
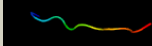

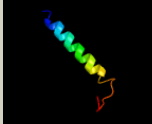








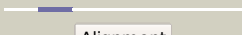



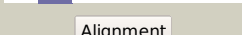

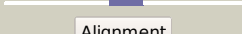

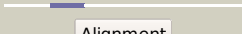
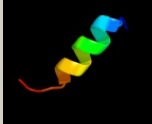





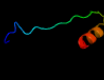





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2084 (- )_2341816_2342952
Date	Mon Aug 5 13:25:20 BST 2019
Unique Job ID	fca3bb463b7e18d7

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1ei9a_</a>	 Alignment		28.2	64	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
2	<a href="#">c3iynO_</a>	 Alignment		20.4	19	<b>PDB header:</b> virus <b>Chain:</b> O: <b>PDB Molecule:</b> hexon-associated protein; <b>PDBTitle:</b> 3.6-angstrom cryoem structure of human adenovirus type 5
3	<a href="#">d1cf7b_</a>	 Alignment		19.8	44	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Cell cycle transcription factor e2f-dp
4	<a href="#">c4q34A_</a>	 Alignment		17.1	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative esterase (bdi_1566) from2 parabacteroides distasonis atcc 8503 at 1.60 a resolution
5	<a href="#">c4jmrA_</a>	 Alignment		13.4	50	<b>PDB header:</b> viral protein/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> gag protein; <b>PDBTitle:</b> a unique spumavirus gag n-terminal domain with functional properties2 of orthoretroviral matrix and capsid
6	<a href="#">d2f5va2</a>	 Alignment		12.3	32	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GMC oxidoreductases
7	<a href="#">d1qlwa_</a>	 Alignment		11.7	42	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> A novel bacterial esterase
8	<a href="#">c4bjjB_</a>	 Alignment		11.3	55	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription factor tau subunit sfc7; <b>PDBTitle:</b> sfc1-sfc7 dimerization module
9	<a href="#">c2vf7B_</a>	 Alignment		11.2	42	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> excinuclease abc, subunit a.; <b>PDBTitle:</b> crystal structure of uvra2 from deinococcus radiodurans
10	<a href="#">c2lq2A_</a>	 Alignment		10.7	80	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed antifreeze peptide 4m; <b>PDBTitle:</b> solution structure of de novo designed peptide 4m
11	<a href="#">c3vzaD_</a>	 Alignment		10.3	50	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> spc24 protein; <b>PDBTitle:</b> crystal structure of the chicken spc24-spc25 globular domain in2 complex with cenp-t peptide

12	<a href="#">c6bi7D_</a>	Alignment		10.0	71	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of rev7-wt/rev3 as a monomer under high-salt2 conditions
13	<a href="#">c6bc8B_</a>	Alignment		9.9	71	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of rev7-r124a/rev3-rbm2 (residues 1988-2014) complex
14	<a href="#">c6ekmB_</a>	Alignment		9.9	71	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of mammalian rev7 in complex with human rev3 second2 binding site
15	<a href="#">c6bccB_</a>	Alignment		9.9	71	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of rev7-k44a/r124a/a135d in complex with rev3-rbm22 (residues 1988-2014)
16	<a href="#">c3zqjF_</a>	Alignment		9.8	53	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
17	<a href="#">c5nkmE_</a>	Alignment		9.3	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein smg-8; <b>PDBTitle:</b> smg8-smg9 complex
18	<a href="#">d1r5qa_</a>	Alignment		8.4	37	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
19	<a href="#">c2fz0A_</a>	Alignment		8.2	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> v-snare component of the vacuolar snare complex <b>PDBTitle:</b> identification of yeast r-snare nyv1p as a novel longin2 domain protein
20	<a href="#">c3pihA_</a>	Alignment		7.9	47	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> t. maritima uvra in complex with fluorescein-modified dna
21	<a href="#">c4ynlB_</a>	Alignment	not modelled	7.7	32	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the hood domain of anabaena hetr in complex with2 the hexapeptide ergsgr derived from pats
22	<a href="#">d1l4sa_</a>	Alignment	not modelled	7.6	30	<b>Fold:</b> Ribosome binding protein Y (YfiA homologue) <b>Superfamily:</b> Ribosome binding protein Y (YfiA homologue) <b>Family:</b> Ribosome binding protein Y (YfiA homologue)
23	<a href="#">c5azzA_</a>	Alignment	not modelled	7.6	60	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> insulin a chain; <b>PDBTitle:</b> crystal structure of seleno-insulin
24	<a href="#">c3b8fB_</a>	Alignment	not modelled	7.5	21	<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
25	<a href="#">c5yixB_</a>	Alignment	not modelled	7.3	71	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell cycle regulatory protein gcra; <b>PDBTitle:</b> caulobacter crescentum gcra sigma-interacting domain (sid) in complex2 with domain 2 of sigma 70
26	<a href="#">c4yv4D_</a>	Alignment	not modelled	7.2	62	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> spindle assembly abnormal protein 5; <b>PDBTitle:</b> structure of the c. elegans sas-5 coiled coil domain
27	<a href="#">c2oq2B_</a>	Alignment	not modelled	7.1	80	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine phosphosulfate reductase; <b>PDBTitle:</b> crystal structure of yeast paps reductase with pap, a product complex
28	<a href="#">d2pw4a1</a>	Alignment	not modelled	6.8	42	<b>Fold:</b> jann2411-like <b>Superfamily:</b> jann2411-like <b>Family:</b> jann2411-like

29	<a href="#">c2a45H_</a>	Alignment	not modelled	6.5	46	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of the complex between thrombin and the central "e"2 region of fibrin
30	<a href="#">d2o35a1</a>	Alignment	not modelled	6.4	35	<b>Fold:</b> SMc04008-like <b>Superfamily:</b> SMc04008-like <b>Family:</b> SMc04008-like
31	<a href="#">c2o35A_</a>	Alignment	not modelled	6.4	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf1244; <b>PDBTitle:</b> protein of unknown function (duf1244) from sinorhizobium meliloti
32	<a href="#">c5h6bA_</a>	Alignment	not modelled	6.3	64	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted lipase; <b>PDBTitle:</b> crystal structure of a thermostable lipase from marine streptomyces
33	<a href="#">c3kitB_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of a vimentin fragment
34	<a href="#">c6mdxA_</a>	Alignment	not modelled	6.0	29	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> spirt-like domain-containing protein spartan; <b>PDBTitle:</b> mechanism of protease dependent dpc repair
35	<a href="#">c6bi7F_</a>	Alignment	not modelled	5.6	71	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of rev7-wt/rev3 as a monomer under high-salt2 conditions
36	<a href="#">d1imua_</a>	Alignment	not modelled	5.5	40	<b>Fold:</b> Ribosome binding protein Y (YfiA homologue) <b>Superfamily:</b> Ribosome binding protein Y (YfiA homologue) <b>Family:</b> Ribosome binding protein Y (YfiA homologue)
37	<a href="#">c6fc3B_</a>	Alignment	not modelled	5.5	60	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> cap-associated protein caf20; <b>PDBTitle:</b> crystal structure of the eif4e-p20 complex from saccharomyces2 cerevisiae
38	<a href="#">c5jw9A_</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> af4/fmr2 family member 4; <b>PDBTitle:</b> the crystal structure of ell2 ocludin domain and aff4 peptide