

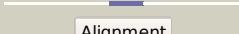

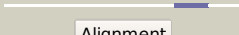













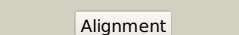

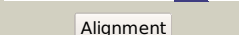












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2742c_(-)_3055525_3056358
Date	Wed Aug 7 12:50:40 BST 2019
Unique Job ID	d6aa93c5123cdad0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6dmaD_</a>	 Alignment		27.0	57	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> dhd15_closed_b; <b>PDBTitle:</b> dhd15_closed
2	<a href="#">c2elpA_</a>	 Alignment		19.1	46	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
3	<a href="#">c2becB_</a>	 Alignment		14.2	55	<b>PDB header:</b> metal binding protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium/hydrogen exchanger 1; <b>PDBTitle:</b> crystal structure of chp2 in complex with its binding2 region in nhe1 and insights into the mechanism of ph3 regulation
4	<a href="#">d1b8xa1</a>	 Alignment		13.9	33	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
5	<a href="#">c6hlwB_</a>	 Alignment		12.7	54	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
6	<a href="#">d1a6ca3</a>	 Alignment		11.4	13	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Comoviridae-like VP
7	<a href="#">c6hltD_</a>	 Alignment		11.4	43	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)
8	<a href="#">c1uusA_</a>	 Alignment		11.1	33	<b>PDB header:</b> signal transduction <b>Chain:</b> A: <b>PDB Molecule:</b> stat protein; <b>PDBTitle:</b> structure of an activated dictyostelium stat in its2 dna-unbound form
9	<a href="#">c2x3mA_</a>	 Alignment		10.1	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein orf239; <b>PDBTitle:</b> crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
10	<a href="#">c6hmvB_</a>	 Alignment		10.0	46	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> genome polyprotein; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
11	<a href="#">c5o9zN_</a>	 Alignment		9.3	78	<b>PDB header:</b> splicing <b>Chain:</b> N: <b>PDB Molecule:</b> zinc finger matrin-type protein 2; <b>PDBTitle:</b> cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)

12	<a href="#">c6hs6E_</a>	Alignment		9.2	28	<b>PDB header:</b> transport protein <b>Chain:</b> E; <b>PDB Molecule:</b> type vi secretion protein impa; <b>PDBTitle:</b> c-terminal domain of the tssa component of the type vi secretion2 system from burkholderia cenocepacia
13	<a href="#">c1ng7A_</a>	Alignment		8.8	46	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> genome polyprotein [core protein p3a]; <b>PDBTitle:</b> the solution structure of the soluble domain of poliovirus 3a protein
14	<a href="#">d1ng7a_</a>	Alignment		8.8	46	<b>Fold:</b> Soluble domain of poliovirus core protein 3a <b>Superfamily:</b> Soluble domain of poliovirus core protein 3a <b>Family:</b> Soluble domain of poliovirus core protein 3a
15	<a href="#">c1ljzB_</a>	Alignment		8.7	57	<b>PDB header:</b> receptor, toxin <b>Chain:</b> B; <b>PDB Molecule:</b> acetylcholine receptor protein; <b>PDBTitle:</b> nmr structure of anachr-peptide (torpedo californica, alpha-subunit2 residues 182-202) in complex with alpha-bungarotoxin
16	<a href="#">c3q66A_</a>	Alignment		8.3	30	<b>PDB header:</b> chaperone/transferase <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 75; <b>PDBTitle:</b> structure of the vps75-rtt109 histone chaperone-lysine2 acetyltransferase complex (full-length proteins in space group p6122)
17	<a href="#">d2e50a1</a>	Alignment		7.9	27	<b>Fold:</b> NAP-like <b>Superfamily:</b> NAP-like <b>Family:</b> NAP-like
18	<a href="#">d1bg1a2</a>	Alignment		7.9	56	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> p53-like transcription factors <b>Family:</b> STAT DNA-binding domain
19	<a href="#">c3dm7B_</a>	Alignment		7.7	27	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 75; <b>PDBTitle:</b> crystal structure of the vps75 histone chaperone
20	<a href="#">c5dayA_</a>	Alignment		7.6	40	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> nap1-related protein 1; <b>PDBTitle:</b> the structure of nap1-related protein(nrp1) in arabidopsis
21	<a href="#">c1yvlB_</a>	Alignment	not modelled	7.4	44	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
22	<a href="#">d1bf5a2</a>	Alignment	not modelled	7.2	44	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> p53-like transcription factors <b>Family:</b> STAT DNA-binding domain
23	<a href="#">c3gyvA_</a>	Alignment	not modelled	7.2	43	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> nucleosome assembly protein 1, putative; <b>PDBTitle:</b> crystal structure of nucleosome assembly protein from plasmodium2 falciparum
24	<a href="#">c5gplA_</a>	Alignment	not modelled	7.1	27	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> putative nucleosome assembly protein c36b7.08c; <b>PDBTitle:</b> crystal structure of ccp1
25	<a href="#">c2m1jA_</a>	Alignment	not modelled	6.5	57	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> prion-like protein doppel; <b>PDBTitle:</b> ovine doppel signal peptide (1-30)
26	<a href="#">c5wcvA_</a>	Alignment	not modelled	6.4	58	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> shk homolog ask132958; <b>PDBTitle:</b> ask132958: a minimal homologue of shk identified in the transcriptome2 of anemonia sulcata
27	<a href="#">c2kuyA_</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> prebacteriocin glycocin f; <b>PDBTitle:</b> structure of glycocin f
28	<a href="#">c3c9dB_</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 75; <b>PDBTitle:</b> crystal structure of vps75
						<b>Fold:</b> SMAD/FHA domain

29	<a href="#">d1kha_</a>	Alignment	not modelled	6.1	44	<b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> SMAD domain
30	<a href="#">c1kxA</a>	Alignment	not modelled	6.1	44	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> smad2; <b>PDBTitle:</b> crystal structure of a phosphorylated smad2
31	<a href="#">c5ypsA</a>	Alignment	not modelled	6.0	36	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 75; <b>PDBTitle:</b> the structural basis of histone chaperonevps75
32	<a href="#">c3l32B</a>	Alignment	not modelled	5.5	56	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> structure of the dimerisation domain of the rabies virus2 phosphoprotein
33	<a href="#">c3bvsA</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkylpurine dna glycosylase alkD; <b>PDBTitle:</b> crystal structure of bacillus cereus alkylpurine dna glycosylase alkD
34	<a href="#">c3kypA</a>	Alignment	not modelled	5.3	45	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> nucleosome assembly protein; <b>PDBTitle:</b> crystal structure of nucleosome assembly protein s (pfnap3) from plasmodium falciparum