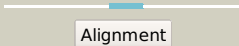





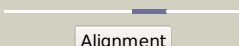

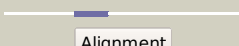
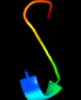
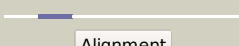

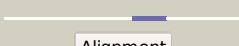


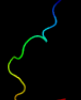

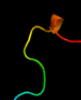





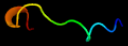
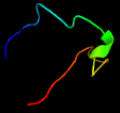

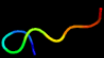






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0292 (-)_355880_356875
Date	Tue Jul 23 14:50:35 BST 2019
Unique Job ID	1c4e94f8a839f097

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k42B_</a>	 Alignment		33.6	50	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> espfu; <b>PDBTitle:</b> solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
2	<a href="#">c2lnhC_</a>	 Alignment		28.7	50	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> secreted effector protein espf(u); <b>PDBTitle:</b> enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
3	<a href="#">d2ieaa3</a>	 Alignment		12.9	18	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
4	<a href="#">c5cdjA_</a>	 Alignment		10.9	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco large subunit-binding protein subunit alpha, <b>PDBTitle:</b> apical domain of chloroplast chaperonin 60a
5	<a href="#">c2lqxA_</a>	 Alignment		10.3	70	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fermitin family homolog 2; <b>PDBTitle:</b> nmr structure for kindle-2 n-terminus
6	<a href="#">c2lzsE_</a>	 Alignment		10.3	38	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> sec-independent protein translocase protein tata; <b>PDBTitle:</b> tata oligomer
7	<a href="#">d1sjpa2</a>	 Alignment		10.2	47	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
8	<a href="#">d1kida_</a>	 Alignment		10.1	26	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
9	<a href="#">d1ioka2</a>	 Alignment		9.5	40	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
10	<a href="#">d1dk7a_</a>	 Alignment		9.3	33	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
11	<a href="#">d1srva_</a>	 Alignment		9.3	23	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain

12	<a href="#">d1oela2</a>	Alignment		9.0	33	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
13	<a href="#">d1we3a2</a>	Alignment		8.4	33	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> GroEL apical domain-like <b>Family:</b> GroEL-like chaperone, apical domain
14	<a href="#">c3m6cA_</a>	Alignment		8.2	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> 60 kda chaperonin 1; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis groel1 apical domain
15	<a href="#">c2i2xD_</a>	Alignment		7.8	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> methyltransferase 1; <b>PDBTitle:</b> crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
16	<a href="#">c2kmcA_</a>	Alignment		7.1	56	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fermitin family homolog 1; <b>PDBTitle:</b> solution structure of the n-terminal domain of kindlin-1
17	<a href="#">d1zj8a2</a>	Alignment		6.7	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
18	<a href="#">d2hja1</a>	Alignment		6.2	46	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> YcfA/nrd intein domain <b>Family:</b> Ykff-like
19	<a href="#">c2hja_</a>	Alignment		6.2	46	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ykff; <b>PDBTitle:</b> solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
20	<a href="#">d1ccwa_</a>	Alignment		5.9	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
21	<a href="#">c4jgiB_</a>	Alignment	not modelled	5.9	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfotobacterium hafniense dcb-2
22	<a href="#">c6gwjK_</a>	Alignment	not modelled	5.1	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> probable trna n6-adenosine threonylcarbamoyltransferase; <b>PDBTitle:</b> protein complex