

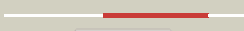


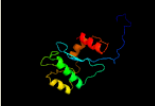
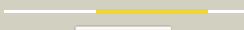

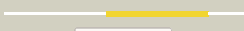

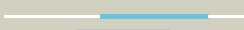








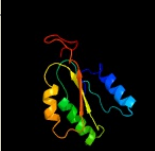

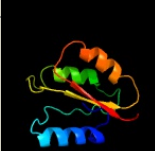
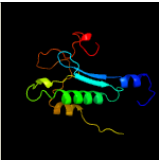

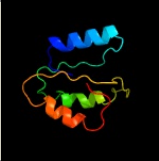


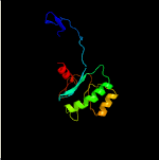
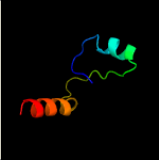
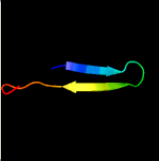
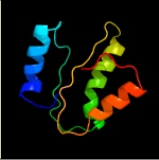


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1041c_(-)_1164576_1165439
Date	Wed Jul 31 22:05:11 BST 2019
Unique Job ID	f4b6b37616fba9dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1musa_</a>	 Alignment		97.7	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Transposase inhibitor (Tn5 transposase)
2	<a href="#">d1b7ea_</a>	 Alignment		97.4	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Transposase inhibitor (Tn5 transposase)
3	<a href="#">c3hosA_</a>	 Alignment		94.0	13	<b>PDB header:</b> transferase, dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element mariner, complete cds; <b>PDBTitle:</b> crystal structure of the mariner mos1 paired end complex with mg
4	<a href="#">d1asua_</a>	 Alignment		78.2	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
5	<a href="#">d1cxqa_</a>	 Alignment		73.5	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Retroviral integrase, catalytic domain
6	<a href="#">c4mq3A_</a>	 Alignment		32.8	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> the 1.1 angstrom structure of catalytic core domain of fiv integrase
7	<a href="#">c1c0mA_</a>	 Alignment		28.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (integrase); <b>PDBTitle:</b> crystal structure of rsv two-domain integrase
8	<a href="#">c3k2kA_</a>	 Alignment		28.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxypeptidase; <b>PDBTitle:</b> crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
9	<a href="#">d1a6qa1</a>	 Alignment		27.9	40	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> Protein serine/threonine phosphatase 2C, C-terminal domain <b>Family:</b> Protein serine/threonine phosphatase 2C, C-terminal domain
10	<a href="#">c6me1A_</a>	 Alignment		25.6	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate--coa ligase subunit alpha; <b>PDBTitle:</b> succinyl-coa synthase from campylobacter jejuni
11	<a href="#">d2nu7a2</a>	 Alignment		25.3	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains

12	<a href="#">d1bcoa2</a>	Alignment		24.6	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> mu transposase, core domain
13	<a href="#">c1bcoA_</a>	Alignment		24.3	19	<b>PDB header:</b> transposase <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophage mu transposase; <b>PDBTitle:</b> bacteriophage mu transposase core domain
14	<a href="#">d1oi7a2</a>	Alignment		23.3	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
15	<a href="#">c3nf9A_</a>	Alignment		23.0	14	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
16	<a href="#">d2csua2</a>	Alignment		22.5	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
17	<a href="#">c5cr4B_</a>	Alignment		21.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sleeping beauty transposase, sb100x; <b>PDBTitle:</b> crystal structure of the sleeping beauty transposase catalytic domain
18	<a href="#">c5cz1B_</a>	Alignment		16.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the catalytic core domain of mmtv integrase
19	<a href="#">c2oxgD_</a>	Alignment		15.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> soxy protein; <b>PDBTitle:</b> the soxyz complex of paracoccus pantotrophus
20	<a href="#">c3mwdB_</a>	Alignment		14.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
21	<a href="#">d2hزاب1</a>	Alignment	not modelled	14.2	33	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
22	<a href="#">c2hm4A_</a>	Alignment	not modelled	11.7	36	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematocyst outer wall antigen; <b>PDBTitle:</b> nematocyst outer wall antigen, nw1 k21p
23	<a href="#">d2hzaa1</a>	Alignment	not modelled	11.6	33	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
24	<a href="#">c2jm2A_</a>	Alignment	not modelled	11.4	54	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> insulin-like growth factor-binding protein 6; <b>PDBTitle:</b> structure of the n-terminal subdomain of insulin-like2 growth factor (igf) binding protein-6 and its interactions3 with igfs
25	<a href="#">c6f45D_</a>	Alignment	not modelled	11.1	9	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> receptor recognition protein; <b>PDBTitle:</b> crystal structure of the gp37-gp38 adhesin tip complex of the2 bacteriophage s16 long tail fiber
26	<a href="#">c5cbkA_</a>	Alignment	not modelled	10.6	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> shhtl5; <b>PDBTitle:</b> crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
27	<a href="#">c1ybxA_</a>	Alignment	not modelled	10.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> conserved hypothetical protein cth-383 from clostridium thermocellum
28	<a href="#">c3qd9D_</a>	Alignment	not modelled	10.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> qsox from trypanosoma brucei (tbqsox); <b>PDBTitle:</b> c72s/c353s mutant of trypanosoma brucei qsox containing an interdomain2 disulfide
						<b>PDB header:</b> signaling protein

