelled	6.2	19	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
56	c2fqpD_	Alignment	not modelled	6.0	13	PDB header: metal binding protein Chain: D: PDB Molecule: hypothetical protein bp2299; PDBTitle: crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
57	c5t86A_	Alignment	not modelled	5.9	36	PDB header: toxin Chain: A: PDB Molecule: cdia toxin; PDBTitle: crystal structure of cdi complex from e. coli a0 34/86
58	d2q3za1	Alignment	not modelled	5.6	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
59	d1zaka2	Alignment	not modelled	5.5	21	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
60	d2gy9m1	Alignment	not modelled	5.5	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
61	c2ky9A_	Alignment	not modelled	5.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ydhk; PDBTitle: solution nmr structure of ydhk c-terminal domain from b.subtilis,2 northeast structural genomics consortium target target sr518
62	c2bf9A_	Alignment	not modelled	5.3	11	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
63	c3bxpA_	Alignment	not modelled	5.3	17	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution
64	d1w7ca2	Alignment	not modelled	5.2	11	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
65	c4eyzB_	Alignment	not modelled	5.1	25	PDB header: hydrolase Chain: B: PDB Molecule: cellulosome-related protein module from ruminococcus PDBTitle: crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavifaciens that resembles papain-like cysteine3 peptidases