




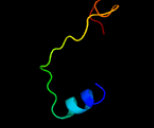



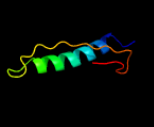







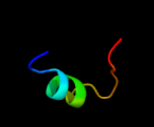

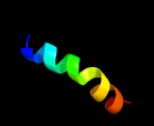










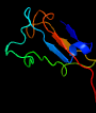


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3008 (-) _3366654_3367277
Date	Thu Aug 8 16:20:17 BST 2019
Unique Job ID	60a3d0c456d25a86

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5t42A_	 Alignment		41.6	58	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
2	c4csoD_	 Alignment		37.7	30	PDB header: transcription Chain: D: PDB Molecule: orfy protein, transcription factor; PDBTitle: the structure of orfy from thermoproteus tenax
3	c2ckcA_	 Alignment		34.3	22	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 7; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
4	d2ckca1	 Alignment		34.3	22	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
5	c3nj2B_	 Alignment		30.2	23	PDB header: unknown function Chain: B: PDB Molecule: duf269-containing protein; PDBTitle: crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
6	d2v0ea1	 Alignment		26.6	31	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
7	d2ckaa1	 Alignment		23.2	38	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
8	c2ckaA_	 Alignment		23.2	38	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 8; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
9	d2v0fa1	 Alignment		15.3	29	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
10	d1pcfa_	 Alignment		13.2	16	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Transcriptional coactivator PC4 C-terminal domain
11	d2dl6a1	 Alignment		12.8	38	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like

12	c4boeA	Alignment		11.4	48	PDB header: cholesterol binding protein Chain: A: PDB Molecule: japanin; PDBTitle: japanin from rhipicephalus appendiculatus bound to cholesterol:2 tetragonal crystal form
13	c3hefB	Alignment		10.9	33	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
14	d2pila	Alignment		10.8	45	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
15	c3sokB	Alignment		10.1	64	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
16	c4aghA	Alignment		9.8	11	PDB header: transcription Chain: A: PDB Molecule: mosub1, transcription cofactor; PDBTitle: structural features of ssdna binding protein mosub1 from magnaporthe2 oryzae
17	c6qv9K	Alignment		9.1	36	PDB header: protein fibril Chain: K: PDB Molecule: prepilin peptidase-dependent protein d; PDBTitle: structure of the type iv pilus from enterohemorrhagic escherichia coli2 (ehc)
18	c6qhgB	Alignment		8.3	71	PDB header: viral protein Chain: B: PDB Molecule: polymerase; PDBTitle: structure of the cap-binding domain of rift valley fever virus l2 protein
19	d1oqwa	Alignment		8.1	64	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
20	c5a98A	Alignment		7.6	25	PDB header: viral protein Chain: A: PDB Molecule: polyhedrin; PDBTitle: crystal structure of trichoplusia ni cpv15 polyhedra
21	c5lskD	Alignment	not modelled	7.5	37	PDB header: cell cycle Chain: D: PDB Molecule: kinetochore-associated protein dsn1 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
22	c1r7gA	Alignment	not modelled	7.5	56	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
23	c6iieA	Alignment	not modelled	7.5	17	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase alpha; PDBTitle: crystal structure of human diacylglycerol kinase alpha ef-hand domains2 bound to ca2+
24	c5wdaL	Alignment	not modelled	7.2	27	PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
25	d2ciwa2	Alignment	not modelled	7.2	63	Fold: EF Hand-like Superfamily: Cloroperoxidase Family: Cloroperoxidase
26	c6oq5E	Alignment	not modelled	7.2	30	PDB header: toxin Chain: E: PDB Molecule: e3; PDBTitle: structure of the full-length clostridium difficile toxin b in complex2 with 3 vhhs
27	c1nauA	Alignment	not modelled	7.0	50	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon; PDBTitle: nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
28	c2vziB	Alignment	not modelled	6.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 167aa long hypothetical dutpase;

28	c2y4B_	Alignment	not modelled	5.4	17	PDBTitle: crystal structure of dctp deaminase from sulfolobus tokodaii
29	c1r7cA_	Alignment	not modelled	5.9	56	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 50% tfe)
30	c2z9fC_	Alignment	not modelled	5.8	42	PDB header: biosynthetic protein Chain: C: PDB Molecule: cellulose synthase operon protein d; PDBTitle: crystal structure of axcesd protein from acetobacter xylinum
31	d2fefa1	Alignment	not modelled	5.6	53	Fold: Bromodomain-like Superfamily: PA2201 N-terminal domain-like Family: PA2201 N-terminal domain-like
32	c5jfzB_	Alignment	not modelled	5.3	38	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfict in complex with ecfica mutant e28g
33	c5jfzF_	Alignment	not modelled	5.3	38	PDB header: transferase Chain: F: PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfict in complex with ecfica mutant e28g