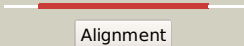

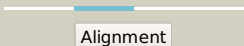

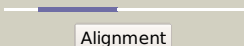

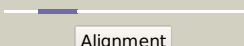
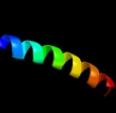
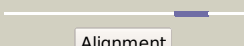

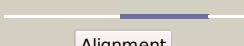

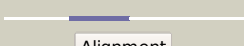






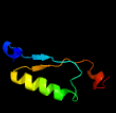





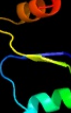
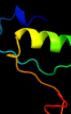
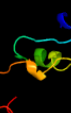

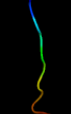
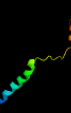


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1761c_(-)_1994678_1995061
Date	Fri Aug 2 13:30:36 BST 2019
Unique Job ID	d500bf6e9e0b6f4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k3mA_</a>	 Alignment		100.0	98	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rv1761c; <b>PDBTitle:</b> rv1761c
2	<a href="#">c3n6yA_</a>	 Alignment		37.9	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-like protein; <b>PDBTitle:</b> crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
3	<a href="#">d1fn9a_</a>	 Alignment		16.8	34	<b>Fold:</b> Outer capsid protein sigma 3 <b>Superfamily:</b> Outer capsid protein sigma 3 <b>Family:</b> Outer capsid protein sigma 3
4	<a href="#">c1g0vB_</a>	 Alignment		15.0	30	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> protease a inhibitor 3; <b>PDBTitle:</b> the structure of proteinase a complexed with a ia3 mutant, mvv
5	<a href="#">c2xppB_</a>	 Alignment		13.1	50	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> chromatin structure modulator; <b>PDBTitle:</b> crystal structure of a spt6-ivs1(spn1) complex from2 encephalitozoon cuniculi, form iii
6	<a href="#">d1zs4a1</a>	 Alignment		12.4	31	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Bacteriophage CII protein
7	<a href="#">c1u0lB_</a>	 Alignment		12.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> crystal structure of yjeq from thermotoga maritima
8	<a href="#">c4bjjA_</a>	 Alignment		12.0	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor tau subunit sfc1; <b>PDBTitle:</b> sfc1-sfc7 dimerization module
9	<a href="#">c4phtC_</a>	 Alignment		12.0	23	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> general secretory pathway protein e; <b>PDBTitle:</b> atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
10	<a href="#">c1mqrA_</a>	 Alignment		11.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-d-glucuronidase; <b>PDBTitle:</b> the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 steartothermophilus t-6
11	<a href="#">d1h41a1</a>	 Alignment		11.5	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain

12	<a href="#">c5aa6F_</a>	Alignment		11.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> vanadium-dependent bromoperoxidase 2; <b>PDBTitle:</b> homo-hexameric structure of the second vanadate-dependent2 bromoperoxidase (anii) from ascophyllum nodosum
13	<a href="#">d1l8na1</a>	Alignment		11.1	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
14	<a href="#">d1yq2a3</a>	Alignment		10.6	25	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> beta-Galactosidase/glucuronidase, N-terminal domain
15	<a href="#">d1t3va_</a>	Alignment		10.2	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
16	<a href="#">c5zfqA_</a>	Alignment		9.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> twitching motility pilus retraction protein; <b>PDBTitle:</b> crystal structure of pili-4, a retraction atpase motor of type iv2 pilus , from geobacter sulfurreducens
17	<a href="#">d1p9ra_</a>	Alignment		9.4	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
18	<a href="#">d1t9ha1</a>	Alignment		9.2	44	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
19	<a href="#">d1n6za_</a>	Alignment		9.1	45	<b>Fold:</b> Hypothetical protein Yml108w <b>Superfamily:</b> Hypothetical protein Yml108w <b>Family:</b> Hypothetical protein Yml108w
20	<a href="#">c5oqml_</a>	Alignment		9.0	18	<b>PDB header:</b> transcription <b>Chain:</b> L; <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
21	<a href="#">d1jlaa2</a>	Alignment	not modelled	8.9	47	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
22	<a href="#">d1knxa1</a>	Alignment	not modelled	8.4	33	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> HPr kinase/phoshatase HprK N-terminal domain
23	<a href="#">c4kssC_</a>	Alignment	not modelled	8.3	29	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> type ii secretion system protein e, hemolysin-coregulated <b>PDBTitle:</b> crystal structure of vibrio cholerae atpase gspse hexamer
24	<a href="#">d1ni3a2</a>	Alignment	not modelled	8.1	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
25	<a href="#">d1o13a_</a>	Alignment	not modelled	8.0	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> MTH1175-like
26	<a href="#">d1xkpa1</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Type III secretion system domain <b>Superfamily:</b> Type III secretion system domain <b>Family:</b> LcrE-like
27	<a href="#">c2xpoD_</a>	Alignment	not modelled	7.6	55	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> chromatin structure modulator; <b>PDBTitle:</b> crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form ii
28	<a href="#">c2xpoB_</a>	Alignment	not modelled	7.4	55	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> chromatin structure modulator; <b>PDBTitle:</b> crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form ii
						<b>Fold:</b> beta-Grasp (ubiquitin-like)

