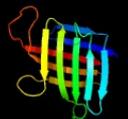
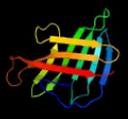
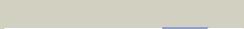
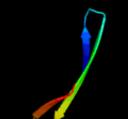


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1881c\_(lppE)\_2131914\_2132336  
 Date Fri Aug 2 13:30:49 BST 2019  
 Unique Job ID c609a97bafd39f9a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xinB_</a>	 Alignment		100.0	28	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lpqh orthologue; <b>PDBTitle:</b> x-ray crystal structure of an lpqh orthologue from mycobacterium avium
2	<a href="#">c4zjmA_</a>	 Alignment		100.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein lpqh; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis lpqh (rv3763)
3	<a href="#">d1h4ga_</a>	 Alignment		42.3	25	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
4	<a href="#">d1hixa_</a>	 Alignment		39.7	22	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
5	<a href="#">d1m4wa_</a>	 Alignment		39.6	19	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
6	<a href="#">c3uafA_</a>	 Alignment		35.9	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ttr-52; <b>PDBTitle:</b> crystal structure of a ttr-52 mutant of c. elegans
7	<a href="#">c3wp6A_</a>	 Alignment		35.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cdbfv; <b>PDBTitle:</b> the complex structure of cdbfv e109a with xylotriase
8	<a href="#">d1xnka1</a>	 Alignment		28.8	31	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
9	<a href="#">c217yA_</a>	 Alignment		27.4	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative endo-beta-n-acetylglucosaminidase; <b>PDBTitle:</b> solution structure of a putative surface protein
10	<a href="#">c4uznA_</a>	 Alignment		25.7	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-glucanase (celulase b); <b>PDBTitle:</b> the native structure of the family 46 carbohydrate-binding2 module (cbm46) of endo-beta-1,4-glucanase b (cel5b) from3 bacillus halodurans
11	<a href="#">c2vuulA_</a>	 Alignment		22.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh11 xylanase; <b>PDBTitle:</b> thermostable mutant of environmentally isolated gh112 xylanase

12	<a href="#">c1vraA_</a>	Alignment		20.3	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine biosynthesis bifunctional protein argj; <b>PDBTitle:</b> crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
13	<a href="#">d1ynaa_</a>	Alignment		19.6	25	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
14	<a href="#">c3mn8A_</a>	Alignment		19.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lp15968p; <b>PDBTitle:</b> structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
15	<a href="#">c1uwya_</a>	Alignment		17.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase m; <b>PDBTitle:</b> crystal structure of human carboxypeptidase m
16	<a href="#">c4f5cF_</a>	Alignment		15.9	16	<b>PDB header:</b> hydrolase/viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> prcv spike protein; <b>PDBTitle:</b> crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig aminopeptidase n3 ectodomain
17	<a href="#">c5vqjA_</a>	Alignment		15.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exo-beta-1,4-xylanase; <b>PDBTitle:</b> discovery of a first gh11 exo-1,4-beta-xylanase from a diverse2 microbial sugar cane bagasse composting community
18	<a href="#">c4q98A_</a>	Alignment		14.8	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> major fimbrial subunit protein; <b>PDBTitle:</b> crystal structure of a fimbriin (fima) from porphyromonas gingivalis2 w83 at 1.30 a resolution (psi community target, nakayama)
19	<a href="#">c6qt9Y_</a>	Alignment		14.2	24	<b>PDB header:</b> virus <b>Chain:</b> Y: <b>PDB Molecule:</b> orf 31; <b>PDBTitle:</b> cryo-em structure of sh1 full particle.
20	<a href="#">c2dcjA_</a>	Alignment		13.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylanase j; <b>PDBTitle:</b> a two-domain structure of alkaliphilic xynj from bacillus sp. 41m-1
21	<a href="#">c5o6vC_</a>	Alignment	not modelled	12.2	12	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
22	<a href="#">d1pvxa_</a>	Alignment	not modelled	12.0	25	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
23	<a href="#">d2dfba1</a>	Alignment	not modelled	12.0	18	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
24	<a href="#">d1te1b_</a>	Alignment	not modelled	11.1	25	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
25	<a href="#">d1uwya1</a>	Alignment	not modelled	10.9	12	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Carboxypeptidase regulatory domain-like <b>Family:</b> Carboxypeptidase regulatory domain
26	<a href="#">c4v2xA_</a>	Alignment	not modelled	10.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-glucanase (cellulase b); <b>PDBTitle:</b> high resolution structure of the full length tri-modular2 endo-beta-1,4-glucanase b (cel5b) from bacillus halodurans
27	<a href="#">d1svba2</a>	Alignment	not modelled	10.7	14	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
28	<a href="#">d1ljma_</a>	Alignment	not modelled	10.6	28	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> p53-like transcription factors <b>Family:</b> RUNT domain
29	<a href="#">c3mxB</a>	Alignment	not modelled	10.1	20	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> recq-mediated genome instability protein

