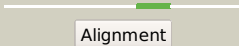
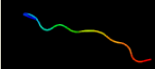

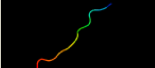
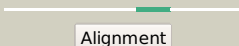

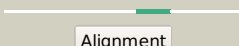

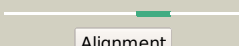

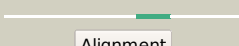

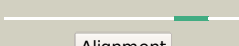
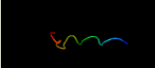
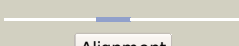


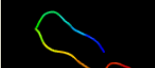



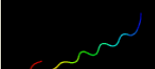


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1961 (-) _2204219_2204713
Date	Mon Aug 5 13:25:06 BST 2019
Unique Job ID	142acb9eeeb90d4e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2f0cC_</a>	 Alignment		55.2	33	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> phage tp901-1 orf49 (bpp); <b>PDBTitle:</b> structure of the receptor binding protein (orf49, bbp) from lactophage2 tp901-1
2	<a href="#">d2f0ca1</a>	 Alignment		49.5	33	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Lactophage receptor-binding protein head domain
3	<a href="#">c3u6xF_</a>	 Alignment		47.2	33	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> bpp; <b>PDBTitle:</b> phage tp901-1 baseplate tripod
4	<a href="#">d1zrua1</a>	 Alignment		47.0	50	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Lactophage receptor-binding protein head domain
5	<a href="#">c3d8mA_</a>	 Alignment		46.7	50	<b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> baseplate protein, receptor binding protein; <b>PDBTitle:</b> crystal structure of a chimeric receptor binding protein from 2 lactococcal phages subspecies tp901-1 and p2
6	<a href="#">c3da0C_</a>	 Alignment		46.0	50	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> cleaved chimeric receptor binding protein from <b>PDBTitle:</b> crystal structure of a cleaved form of a chimeric receptor binding 2 protein from lactococcal phages subspecies tp901-1 and p2
7	<a href="#">c5l6nI_</a>	 Alignment		41.1	63	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> thrombin inhibitor madanin 1; <b>PDBTitle:</b> disulfated madanin-thrombin complex
8	<a href="#">d2dsma1</a>	 Alignment		24.2	45	<b>Fold:</b> Yqal-like <b>Superfamily:</b> Yqal-like <b>Family:</b> Yqal-like
9	<a href="#">c4v194_</a>	 Alignment		17.1	38	<b>PDB header:</b> ribosome <b>Chain:</b> 4: <b>PDB Molecule:</b> mitoribosomal protein bl31m, mrpl55; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
10	<a href="#">c4fc5A_</a>	 Alignment		14.5	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ton_0340
11	<a href="#">c5kpeA_</a>	 Alignment		13.7	41	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo beta sheet design protein or664; <b>PDBTitle:</b> solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesg) target or664

12	<a href="#">c3ij6A_</a>	Alignment		13.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of an uncharacterized metal-dependent hydrolase from2 lactobacillus acidophilus
13	<a href="#">c5jp6A_</a>	Alignment		13.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polysaccharide deacetylase; <b>PDBTitle:</b> bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
14	<a href="#">d2gwg1_</a>	Alignment		13.2	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
15	<a href="#">c2nchA_</a>	Alignment		13.1	30	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi
16	<a href="#">c2o5rA_</a>	Alignment		12.6	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1; <b>PDBTitle:</b> crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glurs 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
17	<a href="#">c2qahA_</a>	Alignment		11.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-pyrone-4,6-dicarboxylic acid hydrolase; <b>PDBTitle:</b> crystal structure of the 2-pyrone-4,6-dicarboxylic acid hydrolase from2 sphingomonas paucimobilis
18	<a href="#">d2f6ka1</a>	Alignment		11.9	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
19	<a href="#">c6grvA_</a>	Alignment		11.3	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> metallothionein; <b>PDBTitle:</b> cadmium(ii) form of full-length metallothionein from pseudomonas2 fluorescens q2-87 (pflq2 mt)
20	<a href="#">c6omqA_</a>	Alignment		10.9	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ptmu3; <b>PDBTitle:</b> crystal structure of ptmu3 complexed with ptm substrate
21	<a href="#">c1iv8A_</a>	Alignment	not modelled	10.3	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> maltooligosyl trehalose synthase; <b>PDBTitle:</b> crystal structure of maltooligosyl trehalose synthase
22	<a href="#">c3zifR_</a>	Alignment	not modelled	9.9	25	<b>PDB header:</b> virus <b>Chain:</b> R: <b>PDB Molecule:</b> pviij; <b>PDBTitle:</b> cryo-em structures of two intermediates provide insight into2 adenovirus assembly and disassembly
23	<a href="#">d2hbva1</a>	Alignment	not modelled	9.6	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
24	<a href="#">d1w2ya_</a>	Alignment	not modelled	9.3	45	<b>Fold:</b> all-alpha NTP pyrophosphatases <b>Superfamily:</b> all-alpha NTP pyrophosphatases <b>Family:</b> Type II deoxyuridine triphosphatase
25	<a href="#">c3cjpA_</a>	Alignment	not modelled	9.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted amidohydrolase, dihydroorotase family; <b>PDBTitle:</b> crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
26	<a href="#">c2wm1A_</a>	Alignment	not modelled	9.2	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-3-carboxymuconate-6-semialdehyde <b>PDBTitle:</b> the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis
27	<a href="#">c5vn5A_</a>	Alignment	not modelled	9.2	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,2',3-trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl meta- <b>PDBTitle:</b> crystal structure of ligy from sphingobium sp. strain syk-6 <b>PDB header:</b> signaling protein/signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> siqma-e factor negative regulatory

