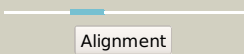

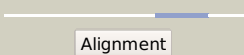

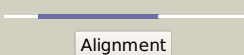



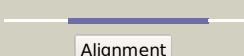
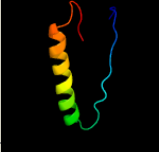
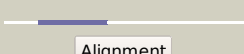
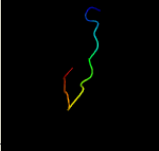
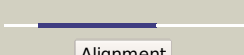

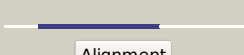
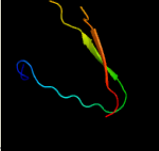
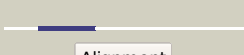
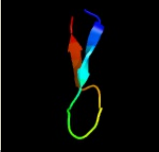

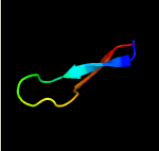

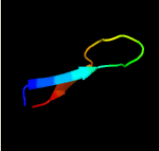
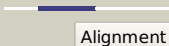
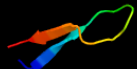
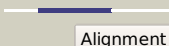


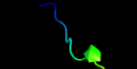
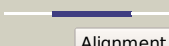

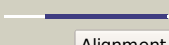
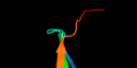
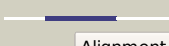
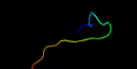

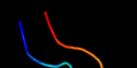
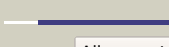


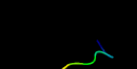
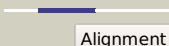
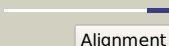
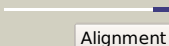
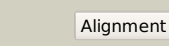
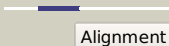
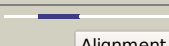




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0108c_(-)_130892_131101
Date	Tue Jul 23 14:50:15 BST 2019
Unique Job ID	9d4c79469598dd30

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2cuqa1</a>	 Alignment		37.2	18	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
2	<a href="#">c3b8fB_</a>	 Alignment		24.2	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative blastidicin s deaminase; <b>PDBTitle:</b> crystal structure of the cytidine deaminase from bacillus anthracis
3	<a href="#">c2fkdK_</a>	 Alignment		16.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> K: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of the c-terminal domain of bacteriophage2 186 repressor
4	<a href="#">c3fl2A_</a>	 Alignment		13.3	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase uhrf1; <b>PDBTitle:</b> crystal structure of the ring domain of the e3 ubiquitin-protein2 ligase uhrf1
5	<a href="#">c4r86B_</a>	 Alignment		12.2	19	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> rnd family aminoglycoside/multidrug efflux pump; <b>PDBTitle:</b> crystal structure of aminoglycoside/multidrug efflux system acrd from2 salmonella typhimurium
6	<a href="#">c6ax6B_</a>	 Alignment		12.2	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> procollagen lysyl hydroxylase and glycosyltransferase; <b>PDBTitle:</b> the crystal structure of a lysyl hydroxylase from acanthamoeba2 polyphaga mimivirus
7	<a href="#">d1vhka1</a>	 Alignment		9.8	22	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> YggJ N-terminal domain-like
8	<a href="#">c2iuwA_</a>	 Alignment		9.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkylated repair protein alkb homolog 3; <b>PDBTitle:</b> crystal structure of human abh3 in complex with iron ion and 2-2 oxoglutarate
9	<a href="#">d1vcpa_</a>	 Alignment		8.7	59	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
10	<a href="#">d1wyka_</a>	 Alignment		8.4	59	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
11	<a href="#">d1lep5a_</a>	 Alignment		8.0	59	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases

12	<a href="#">c1kxfA_</a>			8.0	59	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> sindbis virus capsid protein; <b>PDBTitle:</b> sindbis virus capsid, (wild-type) residues 1-264, tetragonal crystal2 form (form ii)
13	<a href="#">c2oghA_</a>			7.5	33	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor eif-1; <b>PDBTitle:</b> solution structure of yeast eif1
14	<a href="#">c5c5tB_</a>			7.2	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl 4-hydroxylase; <b>PDBTitle:</b> the crystal structure of viral collagen prolyl hydroxylase vcpH from2 paramecium bursaria chlorella virus-1 - 2og complex
15	<a href="#">c4unmB_</a>			7.2	42	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> secreted protein; <b>PDBTitle:</b> structure of galactose oxidase homologue from streptomyces lividans
16	<a href="#">c5xzkA_</a>			7.1	25	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lectin (phosl); <b>PDBTitle:</b> pholiota squarrosa lectin trimer
17	<a href="#">c1w18A_</a>			7.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> levansucrase; <b>PDBTitle:</b> crystal structure of levansucrase from gluconacetobacter2 diazotrophicus
18	<a href="#">c2yewG_</a>			6.8	59	<b>PDB header:</b> virus <b>Chain:</b> G: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> modeling barmah forest virus structural proteins
19	<a href="#">d2fkia1</a>			6.4	12	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> Yjbr-like <b>Family:</b> Yjbr-like
20	<a href="#">d1oa8a_</a>			6.4	55	<b>Fold:</b> AXH domain <b>Superfamily:</b> AXH domain <b>Family:</b> AXH domain
21	<a href="#">c6mx7C_</a>		not modelled	6.2	59	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> capsid; <b>PDBTitle:</b> cryoem structure of chimeric eastern equine encephalitis virus:2 genome-binding capsid n-terminal domain
22	<a href="#">d1iwga2</a>		not modelled	6.1	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
23	<a href="#">c5tzpB_</a>		not modelled	5.9	41	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bik; <b>PDBTitle:</b> crystal structure of fpv039:bik bh3 complex
24	<a href="#">c2djtA_</a>		not modelled	5.4	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> unnamed protein product; <b>PDBTitle:</b> solution structures of the pdz domain of human unnamed2 protein product
25	<a href="#">c1filX_</a>		not modelled	5.4	50	<b>PDB header:</b> apoptosis <b>Chain:</b> X: <b>PDB Molecule:</b> b-cell surface antigen cd40; <b>PDBTitle:</b> molecular basis for cd40 signaling mediated by traf3
26	<a href="#">c1filY_</a>		not modelled	5.3	50	<b>PDB header:</b> apoptosis <b>Chain:</b> Y: <b>PDB Molecule:</b> b-cell surface antigen cd40; <b>PDBTitle:</b> molecular basis for cd40 signaling mediated by traf3
27	<a href="#">c5xoiA_</a>		not modelled	5.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, 2og-fe oxygenase family protein, putative, <b>PDBTitle:</b> the structure of osalkbh1
28	<a href="#">c5xblD_</a>		not modelled	5.1	41	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> associated protein; <b>PDBTitle:</b> structure of nuclease in complex with associated protein

29 [c3cyvA](#)

Alignment

not modelled

5.0

31

**PDB header:**peptide binding protein  
**Chain:** A: **PDB Molecule:**tight junction protein zo-1;  
**PDBTitle:** the crystal structure of zo-1 pdz2 in complex with the cx43 peptide