




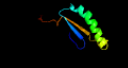















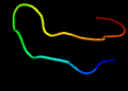
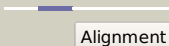

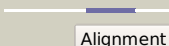

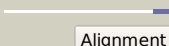

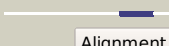

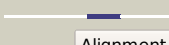

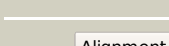



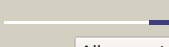


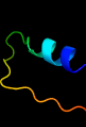
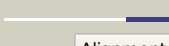
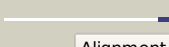
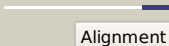
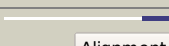

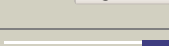
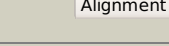
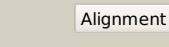


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0004_(-)_4434_4997
Date	Tue Jul 23 14:50:02 BST 2019
Unique Job ID	195970c58cf8ea01

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4tpsD_</a>	 Alignment		68.0	14	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> sporulation inhibitor of dna replication, sira, in complex with domain2 i of dnaa
2	<a href="#">c2ayaA_</a>	 Alignment		45.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit tau; <b>PDBTitle:</b> solution structure of the c-terminal 14 kda domain of the2 tau subunit from escherichia coli dna polymerase iii
3	<a href="#">c2e0gA_</a>	 Alignment		45.1	13	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> dnaa n-terminal domain
4	<a href="#">d1q52a_</a>	 Alignment		41.9	15	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
5	<a href="#">d1rjma_</a>	 Alignment		19.5	18	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
6	<a href="#">c6cfzC_</a>	 Alignment		17.0	38	<b>PDB header:</b> nuclear protein <b>Chain:</b> C: <b>PDB Molecule:</b> dad2; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
7	<a href="#">d2d28c1</a>	 Alignment		13.3	20	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> EspE N-terminal domain-like <b>Family:</b> GSP1I protein E N-terminal domain-like
8	<a href="#">c3h02F_</a>	 Alignment		12.2	16	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
9	<a href="#">c2jpiA_</a>	 Alignment		11.4	11	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
10	<a href="#">d1nr3a_</a>	 Alignment		10.9	17	<b>Fold:</b> DNA-binding protein Tfx <b>Superfamily:</b> DNA-binding protein Tfx <b>Family:</b> DNA-binding protein Tfx
11	<a href="#">c6f8ll_</a>	 Alignment		10.7	21	<b>PDB header:</b> motor protein <b>Chain:</b> J: <b>PDB Molecule:</b> type iv pilus assembly protein pilf; <b>PDBTitle:</b> thermus thermophilus pilf atpase (amppnp-bound form)

12	<a href="#">c2ahqA</a>	 Alignment		10.5	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
13	<a href="#">d16vpa</a>	 Alignment		10.4	26	<b>Fold:</b> Conserved core of transcriptional regulatory protein vp16 <b>Superfamily:</b> Conserved core of transcriptional regulatory protein vp16 <b>Family:</b> Conserved core of transcriptional regulatory protein vp16
14	<a href="#">d1pjqa3</a>	 Alignment		10.2	20	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
15	<a href="#">c1cirA</a>	 Alignment		9.2	33	<b>PDB header:</b> serine protease inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> chymotrypsin inhibitor 2; <b>PDBTitle:</b> complex of two fragments of ci2 [(1-40)(dot)(41-64)]
16	<a href="#">c2p9xB</a>	 Alignment		9.0	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph0832; <b>PDBTitle:</b> crystal structure of ph0832 from pyrococcus horikoshii ot3
17	<a href="#">c6ahqM</a>	 Alignment		8.7	27	<b>PDB header:</b> motor protein <b>Chain:</b> M: <b>PDB Molecule:</b> flagellar protein flil; <b>PDBTitle:</b> structure of the 40-167 fragment of flil
18	<a href="#">c2mt3A</a>	 Alignment		8.7	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-54 factor; <b>PDBTitle:</b> structure of -24 dna binding domain of sigma 54 from e.coli
19	<a href="#">c3f43A</a>	 Alignment		8.5	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative anti-sigma factor antagonist tm1081; <b>PDBTitle:</b> crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
20	<a href="#">c2mtgA</a>	 Alignment		7.9	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> la-related protein 6; <b>PDBTitle:</b> solution structure of the rrm1 of human larp6
21	<a href="#">c1rjnC</a>	 Alignment	not modelled	7.5	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> menb; <b>PDBTitle:</b> the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa
22	<a href="#">d1hska2</a>	 Alignment	not modelled	7.4	15	<b>Fold:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Superfamily:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain <b>Family:</b> Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
23	<a href="#">c3r0oA</a>	 Alignment	not modelled	6.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitiny-coa dehydratase; <b>PDBTitle:</b> crystal structure of carnitiny-coa hydratase from mycobacterium avium
24	<a href="#">d1pjha</a>	 Alignment	not modelled	6.6	13	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
25	<a href="#">c2o8kA</a>	 Alignment	not modelled	6.4	33	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor rpon; <b>PDBTitle:</b> nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
26	<a href="#">c3lkeA</a>	 Alignment	not modelled	6.4	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus halodurans
27	<a href="#">c5ioLC</a>	 Alignment	not modelled	6.2	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nucleoside diphosphate kinase; <b>PDBTitle:</b> crystal structure of nucleoside diphosphate kinase from schistosoma2 mansoni
		 Alignment				<b>PDB header:</b> signaling protein

28	<a href="#">c3cazA_</a>	Alignment	not modelled	6.2	46	<b>Chain:</b> A; <b>PDB Molecule:</b> bar protein; <b>PDBTitle:</b> crystal structure of a bar protein from galdieria sulphuraria
29	<a href="#">d2ch5a1</a>	Alignment	not modelled	6.1	8	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
30	<a href="#">d1dwka2</a>	Alignment	not modelled	6.0	15	<b>Fold:</b> Cyanase C-terminal domain <b>Superfamily:</b> Cyanase C-terminal domain <b>Family:</b> Cyanase C-terminal domain
31	<a href="#">c1hymA_</a>	Alignment	not modelled	5.8	33	<b>PDB header:</b> hydrolase (serine proteinase) <b>Chain:</b> A; <b>PDB Molecule:</b> hydrolyzed cucurbita maxima trypsin inhibitor v; <b>PDBTitle:</b> hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
32	<a href="#">c2iexA_</a>	Alignment	not modelled	5.8	9	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydroxynaphthoic acid synthetase; <b>PDBTitle:</b> crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
33	<a href="#">d1dwma_</a>	Alignment	not modelled	5.7	50	<b>Fold:</b> CI-2 family of serine protease inhibitors <b>Superfamily:</b> CI-2 family of serine protease inhibitors <b>Family:</b> CI-2 family of serine protease inhibitors
34	<a href="#">c2ci2l_</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> proteinase inhibitor (chymotrypsin) <b>Chain:</b> I; <b>PDB Molecule:</b> chymotrypsin inhibitor 2; <b>PDBTitle:</b> crystal and molecular structure of the serine proteinase inhibitor ci-2 2 from barley seeds
35	<a href="#">d1to2i_</a>	Alignment	not modelled	5.7	50	<b>Fold:</b> CI-2 family of serine protease inhibitors <b>Superfamily:</b> CI-2 family of serine protease inhibitors <b>Family:</b> CI-2 family of serine protease inhibitors
36	<a href="#">c3rdyA_</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> bwi-1=protease inhibitor/trypsin inhibitor; <b>PDBTitle:</b> crystal structure of buckwheat trypsin inhibitor rbti at 1.84 angstrom2 resolution
37	<a href="#">d1ypci_</a>	Alignment	not modelled	5.6	50	<b>Fold:</b> CI-2 family of serine protease inhibitors <b>Superfamily:</b> CI-2 family of serine protease inhibitors <b>Family:</b> CI-2 family of serine protease inhibitors
38	<a href="#">d1csei_</a>	Alignment	not modelled	5.6	50	<b>Fold:</b> CI-2 family of serine protease inhibitors <b>Superfamily:</b> CI-2 family of serine protease inhibitors <b>Family:</b> CI-2 family of serine protease inhibitors
39	<a href="#">c1vbwA_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> trypsin inhibitor bgit; <b>PDBTitle:</b> crystal structure of bitter gourd trypsin inhibitor
40	<a href="#">d2snii_</a>	Alignment	not modelled	5.6	50	<b>Fold:</b> CI-2 family of serine protease inhibitors <b>Superfamily:</b> CI-2 family of serine protease inhibitors <b>Family:</b> CI-2 family of serine protease inhibitors
41	<a href="#">d1lucna_</a>	Alignment	not modelled	5.4	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleoside diphosphate kinase, NDK <b>Family:</b> Nucleoside diphosphate kinase, NDK