28	<a href="#">c3m4wE_</a>	Alignment	not modelled	8.7	32	protein; <b>PDBTitle:</b> structural basis for the negative regulation of bacterial stress2 response by rseb
29	<a href="#">c2ja2A_</a>	Alignment	not modelled	8.5	42	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase
30	<a href="#">c5oarC_</a>	Alignment	not modelled	8.2	52	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-hexosaminidase; <b>PDBTitle:</b> crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
31	<a href="#">c2cfoA_</a>	Alignment	not modelled	7.8	50	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
32	<a href="#">c6dxsB_</a>	Alignment	not modelled	7.7	23	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> 4-oxalomesaconate hydratase; <b>PDBTitle:</b> crystal structure of the ligj hydratase e284q mutant substrate complex2 with (3z)-2-keto-4-carboxy-3-hexenedioate
33	<a href="#">c4dziD_</a>	Alignment	not modelled	7.6	46	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative tim-barrel metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase map2389c (target efi-500390) from2 mycobacterium avium subsp. paratuberculosis k-10
34	<a href="#">c4l5pD_</a>	Alignment	not modelled	7.6	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 5-carboxyvanillate decarboxylase; <b>PDBTitle:</b> crystal structure of 5-carboxyvanillate decarboxylase from2 sphingomonas paucimobilis complexed with 4-hydroxy-3-methoxy-5-3 nitrobenzoic acid
35	<a href="#">c4mupC_</a>	Alignment	not modelled	7.5	47	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens atu3138 (efi target2 505157), apo structure
36	<a href="#">d1grja2</a>	Alignment	not modelled	7.4	24	<b>Fold:</b> FKBP-like <b>Superfamily:</b> FKBP-like <b>Family:</b> GreA transcript cleavage factor, C-terminal domain
37	<a href="#">c1grjA_</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> grea protein; <b>PDBTitle:</b> grea transcript cleavage factor from escherichia coli
38	<a href="#">d1nuwa_</a>	Alignment	not modelled	7.1	22	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
39	<a href="#">c5ydfA_</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> parafibromin; <b>PDBTitle:</b> crystal structure of a disease-related gene, hcdc73(1-100)
40	<a href="#">d2dvta1</a>	Alignment	not modelled	6.7	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
41	<a href="#">c4hk6D_</a>	Alignment	not modelled	6.7	27	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil-5-carboxylate decarboxylase; <b>PDBTitle:</b> crystal structure of cordyceps militaris idcase in complex with 5-2 nitro-uracil
42	<a href="#">c5k8qB_</a>	Alignment	not modelled	6.6	40	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> zgc:136689; <b>PDBTitle:</b> crystal structure of calcium-loaded calmodulin in complex with stra62 campb2-site peptide.
43	<a href="#">d1ay7b_</a>	Alignment	not modelled	6.6	27	<b>Fold:</b> Barstar-like <b>Superfamily:</b> Barstar-related <b>Family:</b> Barstar-related
44	<a href="#">c2kamA_</a>	Alignment	not modelled	6.4	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-hemolysin; <b>PDBTitle:</b> nmr structure of delta-toxin from staphylococcus aureus in2 cd3oh
45	<a href="#">d1bk4a_</a>	Alignment	not modelled	6.3	22	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
46	<a href="#">c2fhyL_</a>	Alignment	not modelled	6.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> fructose-1,6-bisphosphatase 1; <b>PDBTitle:</b> structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor
47	<a href="#">c1dtaA_</a>	Alignment	not modelled	6.3	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-delta-toxin; <b>PDBTitle:</b> delta-toxin and analogues as peptide models for protein ion2 channels
48	<a href="#">c3nurA_</a>	Alignment	not modelled	6.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal structure of a putative amidohydrolase from staphylococcus2 aureus
49	<a href="#">c4infA_</a>	Alignment	not modelled	6.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of amidohydrolase sar0_0799 (target efi-505250) from2 novosphingobium aromaticivorans dsm 12444 with bound calcium
50	<a href="#">c3afhA_</a>	Alignment	not modelled	6.1	38	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 2; <b>PDBTitle:</b> crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
51	<a href="#">c2dtbA_</a>	Alignment	not modelled	6.0	44	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-toxin; <b>PDBTitle:</b> delta-toxin and analogues as peptide models for protein ion2 channels
52	<a href="#">c2y1hA_</a>	Alignment	not modelled	6.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyribonuclease tatdn3; <b>PDBTitle:</b> crystal structure of the human tatd-domain protein 3 (tatdn3)
53	<a href="#">c3a6A_</a>	Alignment	not modelled	6.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiohydrolase;

