
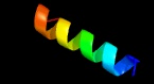
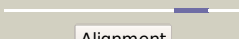
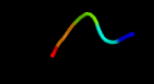
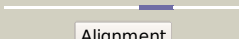
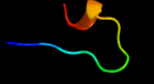
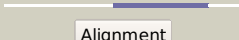

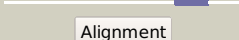


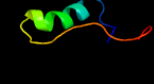
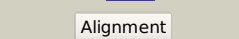




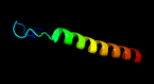


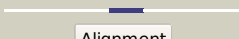



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3901c_(-)_4386543_4386992
Date	Sat Aug 10 22:05:08 BST 2019
Unique Job ID	037eeb24bb6990f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1rhga_</a>	 Alignment		14.8	47	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Long-chain cytokines
2	<a href="#">d1r44a_</a>	 Alignment		12.9	80	<b>Fold:</b> Hedgehog/DD-peptidase <b>Superfamily:</b> Hedgehog/DD-peptidase <b>Family:</b> VanX-like
3	<a href="#">d1kyqa2</a>	 Alignment		11.8	21	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
4	<a href="#">d2fd5a2</a>	 Alignment		11.6	17	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
5	<a href="#">c4lhfA_</a>	 Alignment		11.2	40	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein cox; <b>PDBTitle:</b> crystal structure of a dna binding protein from phage p2
6	<a href="#">d1msza_</a>	 Alignment		9.5	10	<b>Fold:</b> IF3-like <b>Superfamily:</b> R3H domain <b>Family:</b> R3H domain
7	<a href="#">c1mszA_</a>	 Alignment		9.5	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein smubp-2; <b>PDBTitle:</b> solution structure of the r3h domain from human smubp-2
8	<a href="#">c6cfdD_</a>	 Alignment		9.3	36	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
9	<a href="#">c2v0xB_</a>	 Alignment		9.1	25	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> lamina-associated polypeptide 2 isoforms alpha/zeta; <b>PDBTitle:</b> the dimerization domain of lap2alpha
10	<a href="#">c1kyqC_</a>	 Alignment		8.5	21	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
11	<a href="#">d1bgca_</a>	 Alignment		8.4	37	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Long-chain cytokines

12	<a href="#">d1v2za_</a>	Alignment		8.4	43	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
13	<a href="#">d1r8ja1</a>	Alignment		8.2	43	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
14	<a href="#">d1r5qa_</a>	Alignment		8.2	43	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
15	<a href="#">d1sv1a_</a>	Alignment		8.1	43	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
16	<a href="#">c2lg4A_</a>	Alignment		8.1	30	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> aurelin; <b>PDBTitle:</b> 3d solution structure of antimicrobial peptide aurelin
17	<a href="#">c3dfzB_</a>	Alignment		7.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
18	<a href="#">d2hjea1</a>	Alignment		7.1	16	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> LuxQ-periplasmic domain-like
19	<a href="#">d1bgea_</a>	Alignment		6.5	37	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Long-chain cytokines
20	<a href="#">c2hyij_</a>	Alignment		5.9	50	<b>PDB header:</b> hydrolase/rna binding protein/rna <b>Chain:</b> J: <b>PDB Molecule:</b> protein casc3; <b>PDBTitle:</b> structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna
21	<a href="#">c2kvtA_</a>	Alignment	not modelled	5.5	41	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yaia; <b>PDBTitle:</b> solution nmr structure of yaia from escherichia eoli. northeast2 structural genomics target er244