

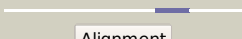
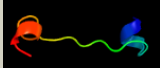
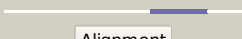


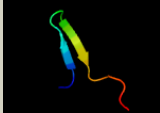

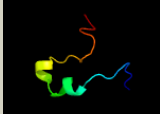






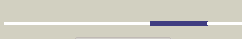


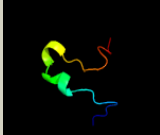

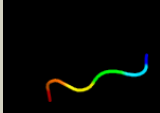











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0057 (- )_59893_60414
Date	Tue Jul 23 14:50:08 BST 2019
Unique Job ID	c888945be701d6f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fviA_</a>	 Alignment		26.3	39	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 192 kda; <b>PDBTitle:</b> ash / papd-like domain of human cep192 (papd-like domain 7)
2	<a href="#">d2g39a1</a>	 Alignment		12.8	19	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
3	<a href="#">d1kyza2</a>	 Alignment		10.5	26	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
4	<a href="#">c2rpsA_</a>	 Alignment		9.7	42	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chemokine; <b>PDBTitle:</b> solution structure of a novel insect chemokine isolated from2 integument
5	<a href="#">c2ehjA_</a>	 Alignment		9.0	54	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of uracil phosphoribosyl transferase
6	<a href="#">d1d5mb2</a>	 Alignment		8.5	39	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
7	<a href="#">d1fp2a2</a>	 Alignment		7.9	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
8	<a href="#">c5xohA_</a>	 Alignment		7.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bergaptol o-methyltransferase; <b>PDBTitle:</b> crystal structure of bergaptol o-methyltransferase complex
9	<a href="#">d1fp1d2</a>	 Alignment		7.4	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Plant O-methyltransferase, C-terminal domain
10	<a href="#">c2e55D_</a>	 Alignment		7.0	50	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of aq2163 protein from aquifex aeolicus
11	<a href="#">c1g1pA_</a>	 Alignment		6.6	100	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin evia; <b>PDBTitle:</b> nmr solution structures of delta-conotoxin evia from conus2 ermineus that selectively acts on vertebrate neuronal na+3 channels

12	<a href="#">dlg1pa_</a>	Alignment		6.6	100	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Conotoxin
13	<a href="#">c2oqjL_</a>	Alignment		6.5	63	<b>PDB header:</b> immune system <b>Chain:</b> L: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
14	<a href="#">c2oqjC_</a>	Alignment		6.4	63	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
15	<a href="#">c2oqjI_</a>	Alignment		6.4	63	<b>PDB header:</b> immune system <b>Chain:</b> I: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
16	<a href="#">c2oqjF_</a>	Alignment		6.4	63	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> peptide 2g12.1 (acppshvldmrsgtclaaegk); <b>PDBTitle:</b> crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
17	<a href="#">c1g1zA_</a>	Alignment		6.3	100	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin evia; <b>PDBTitle:</b> nmr solution structures of delta-conotoxin evia from conus2 ermineus that selectively acts on vertebrate neuronal na+3 channels, leu12-pro13 cis isomer
18	<a href="#">c1xc3A_</a>	Alignment		6.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructokinase; <b>PDBTitle:</b> structure of a putative fructokinase from bacillus subtilis
19	<a href="#">c3mmiB_</a>	Alignment		6.1	38	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin-4; <b>PDBTitle:</b> crystal structure of the globular tail of myo4p
20	<a href="#">c4cyjF_</a>	Alignment		6.1	16	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> pan2; <b>PDBTitle:</b> chaetomium thermophilum pan2:pan3 complex
21	<a href="#">c3fgrA_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phospholipase b-like 2 28 kda form; <b>PDBTitle:</b> two chain form of the 66.3 kda protein at 1.8 angstrom
22	<a href="#">d1t3ta3</a>	Alignment	not modelled	5.9	47	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> FGAM synthase PurL, PurS-like domain
23	<a href="#">c4j8cA_</a>	Alignment	not modelled	5.8	75	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of the dimerization domain of hsc70-interacting2 protein
24	<a href="#">c4j8cB_</a>	Alignment	not modelled	5.8	75	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of the dimerization domain of hsc70-interacting2 protein
25	<a href="#">d2d8za1</a>	Alignment	not modelled	5.7	44	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
26	<a href="#">d2cura2</a>	Alignment	not modelled	5.3	50	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain