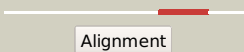

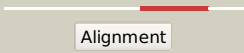

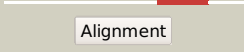





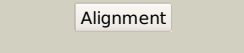

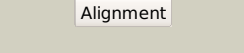



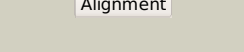

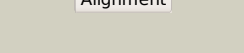

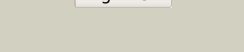






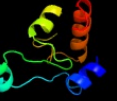





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3896c_(-)_4382121_4383029
Date	Sat Aug 10 22:05:08 BST 2019
Unique Job ID	c5c29b0d4049516a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4cfoB_</a>	 Alignment		99.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mltc; <b>PDBTitle:</b> structure of lytic transglycosylase mltc from escherichia2 coli in complex with tetrasaccharide at 2.9 a resolution.
2	<a href="#">c2y8pA_</a>	 Alignment		99.1	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-type membrane-bound lytic murein transglycosylase a; <b>PDBTitle:</b> crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
3	<a href="#">c3w6dB_</a>	 Alignment		99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lysozyme-like chitinolytic enzyme; <b>PDBTitle:</b> crystal structure of catalytic domain of chitinase from ralstonia sp.2 a-471 (e141q) in complex with tetrasaccharide
4	<a href="#">c4oz9A_</a>	 Alignment		99.1	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-bound lytic murein transglycosylase f; <b>PDBTitle:</b> crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
5	<a href="#">d1qsaa2</a>	 Alignment		99.0	16	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Bacterial muramidase, catalytic domain
6	<a href="#">c1slyA_</a>	 Alignment		99.0	19	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> 70-kda soluble lytic transglycosylase; <b>PDBTitle:</b> complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
7	<a href="#">c6cfcA_</a>	 Alignment		99.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lytic transglycosylase; <b>PDBTitle:</b> crystal structure of soluble lytic transglycosylase cj0843 of2 campylobacter jejuni in complex with bulgecin a
8	<a href="#">d1gbsa_</a>	 Alignment		99.0	14	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> G-type lysozyme
9	<a href="#">c3mgwA_</a>	 Alignment		98.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme g; <b>PDBTitle:</b> thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
10	<a href="#">c6fcqA_</a>	 Alignment		98.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble lytic murein transglycosylase; <b>PDBTitle:</b> the x-ray structure of lytic transglycosylase slt inactive mutant2 e503q from pseudomonas aeruginosa in complex with bulgecin a
11	<a href="#">c4xp8A_</a>	 Alignment		98.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> etga protein; <b>PDBTitle:</b> structure of etga d60n mutant

12	<a href="#">c3gxkB_</a>	Alignment		98.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> goose-type lysozyme 1; <b>PDBTitle:</b> the crystal structure of g-type lysozyme from atlantic cod (gadus2 morhua l.) in complex with nag oligomers sheds new light on substrate3 binding and the catalytic mechanism. native structure to 1.9
13	<a href="#">c1xsfA_</a>	Alignment		98.5	17	<b>PDB header:</b> cell cycle, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable resuscitation-promoting factor rpfb; <b>PDBTitle:</b> solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
14	<a href="#">d1xsfal</a>	Alignment		98.3	21	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> RPF-like
15	<a href="#">c4ow1A_</a>	Alignment		98.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> resuscitation-promoting factor rpfC; <b>PDBTitle:</b> crystal structure of resuscitation promoting factor c
16	<a href="#">c4hpeA_</a>	Alignment		98.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell wall hydrolase tn916-like,ctn1-orf17; <b>PDBTitle:</b> crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution
17	<a href="#">c3eo5A_</a>	Alignment		97.8	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> resuscitation-promoting factor rpfb; <b>PDBTitle:</b> crystal structure of the resuscitation promoting factor rpfb
18	<a href="#">c4fdyA_</a>	Alignment		97.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> similar to lipoprotein, nlp/p60 family; <b>PDBTitle:</b> crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
19	<a href="#">c5e27B_</a>	Alignment		97.6	23	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> resuscitation-promoting factor rpfb; <b>PDBTitle:</b> the structure of resuscitation promoting factor b from m. tuberculosis2 reveals unexpected ubiquitin-like domains
20	<a href="#">c3bkhA_</a>	Alignment		97.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lytic transglycosylase; <b>PDBTitle:</b> crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
21	<a href="#">c2fbdB_</a>	Alignment	not modelled	96.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lysozyme 1; <b>PDBTitle:</b> the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
22	<a href="#">d1iiza_</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
23	<a href="#">c3ct5A_</a>	Alignment	not modelled	96.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> morphogenesis protein 1; <b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
24	<a href="#">d1lsga1</a>	Alignment	not modelled	96.7	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
25	<a href="#">d1gd6a_</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
26	<a href="#">d1juga_</a>	Alignment	not modelled	96.5	16	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
27	<a href="#">d1ghla_</a>	Alignment	not modelled	96.4	22	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
28	<a href="#">d1hhla_</a>	Alignment	not modelled	96.2	22	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
29	<a href="#">d2nwdx1</a>	Alignment	not modelled	96.2	19	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like