29	<a href="#">c3mx1b</a>	Alignment	not modelled	10.1	20	<b>PDBTitle:</b> crystal structure of the rmi core complex
30	<a href="#">c5xxzB</a>	Alignment	not modelled	10.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> chemokine protease c; <b>PDBTitle:</b> crystal structure of a serine protease from streptococcus species
31	<a href="#">c4m03A</a>	Alignment	not modelled	9.6	15	<b>PDB header:</b> calcium binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine-rich adhesin for platelets; <b>PDBTitle:</b> c-terminal fragment(residues 576-751) of binding region of srap
32	<a href="#">c2g16A</a>	Alignment	not modelled	9.0	20	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of s65a y66s gfp variant after backbone2 fragmentation
33	<a href="#">c3ls1A</a>	Alignment	not modelled	8.5	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> sl1638 protein; <b>PDBTitle:</b> crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
34	<a href="#">d1ok8a2</a>	Alignment	not modelled	8.3	6	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
35	<a href="#">c1urzC</a>	Alignment	not modelled	8.1	13	<b>PDB header:</b> virus/viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
36	<a href="#">c2ovsB</a>	Alignment	not modelled	8.1	10	<b>PDB header:</b> gene regulation, ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> i0044; <b>PDBTitle:</b> crystal strcuture of a type three secretion system protein
37	<a href="#">d2go8a1</a>	Alignment	not modelled	7.4	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
38	<a href="#">c1p58C</a>	Alignment	not modelled	7.2	7	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> major envelope protein e; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
39	<a href="#">c4whiA</a>	Alignment	not modelled	7.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of c-terminal domain of penicillin binding protein2 rv0907
40	<a href="#">c4m02A</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> calcium binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> serine-rich adhesin for platelets; <b>PDBTitle:</b> middle fragment(residues 494-663) of the binding region of srap
41	<a href="#">d1ee6a</a>	Alignment	not modelled	6.6	17	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Pectate lyase-like
42	<a href="#">c6b6iD</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> viral protein,protease <b>Chain:</b> D: <b>PDB Molecule:</b> 3c-like protease; <b>PDBTitle:</b> 2.4a resolution structure of human norovirus gii.4 protease
43	<a href="#">c3b90A</a>	Alignment	not modelled	6.3	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-pectate lyase; <b>PDBTitle:</b> crystal structure of the catalytic domain of pectate lyase peli from2 erwinia chrysanthemi
44	<a href="#">d1cwva2</a>	Alignment	not modelled	6.2	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Invasin/intimin cell-adhesion fragments <b>Family:</b> Invasin/intimin cell-adhesion fragments
45	<a href="#">c2of6C</a>	Alignment	not modelled	6.1	10	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein e; <b>PDBTitle:</b> structure of immature west Nile virus
46	<a href="#">d1xnda</a>	Alignment	not modelled	5.7	20	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
47	<a href="#">d1wv3a1</a>	Alignment	not modelled	5.5	44	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> EssC N-terminal domain-like
48	<a href="#">d1igoa</a>	Alignment	not modelled	5.4	16	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
49	<a href="#">c5u6fA</a>	Alignment	not modelled	5.3	6	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> lpxtg-motif cell wall anchor domain protein; <b>PDBTitle:</b> bacterial adhesin from mobiluncus mulieris containing intramolecular2 disulfide, isopeptide, and ester bond cross-links (space group p21)
50	<a href="#">c1ywkE</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-deoxy-l-threo-5-hexosulose-uronate ketol- <b>PDBTitle:</b> crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
51	<a href="#">d1oa3a</a>	Alignment	not modelled	5.3	17	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
52	<a href="#">d2jeka1</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Rv1873-like <b>Superfamily:</b> Rv1873-like <b>Family:</b> Rv1873-like
53	<a href="#">c2c1fA</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional endo-1,4-beta-xylanase a; <b>PDBTitle:</b> the structure of the family 11 xylanase from neocallimastix2 patriciarum
54	<a href="#">c1as5A</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> neurotoxin <b>Chain:</b> A: <b>PDB Molecule:</b> conotoxin y-piie; <b>PDBTitle:</b> solution structure of conotoxin y-piie from conus2 purpurascens, nmr, 14 structures