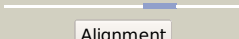

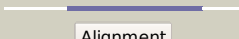

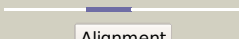
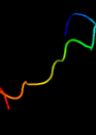











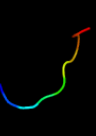



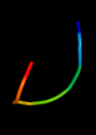
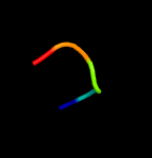



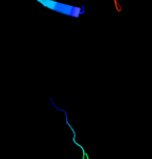

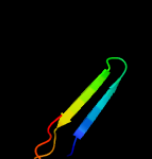
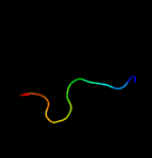
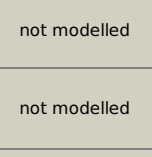


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0397A_(RVBD0397A)_476397_476645
 Date Tue Jul 23 14:50:47 BST 2019
 Unique Job ID d4892128b3deeb95

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xrzA_	 Alignment		20.6	86	PDB header: transcription Chain: A: PDB Molecule: zinc finger y-chromosomal protein; PDBTitle: nmr structure of a zinc finger with cyclohexanylalanine2 substituted for the central aromatic residue
2	d1u34a_	 Alignment		14.1	24	Fold: Hormone receptor domain Superfamily: Hormone receptor domain Family: Hormone receptor domain
3	c1jy2O_	 Alignment		12.6	63	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of the central region of bovine fibrinogen (e52 fragment) at 1.4 angstroms resolution
4	c4rwcC_	 Alignment		11.8	42	PDB header: membrane protein/hormone Chain: C: PDB Molecule: maltose-binding periplasmic protein, receptor activity- PDBTitle: crystal structure of the clr:ramp1 extracellular domain heterodimer2 with bound high affinity cgpr analog
5	c2lufA_	 Alignment		10.5	75	PDB header: de novo protein Chain: A: PDB Molecule: retro trp-cage peptide; PDBTitle: retro trp-cage peptide
6	c1ansA_	 Alignment		10.2	75	PDB header: toxin Chain: A: PDB Molecule: neurotoxin iii; PDBTitle: three-dimensional structure in solution of neurotoxin iii from the sea2 anemone anemonia sulcata
7	c4vlyB_	 Alignment		9.2	43	PDB header: hydrolase Chain: B: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, staphylococcus aureus at 2.25 angstrom resolution
8	c3v2iA_	 Alignment		8.9	71	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
9	c2kghA_	 Alignment		8.9	60	PDB header: toxin Chain: A: PDB Molecule: venom peptide 2; PDBTitle: solution structure of brachyperma ruhnaui toxin 2
10	c1pqrA_	 Alignment		8.3	71	PDB header: toxin Chain: A: PDB Molecule: alpha-a-conotoxin eiva; PDBTitle: solution conformation of alphaa-conotoxin eiva
11	c4dhwA_	 Alignment		7.8	86	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from pseudomonas2 aeruginosa with adipic acid at 2.4 angstrom resolution

12	d3b2ua2	Alignment		7.6	100	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
13	d1ryba_	Alignment		7.3	71	Fold: Phosphorylase/hydrolase-like Superfamily: Peptidyl-tRNA hydrolase-like Family: Peptidyl-tRNA hydrolase-like
14	d1yy9a4	Alignment		7.3	71	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
15	c4fopA_	Alignment		7.2	71	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from acinetobacter2 baumannii at 1.86 a resolution
16	d1a0ia1	Alignment		7.1	39	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
17	c1wysA_	Alignment		7.0	31	PDB header: metal binding protein Chain: A: PDB Molecule: riken cdna 2310008m20 protein; PDBTitle: solution structure of the first zf-an1 domain of mouse2 riken cdna 2310008m20 protein
18	c5x29B_	Alignment		6.9	80	PDB header: viral protein Chain: B: PDB Molecule: envelope small membrane protein; PDBTitle: nmr structure of the sars coronavirus e protein pentameric ion channel
19	c5oemA_	Alignment		6.8	17	PDB header: transcription Chain: A: PDB Molecule: interferon regulatory factor 9; PDBTitle: crystal structure of interferon regulatory factor 9 iad domain
20	d1pe4a_	Alignment		6.7	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
21	d1jzaa_	Alignment	not modelled	6.6	27	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
22	c5zx8A_	Alignment	not modelled	6.6	71	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from thermus thermophilus
23	c4q55B_	Alignment	not modelled	6.5	71	PDB header: hydrolase Chain: B: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from a gram-positive2 bacterium, streptococcus pyogenes at 2.19a resolution shows the3 closed structure of the substrate binding cleft
24	c5bviB_	Alignment	not modelled	6.0	29	PDB header: transcription Chain: B: PDB Molecule: interferon regulatory factor 4; PDBTitle: x-ray structure of interferon regulatory factor 4 iad domain
25	c3n7sB_	Alignment	not modelled	6.0	38	PDB header: membrane protein Chain: B: PDB Molecule: calcitonin gene-related peptide type 1 receptor; PDBTitle: crystal structure of the ectodomain complex of the cgrp receptor, a2 class-b gpcr, reveals the site of drug antagonism
26	c4g0rA_	Alignment	not modelled	5.9	39	PDB header: virus/dna Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: structural characterization of h-1 parvovirus: comparison of2 infectious virions to replication defective particles
27	c4ersA_	Alignment	not modelled	5.7	36	PDB header: immune system Chain: A: PDB Molecule: glucagon receptor; PDBTitle: a molecular basis for negative regulation of the glucagon receptor
28	c2z2jA_	Alignment	not modelled	5.4	71	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of peptidyl-trna hydrolase from