29	<a href="#">c2laqA_</a>	Alignment	not modelled	9.8	43	<b>Chain:</b> A: <b>PDB Molecule:</b> accessory gland-specific peptide 70a; <b>PDBTitle:</b> solution structure of the sex peptide from drosophila melanogaster
30	<a href="#">c3jcaE_</a>	Alignment	not modelled	9.0	21	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> core model of the mouse mammary tumor virus intasome
31	<a href="#">c3f9kV_</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> viral protein, recombination <b>Chain:</b> V: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> two domain fragment of hiv-2 integrase in complex with ledgf ibd
32	<a href="#">c2n2iA_</a>	Alignment	not modelled	8.4	21	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> epstein-barr nuclear antigen 2; <b>PDBTitle:</b> solution structure of the ebna-2 n-terminal dimerization (end) domain2 from the epstein-barr virus
33	<a href="#">c3h1qB_</a>	Alignment	not modelled	8.4	13	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutj; <b>PDBTitle:</b> crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
34	<a href="#">d1euca2</a>	Alignment	not modelled	8.4	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
35	<a href="#">c6ajjA_</a>	Alignment	not modelled	8.3	32	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
36	<a href="#">c4uwqK_</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> soxy protein; <b>PDBTitle:</b> crystal structure of the disulfide-linked complex of the2 thiosulfurylase soxb with the carrier-protein soxyz from3 thermus thermophilus
37	<a href="#">c4aj52_</a>	Alignment	not modelled	8.2	8	<b>PDB header:</b> cell cycle <b>Chain:</b> 2: <b>PDB Molecule:</b> spindle and kinetochore-associated protein 3; <b>PDB Fragment:</b> residues 1-121; <b>PDBTitle:</b> crystal structure of the ska core complex
38	<a href="#">c6n63A_</a>	Alignment	not modelled	7.9	32	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> encapsulin cargo protein; <b>PDBTitle:</b> crystal structure of an iron binding protein
39	<a href="#">d1i2va_</a>	Alignment	not modelled	7.4	41	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Insect defensins
40	<a href="#">d2bj7a1</a>	Alignment	not modelled	7.2	19	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
41	<a href="#">d1ckma1</a>	Alignment	not modelled	6.7	30	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
42	<a href="#">c5gsfA_</a>	Alignment	not modelled	6.7	60	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> roseltide rt1; <b>PDBTitle:</b> structure of roseltide rt1
43	<a href="#">c2fpgA_</a>	Alignment	not modelled	6.4	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [gdp-forming] alpha-chain, <b>PDBTitle:</b> crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
44	<a href="#">d1ni5a1</a>	Alignment	not modelled	6.0	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
45	<a href="#">c1oi7A_</a>	Alignment	not modelled	5.9	20	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
46	<a href="#">c2yv1A_</a>	Alignment	not modelled	5.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
47	<a href="#">c4yajA_</a>	Alignment	not modelled	5.9	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
48	<a href="#">c6hlwB_</a>	Alignment	not modelled	5.8	13	<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)
49	<a href="#">c2hm3A_</a>	Alignment	not modelled	5.7	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematocyst outer wall antigen; <b>PDBTitle:</b> nematocyst outer wall antigen, cysteine rich domain nw1
50	<a href="#">d1pugb_</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
51	<a href="#">c5loxH_</a>	Alignment	not modelled	5.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> peptidase; <b>PDBTitle:</b> helical assembly of the anbu complex from pseudomonas aeruginosa
52	<a href="#">c5yrxA_</a>	Alignment	not modelled	5.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoid-associated protein rv3716c; <b>PDBTitle:</b> crystal structure of a hypothetical protein rv3716c from mycobacterium2 tuberculosis
53	<a href="#">c5id6A_</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cpf1; <b>PDBTitle:</b> structure of cpf1/rna complex
						<b>Fold:</b> MTH938-like

54	<a href="#">d2fi9a1</a>	Alignment	not modelled	5.3	18	<b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
55	<a href="#">c5u1cA_</a>	Alignment	not modelled	5.1	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hiv-1 integrase, sso7d chimera; <b>PDBTitle:</b> structure of tetrameric hiv-1 strand transfer complex intasome
56	<a href="#">c2omkB_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
57	<a href="#">c2lg5A_</a>	Alignment	not modelled	5.1	83	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> gallinacin-2; <b>PDBTitle:</b> nmr structure of chicken avbd2 defensin