53	<a href="#">c3b9A</a>	Alignment	not modelled	6.0	42	<b>PDBTitle:</b> crystal structure of ccel6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea <b>PDB header:</b> hydrolase
54	<a href="#">c1jqpA</a>	Alignment	not modelled	6.0	43	<b>Chain:</b> A; <b>PDB Molecule:</b> dipeptidyl peptidase i; <b>PDBTitle:</b> dipeptidyl peptidase i (cathepsin c), a tetrameric cysteine protease2 of the papain family
55	<a href="#">d1yixa1</a>	Alignment	not modelled	5.9	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> TatD Mg-dependent DNase-like
56	<a href="#">d1qtra2</a>	Alignment	not modelled	5.9	42	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
57	<a href="#">d1bbua1</a>	Alignment	not modelled	5.8	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
58	<a href="#">d1ftaa</a>	Alignment	not modelled	5.8	22	<b>Fold:</b> Carbohydrate phosphatase <b>Superfamily:</b> Carbohydrate phosphatase <b>Family:</b> Inositol monophosphatase/fructose-1,6-bisphosphatase-like
59	<a href="#">d1nzia</a>	Alignment	not modelled	5.7	58	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
60	<a href="#">c4do7B</a>	Alignment	not modelled	5.7	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> amidohydrolase 2; <b>PDBTitle:</b> crystal structure of an amidohydrolase (cog3618) from burkholderia2 multivorans (target efi-500235) with bound zn, space group c2
61	<a href="#">d2ffia1</a>	Alignment	not modelled	5.5	54	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> PP1699/LP2961-like
62	<a href="#">c2v6xB</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> doa4-independent degradation protein 4; <b>PDBTitle:</b> structural insight into the interaction between escrt-iii and vps4
63	<a href="#">c6s3fB</a>	Alignment	not modelled	5.5	50	<b>PDB header:</b> antifungal protein <b>Chain:</b> B; <b>PDB Molecule:</b> 2s albumin; <b>PDBTitle:</b> moringa seed protein mo-cbp3-4
64	<a href="#">c6b1pA</a>	Alignment	not modelled	5.4	42	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate--trna ligase 1; <b>PDBTitle:</b> crystal structure of glutamate-trna synthetase from helicobacter2 pylori
65	<a href="#">c3qitA</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> carbon monoxide dehydrogenase/acetyl-coa synthase subunit <b>PDBTitle:</b> crystal structure of a truncated acetyl-coa synthase
66	<a href="#">c3al0C</a>	Alignment	not modelled	5.4	38	<b>PDB header:</b> ligase/rna <b>Chain:</b> C; <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c, linker, <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
67	<a href="#">c2dzmA</a>	Alignment	not modelled	5.4	19	<b>PDB header:</b> structural genomics unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> fas-associated factor 1; <b>PDBTitle:</b> solution structure of the ubiquitin-like domain in human2 fas-associated factor 1 (hfa1)
68	<a href="#">d2cx6a1</a>	Alignment	not modelled	5.3	16	<b>Fold:</b> Barstar-like <b>Superfamily:</b> Barstar-related <b>Family:</b> Barstar-related
69	<a href="#">c5lqCA</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> arce4a; <b>PDBTitle:</b> t48 deacetylase with substrate
70	<a href="#">c2vyoA</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> polysaccharide deacetylase domain-containing protein <b>PDBTitle:</b> chitin deacetylase family member from encephalitozoon cuniculi
71	<a href="#">c2vqlD</a>	Alignment	not modelled	5.2	86	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> uncharacterized protein cgl0972; <b>PDBTitle:</b> crystal structure of porb from corynebacterium glutamicum (2 crystal form iii)
72	<a href="#">c3tnxA</a>	Alignment	not modelled	5.2	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> papain; <b>PDBTitle:</b> structure of the precursor of a thermostable variant of papain at 2.62 angstroem resolution
73	<a href="#">c2gq1A</a>	Alignment	not modelled	5.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> fructose-1,6-bisphosphatase; <b>PDBTitle:</b> crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions