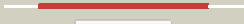


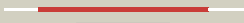















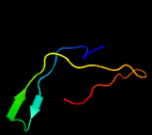





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2386c_(mbt)_2678663_2680015
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	05500ddc7ad1e4cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2g5fa1</a>	 Alignment		100.0	100	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase
2	<a href="#">c2i6yA</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> anthranilate synthase component i, putative; <b>PDBTitle:</b> structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbt1
3	<a href="#">c4penA</a>	 Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> anthranilate synthase component 1; <b>PDBTitle:</b> structure of anthranilate synthase component 1 (trpe) from2 mycobacterium tuberculosis with inhibitor bound
4	<a href="#">d1qdlA</a>	 Alignment		100.0	27	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase
5	<a href="#">d1i1qa</a>	 Alignment		100.0	24	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase
6	<a href="#">d1i7qa</a>	 Alignment		100.0	22	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase
7	<a href="#">d2fn0a1</a>	 Alignment		100.0	37	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase
8	<a href="#">c5kckA</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> anthranilate synthase component i; <b>PDBTitle:</b> crystal structure of anthranilate synthase component i from2 streptococcus pneumoniae tigr4
9	<a href="#">c4grhA</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aminodeoxychorismate synthase; <b>PDBTitle:</b> crystal structure of pabb of stentrophomonas maltophilia
10	<a href="#">d3bzna1</a>	 Alignment		100.0	22	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase
11	<a href="#">d1k0ga</a>	 Alignment		100.0	19	<b>Fold:</b> ADC synthase <b>Superfamily:</b> ADC synthase <b>Family:</b> ADC synthase

12	<a href="#">c3h9mA</a>	Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> p-aminobenzoate synthetase, component i; <b>PDBTitle:</b> crystal structure of para-aminobenzoate synthetase, component i from2 cytophaga hutchinsonii
13	<a href="#">c3hwoB</a>	Alignment		100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> isochorismate synthase entc; <b>PDBTitle:</b> crystal structure of escherichia coli enterobactin-specific2 isochorismate synthase entc in complex with isochorismate
14	<a href="#">c3gseA</a>	Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> menaquinone-specific isochorismate synthase; <b>PDBTitle:</b> crystal structure of menaquinone-specific isochorismate synthase from2 yersinia pestis co92
15	<a href="#">c3os6A</a>	Alignment		100.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isochorismate synthase dhbc; <b>PDBTitle:</b> crystal structure of putative 2,3-dihydroxybenzoate-specific2 isochorismate synthase, dhbc from bacillus anthracis.
16	<a href="#">c3r74B</a>	Alignment		100.0	19	<b>PDB header:</b> lyase, biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate/para-aminobenzoate synthases component i; <b>PDBTitle:</b> crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
17	<a href="#">c3nqkA</a>	Alignment		40.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a structural genomics, unknown function2 (bacova_03322) from bacteroides ovatus at 2.61 a resolution
18	<a href="#">d1cvra1</a>	Alignment		39.1	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Gingipain R (RgpB), C-terminal domain
19	<a href="#">c2km1A</a>	Alignment		25.2	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein dre2; <b>PDBTitle:</b> solution structure of the n-terminal domain of the yeast protein dre2
20	<a href="#">d2ffca1</a>	Alignment		21.5	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
21	<a href="#">d1hxra</a>	Alignment	not modelled	15.3	17	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> RabGEF Mss4
22	<a href="#">c1wqkA</a>	Alignment	not modelled	15.2	31	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> toxin apetx1; <b>PDBTitle:</b> solution structure of apetx1, a specific peptide inhibitor2 of human ether-a-go-go-related gene potassium channels3 from the venom of the sea anemone anthopleura4 elegantissima: a new fold for an herg toxin
23	<a href="#">d2fu5a1</a>	Alignment	not modelled	14.9	17	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> RabGEF Mss4
24	<a href="#">c2lt2A</a>	Alignment	not modelled	13.8	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr structure of ba42 protein from the psychrophilic bacteria bizionia2 argentinensis sp. nov.
25	<a href="#">c4anrA</a>	Alignment	not modelled	13.8	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble lytic transglycosylase b; <b>PDBTitle:</b> crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
26	<a href="#">d2qdyal</a>	Alignment	not modelled	13.6	14	<b>Fold:</b> Nitrile hydratase alpha chain <b>Superfamily:</b> Nitrile hydratase alpha chain <b>Family:</b> Nitrile hydratase alpha chain
27	<a href="#">c1wxnA</a>	Alignment	not modelled	12.9	31	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> toxin apetx2; <b>PDBTitle:</b> solution structure of apetx2, a specific peptide inhibitor2 of ASIC3 proton-gated channels
28	<a href="#">d1ugpa</a>	Alignment	not modelled	12.3	21	<b>Fold:</b> Nitrile hydratase alpha chain <b>Superfamily:</b> Nitrile hydratase alpha chain <b>Family:</b> Nitrile hydratase alpha chain
						<b>PDB header:</b> structural genomics, unknown function

29	<a href="#">c1yx3A_</a>	Alignment	not modelled	11.9	22	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dsrc; <b>PDBTitle:</b> nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
30	<a href="#">c4k6nA_</a>	Alignment	not modelled	11.8	7	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aminodeoxychorismate lyase; <b>PDBTitle:</b> crystal structure of yeast 4-amino-4-deoxychorismate lyase
31	<a href="#">c3vf0A_</a>	Alignment	not modelled	11.5	11	<b>PDB header:</b> cell adhesion/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> vinculin; <b>PDBTitle:</b> raver1 in complex with metavinclin I954 deletion mutant
32	<a href="#">c4w5xA_</a>	Alignment	not modelled	10.9	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> late protein h7; <b>PDBTitle:</b> the structure of vaccinia virus h7 protein displays a novel2 phosphoinositide binding fold required for membrane biogenesis
33	<a href="#">c5jnoB_</a>	Alignment	not modelled	10.8	21	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> dna excision repair protein ercc-6-like; <b>PDBTitle:</b> crystal structure of the bd1-ntp complex from bend3 and pich
34	<a href="#">c4aq2I_</a>	Alignment	not modelled	10.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> homogentisate 1,2-dioxygenase; <b>PDBTitle:</b> resting state of homogentisate 1,2-dioxygenase
35	<a href="#">c3kz5E_</a>	Alignment	not modelled	10.2	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of cdomain
36	<a href="#">d1ji8a_</a>	Alignment	not modelled	9.9	23	<b>Fold:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Superfamily:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase <b>Family:</b> DsrC, the gamma subunit of dissimilatory sulfite reductase
37	<a href="#">c5n81B_</a>	Alignment	not modelled	9.3	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 1; <b>PDBTitle:</b> crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
38	<a href="#">c2k27A_</a>	Alignment	not modelled	9.0	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> paired box protein pax-8; <b>PDBTitle:</b> solution structure of human pax8 paired box domain
39	<a href="#">d1qusa_</a>	Alignment	not modelled	8.8	29	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Bacterial muramidase, catalytic domain
40	<a href="#">d2bccg3</a>	Alignment	not modelled	8.1	30	<b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GDI-like
41	<a href="#">c5anzA_</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble lytic transglycosylase b3; <b>PDBTitle:</b> crystal structure of sltb3 from pseudomonas aeruginosa.
42	<a href="#">d1v29a_</a>	Alignment	not modelled	7.6	12	<b>Fold:</b> Nitrile hydratase alpha chain <b>Superfamily:</b> Nitrile hydratase alpha chain <b>Family:</b> Nitrile hydratase alpha chain
43	<a href="#">c5h1nB_</a>	Alignment	not modelled	7.2	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0253 protein yaep; <b>PDBTitle:</b> crystal structure of sf173 from shigella flexneri
44	<a href="#">c4ccfD_</a>	Alignment	not modelled	7.1	27	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> fusion glycoprotein f0; <b>PDBTitle:</b> structure of respiratory syncytial virus f protein head domain
45	<a href="#">c3oheA_</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine triad (hit) protein; <b>PDBTitle:</b> crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
46	<a href="#">c6f37B_</a>	Alignment	not modelled	6.7	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nano3,fructose-binding lectin protein; <b>PDBTitle:</b> fusion protein of rsl and trimeric coiled coil
47	<a href="#">c4rrfD_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> threonine--trna ligase; <b>PDBTitle:</b> editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa
48	<a href="#">d2af7a1</a>	Alignment	not modelled	6.5	17	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
49	<a href="#">c2xt6B_</a>	Alignment	not modelled	6.5	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate decarboxylase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
50	<a href="#">c4mmvB_</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> fusion glycoprotein f1 fused with fibrin trimerization <b>PDBTitle:</b> crystal structure of prefusion-stabilized rsv f variant ds-cav1-tric2 at ph 9.5
51	<a href="#">c2z1tA_</a>	Alignment	not modelled	6.1	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase expression/formation protein hype; <b>PDBTitle:</b> crystal structure of hydrogenase maturation protein hype
52	<a href="#">c5tpnA_</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> fusion glycoprotein f0,fibrin;trimerization <b>PDBTitle:</b> crystal structure of rsv f in complex with human antibody hrsv90
53	<a href="#">c2nd2A_</a>	Alignment	not modelled	6.0	11	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo mini protein hhh_06; <b>PDBTitle:</b> solution structure of the de novo mini protein ghhh_06
54	<a href="#">c3rrrB_</a>	Alignment	not modelled	6.0	28	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> fusion glycoprotein f0; <b>PDBTitle:</b> structure of the rsv f protein in the post-fusion conformation
55	<a href="#">c3c66B_</a>	Alignment	not modelled	5.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a) polymerase; <b>PDBTitle:</b> yeast poly(a) polymerase in complex with fip1 residues

				80-105	
56	<a href="#">c4d56A_</a>	Alignment	not modelled	5.9	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> apnaa1; <b>PDBTitle:</b> understanding bi-specificity of a-domains
57	<a href="#">c3tfxB_</a>	Alignment	not modelled	5.7	19 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5'-phosphate decarboxylase from <i>lactobacillus acidophilus</i>
58	<a href="#">c3rkiB_</a>	Alignment	not modelled	5.7	27 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> fusion glycoprotein f0; <b>PDBTitle:</b> structural basis for immunization with post-fusion rsv f to elicit high neutralizing antibody titers
59	<a href="#">c3o44G_</a>	Alignment	not modelled	5.5	38 <b>PDB header:</b> toxin <b>Chain:</b> G: <b>PDB Molecule:</b> hemolysin; <b>PDBTitle:</b> crystal structure of the vibrio cholerae cytolysin (hlyA) heptameric2 pore
60	<a href="#">c1t2ba_</a>	Alignment	not modelled	5.3	6 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> p450cin; <b>PDBTitle:</b> crystal structure of cytochrome p450cin complexed with its2 substrate 1,8-cineole
61	<a href="#">c4nv1D_</a>	Alignment	not modelled	5.3	9 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltransferase; <b>PDBTitle:</b> crystal structure of a 4-n formyltransferase from francisella2 tularensis
62	<a href="#">c5nopB_</a>	Alignment	not modelled	5.2	18 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> attachment glycoprotein; <b>PDBTitle:</b> structure of mojiang virus attachment glycoprotein
63	<a href="#">c3zj1A_</a>	Alignment	not modelled	5.2	20 <b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear polyadenylated rna-binding protein nab2; <b>PDBTitle:</b> structure of nab2p tandem zinc finger 12
64	<a href="#">d2acfa1</a>	Alignment	not modelled	5.2	11 <b>Fold:</b> Macro domain-like <b>Superfamily:</b> Macro domain-like <b>Family:</b> Macro domain
65	<a href="#">d1d5ta2</a>	Alignment	not modelled	5.1	26 <b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GDI-like
66	<a href="#">c3qyhG_</a>	Alignment	not modelled	5.1	9 <b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> co-type nitrile hydratase alpha subunit; <b>PDBTitle:</b> crystal structure of co-type nitrile hydratase beta-h711 from <i>2 pseudomonas putida</i> .