

























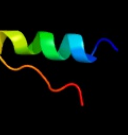
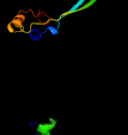

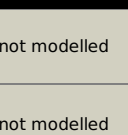
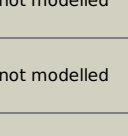


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0962c_(lprP)_1074444_1075118
Date	Wed Jul 31 22:05:02 BST 2019
Unique Job ID	489d0e2c5ab28497

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2v7sA_</a>	 Alignment		89.7	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved lipoprotein lppa; <b>PDBTitle:</b> crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
2	<a href="#">c3udiA_</a>	 Alignment		78.0	35	<b>PDB header:</b> penicillin-binding protein/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1a; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
3	<a href="#">c3zg8B_</a>	 Alignment		57.4	32	<b>PDB header:</b> penicillin-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> penicillin-binding protein 4; <b>PDBTitle:</b> crystal structure of penicillin binding protein 4 from2 listeria monocytogenes in the ampicillin bound form
4	<a href="#">c5u2gA_</a>	 Alignment		49.6	33	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1a; <b>PDBTitle:</b> 2.6 angstrom resolution crystal structure of penicillin-binding2 protein 1a from haemophilus influenzae
5	<a href="#">c3fwlA_</a>	 Alignment		49.4	35	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1b; <b>PDBTitle:</b> crystal structure of the full-length transglycosylase pbp1b from2 escherichia coli
6	<a href="#">c2olvA_</a>	 Alignment		42.4	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
7	<a href="#">d2bqxa1</a>	 Alignment		41.4	52	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> Peptidoglycan binding domain, PGBD
8	<a href="#">c2ot8D_</a>	 Alignment		40.5	78	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein m; <b>PDBTitle:</b> karyopherin beta2/transportin-hnrnrm nls complex
9	<a href="#">c3dwkC_</a>	 Alignment		39.8	32	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> penicillin-binding protein 2; <b>PDBTitle:</b> identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
10	<a href="#">c1vw4b_</a>	 Alignment		30.4	18	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
11	<a href="#">c5namA_</a>	 Alignment		28.3	100	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> toll-like receptor 4; <b>PDBTitle:</b> nmr structure of tlr4 transmembrane domain (624-670) in dmpg/dhcp2 bicelles

12	<a href="#">c3hzaA</a>	Alignment		26.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> monofunctional glycosyltransferase; <b>PDBTitle:</b> s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
13	<a href="#">d2olua1</a>	Alignment		21.7	30	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PBP transglycosylase domain-like
14	<a href="#">c2q5tA</a>	Alignment		18.7	29	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> cholix toxin; <b>PDBTitle:</b> full-length cholix toxin from vibrio cholerae
15	<a href="#">d2oqa1</a>	Alignment		16.0	38	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> PBP transglycosylase domain-like
16	<a href="#">c3assB</a>	Alignment		15.2	22	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> crystal structure of p domain from norovirus funabashi258 stain in the2 complex with lewis-b
17	<a href="#">d1bm9a</a>	Alignment		12.0	38	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Replication terminator protein (RTP)
18	<a href="#">c2p5xB</a>	Alignment		12.0	22	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> n-acetylserotonin o-methyltransferase-like protein; <b>PDBTitle:</b> crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
19	<a href="#">d1muwa</a>	Alignment		11.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
20	<a href="#">c5jeaK</a>	Alignment		11.2	22	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> K; <b>PDB Molecule:</b> superkiller protein 7,endolysin; <b>PDBTitle:</b> structure of a cytoplasmic 11-subunit rna exosome complex including2 ski7, bound to rna
21	<a href="#">d1n7za</a>	Alignment	not modelled	10.3	38	<b>Fold:</b> Baseplate structural protein gp8 <b>Superfamily:</b> Baseplate structural protein gp8 <b>Family:</b> Baseplate structural protein gp8
22	<a href="#">c1ye9E</a>	Alignment	not modelled	10.3	48	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> catalase hpii; <b>PDBTitle:</b> crystal structure of proteolytically truncated catalase2 hpii from e. coli
23	<a href="#">c2xsgB</a>	Alignment	not modelled	9.9	46	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ccman5; <b>PDBTitle:</b> structure of the gh92 family glycosyl hydrolase ccman5
24	<a href="#">d1br2a2</a>	Alignment	not modelled	9.6	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Motor proteins
25	<a href="#">c4qlpB</a>	Alignment	not modelled	9.6	16	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> alanine and proline rich protein, tuberculosis necrotizing <b>PDBTitle:</b> atomic structure of tuberculosis necrotizing toxin (tnt) complexed2 with its immunity factor ift
26	<a href="#">c5civA</a>	Alignment	not modelled	9.1	17	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> sibling bacteriocin; <b>PDBTitle:</b> sibling lethal factor precursor - dfsb
27	<a href="#">d2amha1</a>	Alignment	not modelled	9.0	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> ITPase-like <b>Family:</b> Maf-like
28	<a href="#">c2kq5A</a>	Alignment	not modelled	8.9	47	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha <b>PDB header:</b> transferase

29	<a href="#">c3vmtA</a>	Alignment	not modelled	8.9	16	<b>Chain:</b> A: <b>PDB Molecule:</b> monofunctional glycosyltransferase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus membrane-bound2 transglycosylase in complex with a lipid ii analog
30	<a href="#">c2wvyA</a>	Alignment	not modelled	8.5	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
31	<a href="#">c5uwzA</a>	Alignment	not modelled	8.2	52	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde decarbonylase; <b>PDBTitle:</b> protein 12 with aldehyde deformylating oxygenase activity from2 gloeobacter violaceus
32	<a href="#">c5fu4B</a>	Alignment	not modelled	7.9	52	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cbm74-rfgh5; <b>PDBTitle:</b> the complexity of the ruminococcus flavefaciens cellulosome reflects2 an expansion in glycan recognition
33	<a href="#">c4p2nD</a>	Alignment	not modelled	7.8	36	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> major capsid protein; <b>PDBTitle:</b> structure of the p domain from a gi.7 norovirus variant in complex2 with lex hbga
34	<a href="#">d1ikpa1</a>	Alignment	not modelled	7.7	38	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Exotoxin A, N-terminal domain
35	<a href="#">d1ei5a1</a>	Alignment	not modelled	7.5	57	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
36	<a href="#">c2zl5A</a>	Alignment	not modelled	7.5	26	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> 58 kd capsid protein; <b>PDBTitle:</b> atomic resolution structural characterization of2 recognition of histo-blood group antigen by norwalk virus
37	<a href="#">c4pwyA</a>	Alignment	not modelled	7.1	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calmodulin-lysine n-methyltransferase; <b>PDBTitle:</b> crystal structure of a calmodulin-lysine n-methyltransferase fragment
38	<a href="#">d1wpga2</a>	Alignment	not modelled	7.1	32	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
39	<a href="#">c5lnkn</a>	Alignment	not modelled	7.1	55	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> mitochondrial complex i, nd2 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
40	<a href="#">c4pd3B</a>	Alignment	not modelled	7.0	26	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> nonmuscle myosin heavy chain b, alpha-actinin a chimera <b>PDBTitle:</b> crystal structure of rigor-like human nonmuscle myosin-2b
41	<a href="#">c6f92B</a>	Alignment	not modelled	6.8	46	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 alpha-mannosidase bt3965 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
42	<a href="#">c4wj4A</a>	Alignment	not modelled	6.8	25	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase; <b>PDBTitle:</b> crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asp) and aspartic acid
43	<a href="#">d1p80a2</a>	Alignment	not modelled	6.8	48	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
44	<a href="#">d2uubk1</a>	Alignment	not modelled	6.6	40	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> Ribosomal protein L18 and S11
45	<a href="#">c6itcB</a>	Alignment	not modelled	6.6	34	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> translocating peptide; <b>PDBTitle:</b> structure of a substrate engaged seca-secy protein translocation2 machine
46	<a href="#">c2dfsA</a>	Alignment	not modelled	6.5	30	<b>PDB header:</b> contractile protein/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin-5a; <b>PDBTitle:</b> 3-d structure of myosin-v inhibited state
47	<a href="#">c4b24A</a>	Alignment	not modelled	6.5	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna-3-methyladenine glycosylase 2; <b>PDBTitle:</b> unprecedented sculpting of dna at abasic sites by dna glycosylase2 homolog mag2
48	<a href="#">c2dceA</a>	Alignment	not modelled	6.3	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> kiaa1915 protein; <b>PDBTitle:</b> solution structure of the swirm domain of human kiaa19152 protein
49	<a href="#">d1q3ma</a>	Alignment	not modelled	6.2	44	<b>Fold:</b> GLA-domain <b>Superfamily:</b> GLA-domain <b>Family:</b> GLA-domain
50	<a href="#">d2drwa1</a>	Alignment	not modelled	6.1	19	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
51	<a href="#">c5swiD</a>	Alignment	not modelled	6.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sugar hydrolase; <b>PDBTitle:</b> crystal structure of sphg92 in complex with mannose
52	<a href="#">c2qziA</a>	Alignment	not modelled	5.8	58	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a conserved protein of unknown function from2 streptococcus thermophilus lmg 18311.
53	<a href="#">c1br2C</a>	Alignment	not modelled	5.8	28	<b>PDB header:</b> muscle protein <b>Chain:</b> C: <b>PDB Molecule:</b> myosin; <b>PDBTitle:</b> smooth muscle myosin motor domain complexed with mgadp.alf4
54	<a href="#">c3lq6A</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> crystal structure of murine norovirus protruding (p)

					domain
55	<a href="#">c2ww1B_</a>	Alignment	not modelled	5.6	41 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
56	<a href="#">d1t98a2</a>	Alignment	not modelled	5.6	24 <b>Fold:</b> STAT-like <b>Superfamily:</b> MukF C-terminal domain-like <b>Family:</b> MukF C-terminal domain-like
57	<a href="#">d1a4ea_</a>	Alignment	not modelled	5.5	50 <b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
58	<a href="#">d1m5ha2</a>	Alignment	not modelled	5.5	29 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
59	<a href="#">d1qw1a1</a>	Alignment	not modelled	5.5	22 <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> FeoA-like
60	<a href="#">c5udbB_</a>	Alignment	not modelled	5.3	17 <b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
61	<a href="#">c2n8cA_</a>	Alignment	not modelled	5.1	64 <b>PDB header:</b> protein binding, de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine knot; <b>PDBTitle:</b> cystein knot with 2fp integrin avb6 cancer recognition site
62	<a href="#">c3l2tB_</a>	Alignment	not modelled	5.1	15 <b>PDB header:</b> recombination/dna <b>Chain:</b> B: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)