29	<a href="#">d2al6a3</a>	Alignment	not modelled	7.4	38	<b>Superfamily:</b> Ubiquitin-like <b>Family:</b> First domain of FERM
30	<a href="#">c1gqkB</a>	Alignment	not modelled	7.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-d-glucuronidase; <b>PDBTitle:</b> structure of pseudomonas cellulosa alpha-d-glucuronidase complexed2 with glucuronic acid
31	<a href="#">c2xpnB</a>	Alignment	not modelled	6.8	55	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> chromatin structure modulator; <b>PDBTitle:</b> crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form i
32	<a href="#">c2eouA</a>	Alignment	not modelled	6.5	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 473; <b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473
33	<a href="#">d1ddba</a>	Alignment	not modelled	6.5	23	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death <b>Family:</b> Bcl-2 inhibitors of programmed cell death
34	<a href="#">c3jvVA</a>	Alignment	not modelled	6.5	35	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> twitching mobility protein; <b>PDBTitle:</b> crystal structure of p. aeruginosa pilt with bound amp-ppc
35	<a href="#">d2c0sa1</a>	Alignment	not modelled	6.1	32	<b>Fold:</b> ROP-like <b>Superfamily:</b> BAS1536-like <b>Family:</b> BAS1536-like
36	<a href="#">c2npbA</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> selenoprotein w; <b>PDBTitle:</b> nmr solution structure of mouse selw
37	<a href="#">c5fl3A</a>	Alignment	not modelled	5.9	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> pili retraction protein pilt; <b>PDBTitle:</b> pilt2 from thermus thermophilus
38	<a href="#">d2bzba1</a>	Alignment	not modelled	5.8	56	<b>Fold:</b> ROP-like <b>Superfamily:</b> BAS1536-like <b>Family:</b> BAS1536-like
39	<a href="#">c1knxF</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> probable hpr(ser) kinase/phosphatase; <b>PDBTitle:</b> hpr kinase/phosphatase from mycoplasma pneumoniae
40	<a href="#">c2yx6C</a>	Alignment	not modelled	5.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein ph0822; <b>PDBTitle:</b> crystal structure of ph0822
41	<a href="#">c3ebwA</a>	Alignment	not modelled	5.5	29	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> per a 4 allergen; <b>PDBTitle:</b> crystal structure of major allergens, per a 4 from cockroaches
42	<a href="#">c5tshF</a>	Alignment	not modelled	5.4	47	<b>PDB header:</b> atp-binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> type iv pilus biogenesis atpase pilb; <b>PDBTitle:</b> pilb from geobacter metallireducens bound to amp-pnp
43	<a href="#">d1ys7a1</a>	Alignment	not modelled	5.3	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
44	<a href="#">d2j8xa1</a>	Alignment	not modelled	5.2	25	<b>Fold:</b> Uracil-DNA glycosylase-like <b>Superfamily:</b> Uracil-DNA glycosylase-like <b>Family:</b> Uracil-DNA glycosylase
45	<a href="#">c4lrV</a>	Alignment	not modelled	5.2	48	<b>PDB header:</b> dna binding protein <b>Chain:</b> L: <b>PDB Molecule:</b> dna sulfur modification protein dnde; <b>PDBTitle:</b> crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
46	<a href="#">c5bncB</a>	Alignment	not modelled	5.1	17	<b>PDB header:</b> heme binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeG_6519; <b>PDBTitle:</b> structure of heme binding protein msmeG_6519 from mycobacterium2 smegmatis
47	<a href="#">c6gefB</a>	Alignment	not modelled	5.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> type iv secretion system protein dotB; <b>PDBTitle:</b> x-ray structure of the yersinia pseudotuberculosis atpase dotB
48	<a href="#">c3graA</a>	Alignment	not modelled	5.1	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of arac family transcriptional regulator from2 pseudomonas putida
49	<a href="#">d2dexx3</a>	Alignment	not modelled	5.0	37	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Peptidylarginine deiminase Pad4, catalytic C-terminal domain