


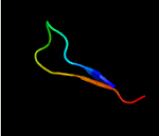

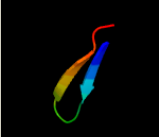

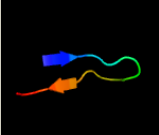

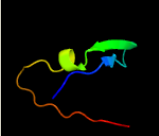

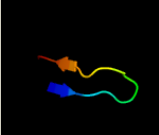

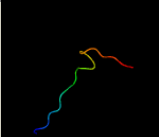

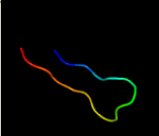

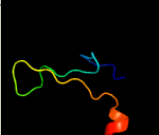



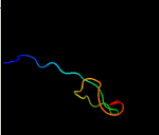
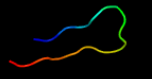
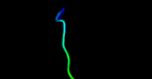
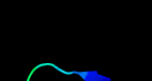


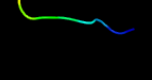

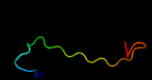



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3748 (-)_4197414_4197773
Date	Fri Aug 9 18:20:44 BST 2019
Unique Job ID	1463099a1c9e9f2e

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zjnA_	 Alignment		64.6	32	PDB header: transport protein Chain: A: PDB Molecule: portal protein; PDBTitle: crystal structure of the bacteriophage g20c portal protein
2	c4dfcC_	 Alignment		37.8	13	PDB header: hydrolase/dna binding protein Chain: C: PDB Molecule: transcription-repair-coupling factor; PDBTitle: core uvra/trcf complex
3	c3fpnB_	 Alignment		30.3	38	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrb interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains
4	d2b2na1	 Alignment		24.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
5	d1pn0a2	 Alignment		24.3	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
6	c3hjhA_	 Alignment		22.1	13	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair-coupling factor; PDBTitle: a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
7	c3gasA_	 Alignment		17.6	28	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
8	d2eyqa4	 Alignment		16.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
9	d2phna1	 Alignment		13.8	39	Fold: CofE-like Superfamily: CofE-like Family: CofE-like
10	d1pjwa_	 Alignment		13.0	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
11	d1zcca1	 Alignment		12.5	24	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase

12	c2eyqA	Alignment		12.5	13	PDB header: hydrolase Chain: A; PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
13	c5bjuA	Alignment		12.4	57	PDB header: membrane protein Chain: A; PDB Molecule: wlal protein; PDBTitle: x-ray structure of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h)
14	d1t5la1	Alignment		12.3	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
15	c6fgkA	Alignment		11.7	18	PDB header: transferase Chain: A; PDB Molecule: gtp pyrophosphokinase ywac; PDBTitle: crystal structure of the small alarmone synthetase 2 from bacillus2 subtilis
16	c2kxjA	Alignment		11.6	50	PDB header: protein binding Chain: A; PDB Molecule: ubx domain-containing protein 4; PDBTitle: solution structure of ubx domain of human ubxd2 protein
17	c5vugA	Alignment		10.4	33	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein rv2277c; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 domain of uncharacterized protein rv2277c from mycobacterium3 tuberculosis
18	c4lkbA	Alignment		9.3	19	PDB header: isomerase Chain: A; PDB Molecule: hypothetical protein alr4568/putative 4-oxalocrotonate PDBTitle: crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120
19	c5dotA	Alignment		8.9	22	PDB header: ligase Chain: A; PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
20	c4r7oE	Alignment		8.7	21	PDB header: hydrolase Chain: E; PDB Molecule: glycerophosphoryl diester phosphodiesterase, putative; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterasefrom bacillus anthraci
21	c5douC	Alignment	not modelled	8.5	22	PDB header: ligase Chain: C; PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
22	c3l9dA	Alignment	not modelled	8.4	19	PDB header: transferase Chain: A; PDB Molecule: putative gtp pyrophosphokinase; PDBTitle: the crystal structure of smu.1046c from streptococcus mutans ua159
23	d1ztxe1	Alignment	not modelled	8.3	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
24	d1kzfa	Alignment	not modelled	8.1	38	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: Autoinducer synthetase
25	c1rfoC	Alignment	not modelled	8.0	83	PDB header: viral protein Chain: C; PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibrin
26	c3ie4A	Alignment	not modelled	7.2	30	PDB header: immune system Chain: A; PDB Molecule: gram-negative binding protein 3; PDBTitle: b-glucan binding domain of drosophila gnbp3 defines a novel2 family of pattern recognition receptor
27	c3f44A	Alignment	not modelled	7.2	18	PDB header: oxidoreductase Chain: A; PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
28	d1oe1a2	Alignment	not modelled	6.4	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins

29	c5dedA	Alignment	not modelled	6.3	18	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase yjbm; PDBTitle: crystal structure of the small alarmone synthetase 1 from bacillus2 subtilis bound to its product pppgpp
30	d1s6na	Alignment	not modelled	6.3	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
31	c5wsnC	Alignment	not modelled	6.2	31	PDB header: virus Chain: C: PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
32	c3rb7E	Alignment	not modelled	6.2	16	PDB header: metal binding protein Chain: E: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of cbd12 from calx1.2
33	c3uzeC	Alignment	not modelled	6.1	38	PDB header: immune system Chain: C: PDB Molecule: envelope protein; PDBTitle: crystal structure of the dengue virus serotype 3 envelope protein2 domain iii in complex with the variable domains of mab 4e11
34	c3egpA	Alignment	not modelled	6.0	28	PDB header: viral protein Chain: A: PDB Molecule: envelope protein; PDBTitle: crystal structure analysis of dengue-1 envelope protein2 domain iii
35	c3cjsA	Alignment	not modelled	5.9	44	PDB header: transferase/ribosomal protein Chain: A: PDB Molecule: ribosomal protein l11 methyltransferase; PDBTitle: minimal recognition complex between prma and ribosomal protein l11
36	d1ok8a1	Alignment	not modelled	5.8	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
37	c6cj6B	Alignment	not modelled	5.8	15	PDB header: viral protein Chain: B: PDB Molecule: protein f9; PDBTitle: structure of the poxvirus protein f9
38	c2j6gA	Alignment	not modelled	5.8	24	PDB header: cell adhesion Chain: A: PDB Molecule: faeg; PDBTitle: faeg from f4ac etec strain 5_95, produced in tobacco plant chloroplast
39	d1zela1	Alignment	not modelled	5.5	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rv2827c N-terminal domain-like
40	d1mwwa	Alignment	not modelled	5.5	15	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
41	c5ireA	Alignment	not modelled	5.3	27	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
42	d1z66a1	Alignment	not modelled	5.3	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
43	c4qniA	Alignment	not modelled	5.2	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an auxiliary nutrient binding protein (bt3507)2 from bacteroides thetaiotaomicron vpi-5482 at 2.30 a resolution
44	c2h0pA	Alignment	not modelled	5.1	21	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: nmr structure of the dengue-4 virus envelope protein domain2 iii
45	c6ouuB	Alignment	not modelled	5.1	12	PDB header: virus like particle Chain: B: PDB Molecule: major capsid protein; PDBTitle: symmetric reconstruction of human norovirus gii.4 minerva strain vlp2 in t=4 symmetry
46	d1svba1	Alignment	not modelled	5.1	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain