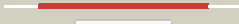

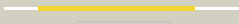
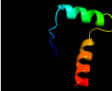

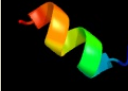



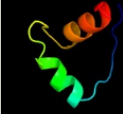
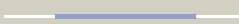








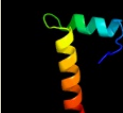


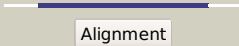

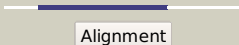


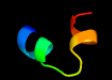
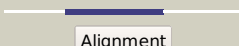

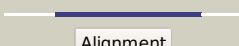
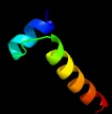
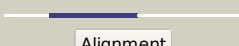

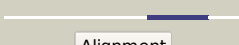



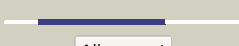
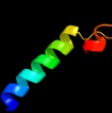


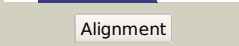
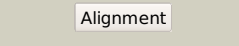
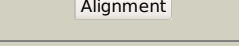





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0657c_(-)_753465_753620
Date	Fri Jul 26 01:50:22 BST 2019
Unique Job ID	d90355e251e1d983

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6a7vU</a>	 Alignment		99.1	47	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapp11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	<a href="#">c2k5jB</a>	 Alignment		71.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
3	<a href="#">c3echC</a>	 Alignment		45.8	50	<b>PDB header:</b> transcription, transcription regulation <b>Chain:</b> C: <b>PDB Molecule:</b> 25-mer fragment of protein armr; <b>PDBTitle:</b> the marr-family repressor mexr in complex with its antirepressor armr
4	<a href="#">d1c1da2</a>	 Alignment		44.8	40	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
5	<a href="#">c1q5vB</a>	 Alignment		29.2	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
6	<a href="#">c2bj3D</a>	 Alignment		27.9	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
7	<a href="#">d1leha2</a>	 Alignment		27.6	40	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
8	<a href="#">c2p2uA</a>	 Alignment		23.9	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-nuclease inhibitor protein gam, putative; <b>PDBTitle:</b> crystal structure of putative host-nuclease inhibitor protein gam from2 desulfovibrio vulgaris
9	<a href="#">d2bj7a1</a>	 Alignment		23.7	17	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
10	<a href="#">c6iyaD</a>	 Alignment		10.6	28	<b>PDB header:</b> antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
11	<a href="#">c1bxgA</a>	 Alignment		10.3	40	<b>PDB header:</b> amino acid dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine dehydrogenase; <b>PDBTitle:</b> phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate

12	<a href="#">c2ca9B_</a>			9.9	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
13	<a href="#">c2ltuA_</a>			9.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-2; <b>PDBTitle:</b> solution structure of autoinhibitory domain of human amp-activated2 protein kinase catalytic subunit
14	<a href="#">c2wj9A_</a>			8.3	31	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> intergenic-region protein; <b>PDBTitle:</b> ardb
15	<a href="#">c3sztB_</a>			7.5	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
16	<a href="#">d2hzaa1</a>			7.4	16	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
17	<a href="#">c1lehB_</a>			7.2	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> leucine dehydrogenase; <b>PDBTitle:</b> leucine dehydrogenase from bacillus sphaericus
18	<a href="#">c5zyxA_</a>			7.0	40	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> arg-trp-lys-arg-his-ile-ser-glu-gln-leu-arg-arg-arg-asp- <b>PDBTitle:</b> solution nmr structure of k30 peptide in 10 mm dioctanoyl2 phosphatidylglycerol (d8pg)
19	<a href="#">d1kwia_</a>			6.7	36	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> Cathelicidin motif
20	<a href="#">c2klzA_</a>			6.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ataxin-3; <b>PDBTitle:</b> solution structure of the tandem uim domain of ataxin-3 complexed with2 ubiquitin
21	<a href="#">c2hv8D_</a>		not modelled	6.4	38	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of gtp-bound rab11 in complex with fip3
22	<a href="#">c2kmgA_</a>		not modelled	6.2	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> klca; <b>PDBTitle:</b> the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro
23	<a href="#">c2khsB_</a>		not modelled	6.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nuclease; <b>PDBTitle:</b> solution structure of snase121:snase(111-143) complex
24	<a href="#">c4cgbA_</a>		not modelled	6.1	33	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 2; <b>PDBTitle:</b> crystal structure of the trimerization domain of eml2
25	<a href="#">c2mdvB_</a>		not modelled	6.0	42	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of beta alpha alpha 38
26	<a href="#">c2q2kB_</a>		not modelled	6.0	40	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of nucleic-acid binding protein
27	<a href="#">c2q2kA_</a>		not modelled	6.0	40	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of nucleic-acid binding protein
28	<a href="#">c4cgbE_</a>		not modelled	6.0	63	<b>PDB header:</b> cell cycle <b>Chain:</b> E: <b>PDB Molecule:</b> echinoderm microtubule-associated protein-like 2; <b>PDBTitle:</b> crystal structure of the trimerization domain of eml2 <b>PDB header:</b> isomerase

29	<a href="#">c2f4qA_</a>	Alignment	not modelled	5.7	15	<b>Chain:</b> A: <b>PDB Molecule:</b> type i topoisomerase, putative; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans topoisomerase ib
30	<a href="#">c6dmaD_</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> dhd15_closed_b; <b>PDBTitle:</b> dhd15_closed
31	<a href="#">c2d7cD_</a>	Alignment	not modelled	5.6	40	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of human rab11 in complex with fip3 rab-2 binding domain
32	<a href="#">d1vjla_</a>	Alignment	not modelled	5.3	30	<b>Fold:</b> Hypothetical protein TM0160 <b>Superfamily:</b> Hypothetical protein TM0160 <b>Family:</b> Hypothetical protein TM0160
33	<a href="#">d2hzaB1</a>	Alignment	not modelled	5.3	19	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
34	<a href="#">c4nawC_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> C: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
35	<a href="#">c4nawG_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> G: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
36	<a href="#">c4nawO_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> O: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3
37	<a href="#">c4gdlC_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
38	<a href="#">c4gdkC_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5 conjugate in complex with an n-2 terminal fragment of atg16l1
39	<a href="#">c4nawK_</a>	Alignment	not modelled	5.2	40	<b>PDB header:</b> protein transport/ligase <b>Chain:</b> K: <b>PDB Molecule:</b> autophagy-related protein 16-1; <b>PDBTitle:</b> crystal structure of human atg12~atg5-atg16n in complex with a2 fragment of atg3