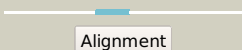
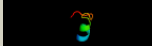

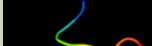

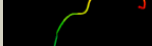
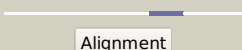

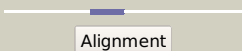

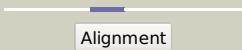
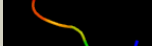
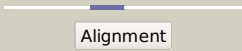

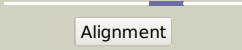

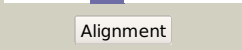

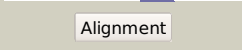




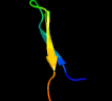
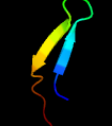
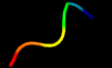

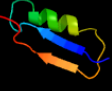

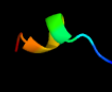



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2774c (- )_3082362_3082766
Date	Wed Aug 7 12:50:43 BST 2019
Unique Job ID	b5b5a055107897c3

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ariA_</a>	 Alignment		30.1	56	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelope polyprotein gp160; <b>PDBTitle:</b> solution structure of micelle-bound fusion domain of hiv-12 gp41
2	<a href="#">c2mxqA_</a>	 Alignment		21.6	67	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A; <b>PDB Molecule:</b> paneth cell-specific alpha-defensin 1; <b>PDBTitle:</b> the solution structure of defa1, a highly potent antimicrobial peptide2 from the horse
3	<a href="#">c2odxA_</a>	 Alignment		19.4	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome c oxidase polypeptide iv; <b>PDBTitle:</b> solution structure of zn(ii)cox4
4	<a href="#">d1omba_</a>	 Alignment		14.7	55	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
5	<a href="#">c1erfA_</a>	 Alignment		14.4	88	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> transmembrane glycoprotein; <b>PDBTitle:</b> conformational mapping of the n-terminal fusion peptide of2 hiv-1 gp41 using 13c-enhanced fourier transform infrared3 spectroscopy (ftir)
6	<a href="#">c2jnrB_</a>	 Alignment		13.8	88	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> env polyprotein; <b>PDBTitle:</b> discovery and optimization of a natural hiv-1 entry2 inhibitor targeting the gp41 fusion peptide
7	<a href="#">c1p5aA_</a>	 Alignment		13.2	88	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelope polyprotein gp160; <b>PDBTitle:</b> conformational mapping of the n-terminal peptide of hiv-12 gp41 in lipid detergent and aqueous environments using 13c-3 enhanced fourier transform infrared spectroscopy
8	<a href="#">d1agga_</a>	 Alignment		13.1	55	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Spider toxins
9	<a href="#">c2pivA_</a>	 Alignment		11.2	75	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> solution structure of hiv-1 gp41 fusion domain bound to dpc micelle
10	<a href="#">c5we0J_</a>	 Alignment		10.5	100	<b>PDB header:</b> gene regulation <b>Chain:</b> J; <b>PDB Molecule:</b> protection of telomeres protein poz1; <b>PDBTitle:</b> structural basis for shelterin bridge assembly
11	<a href="#">d1xhja_</a>	 Alignment		10.4	30	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like

12	<a href="#">c4tvpB</a>	Alignment		10.0	60	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope glycoprotein gp160; <b>PDBTitle:</b> crystal structure of the hiv-1 bg505 sosip.664 env trimer ectodomain,2 comprising atomic-level definition of pre-fusion gp120 and gp41, in3 complex with human antibodies pgt122 and 35o22
13	<a href="#">d1ywsa1</a>	Alignment		9.9	32	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> CSL zinc finger <b>Family:</b> CSL zinc finger
14	<a href="#">d1wgea1</a>	Alignment		9.3	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> CSL zinc finger <b>Family:</b> CSL zinc finger
15	<a href="#">c2rpsA</a>	Alignment		8.5	83	<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
16	<a href="#">d2p5zx1</a>	Alignment		7.8	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> gp5 N-terminal domain-like <b>Family:</b> gp4 N-terminal domain-like
17	<a href="#">d1t3ta5</a>	Alignment		7.7	21	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> PurM N-terminal domain-like <b>Family:</b> PurM N-terminal domain-like
18	<a href="#">d1i8da2</a>	Alignment		7.0	8	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Riboflavin synthase
19	<a href="#">c4p3xA</a>	Alignment		6.6	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate synthase a; <b>PDBTitle:</b> structure of the fe4s4 quinolinate synthase nada from thermotoga2 maritima
20	<a href="#">d1veha</a>	Alignment		6.6	30	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
21	<a href="#">d1ncfa3</a>	Alignment	not modelled	6.4	38	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
22	<a href="#">d1th5a1</a>	Alignment	not modelled	6.2	27	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
23	<a href="#">d1pjqa3</a>	Alignment	not modelled	5.8	62	<b>Fold:</b> Siroheme synthase middle domains-like <b>Superfamily:</b> Siroheme synthase middle domains-like <b>Family:</b> Siroheme synthase middle domains-like
24	<a href="#">c6rdu9</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> proton transport <b>Chain:</b> 9: <b>PDB Molecule:</b> asa-9: polytomella f-atp synthase associated subunit 9; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
25	<a href="#">c2jnvA</a>	Alignment	not modelled	5.6	30	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 1, chloroplast; <b>PDBTitle:</b> solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
26	<a href="#">c3ju3A</a>	Alignment	not modelled	5.5	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; <b>PDBTitle:</b> crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
27	<a href="#">c3kskA</a>	Alignment	not modelled	5.2	48	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type-2 restriction enzyme pvuii; <b>PDBTitle:</b> crystal structure of single chain pvuii
28	<a href="#">c6qbsB</a>	Alignment	not modelled	5.2	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative mrna decapping protein; <b>PDBTitle:</b> crystal structure of the c. thermophilum scavenger decapping enzyme2 dcps apo form <b>PDB header:</b> transferase

29	<a href="#">c3omsA_</a>	Alignment	not modelled	5.1	15	<b>Chain:</b> A: <b>PDB Molecule:</b> phnb protein; <b>PDBTitle:</b> putative 3-demethylubiquinone-9 3-methyltransferase, phnb protein,2 from bacillus cereus.
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