						<b>Family:</b> C-type lysozyme
30	<a href="#">d2vb1a1</a>	Alignment	not modelled	96.2	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
31	<a href="#">d1jsea_</a>	Alignment	not modelled	96.2	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
32	<a href="#">d1qqya_</a>	Alignment	not modelled	96.1	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
33	<a href="#">d2eqla_</a>	Alignment	not modelled	96.0	24	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
34	<a href="#">d1lmqa_</a>	Alignment	not modelled	96.0	16	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
35	<a href="#">d1qusa_</a>	Alignment	not modelled	95.7	26	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Bacterial muramidase, catalytic domain
36	<a href="#">c2z2fA_</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme c-2; <b>PDBTitle:</b> x-ray crystal structure of bovine stomach lysozyme
37	<a href="#">d1yroa1</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
38	<a href="#">d1b9oa_</a>	Alignment	not modelled	95.4	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
39	<a href="#">d1fkqa_</a>	Alignment	not modelled	95.3	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
40	<a href="#">d1hfxa_</a>	Alignment	not modelled	95.0	19	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
41	<a href="#">d1ivma_</a>	Alignment	not modelled	94.9	19	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
42	<a href="#">c2goiC_</a>	Alignment	not modelled	94.8	24	<b>PDB header:</b> cell adhesion, sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> sperm lysozyme-like protein 1; <b>PDBTitle:</b> crystal structure of mouse sperm c-type lysozyme-like protein 1
43	<a href="#">d1f6sa_</a>	Alignment	not modelled	94.8	15	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
44	<a href="#">d1alca_</a>	Alignment	not modelled	94.6	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
45	<a href="#">c5anzA_</a>	Alignment	not modelled	94.6	20	<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.
46	<a href="#">c4anrA_</a>	Alignment	not modelled	93.7	23	<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
47	<a href="#">c3csqC_</a>	Alignment	not modelled	92.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> morphogenesis protein 1; <b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
48	<a href="#">d1hbna1</a>	Alignment	not modelled	39.6	26	<b>Fold:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Superfamily:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Family:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
49	<a href="#">c5n1qD_</a>	Alignment	not modelled	23.3	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> methyl-coenzyme m reductase iii from methanothermococcus <b>PDBTitle:</b> methyl-coenzyme m reductase iii from methanothermococcus2 thermolithotrophicus at 1.9 a resolution
50	<a href="#">c1hbuD_</a>	Alignment	not modelled	22.5	23	<b>PDB header:</b> methanogenesis <b>Chain:</b> D: <b>PDB Molecule:</b> methyl-coenzyme m reductase i alpha subunit; <b>PDBTitle:</b> methyl-coenzyme m reductase in the mcr-red1-silent state in complex2 with coenzyme m
51	<a href="#">d1e6va1</a>	Alignment	not modelled	14.9	23	<b>Fold:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Superfamily:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Family:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
52	<a href="#">c6cgvW_</a>	Alignment	not modelled	12.2	44	<b>PDB header:</b> virus <b>Chain:</b> W: <b>PDB Molecule:</b> pre-protein vi; <b>PDBTitle:</b> revised crystal structure of human adenovirus
53	<a href="#">c5l2dA_</a>	Alignment	not modelled	8.8	29	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> surface-associated protein csha; <b>PDBTitle:</b> streptococcal surface adhesin - csha nr2
54	<a href="#">d1e4ra_</a>	Alignment	not modelled	8.3	46	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
						<b>PDB header:</b> transferase

55	<a href="#">c4upuB_</a>	Alignment	not modelled	6.6	31	<b>Chain:</b> B; <b>PDB Molecule:</b> inositol-trisphosphate 3-kinase a; <b>PDBTitle:</b> crystal structure of ip3 3-k calmodulin binding region in complex2 with calmodulin
56	<a href="#">c4gaxA_</a>	Alignment	not modelled	6.5	13	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> amorpha-4,11-diene synthase; <b>PDBTitle:</b> crystal structure of an alpha-bisabolol synthase mutant
57	<a href="#">d1e6ya1</a>	Alignment	not modelled	5.7	19	<b>Fold:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Superfamily:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain <b>Family:</b> Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
58	<a href="#">c5nm7A_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidoglycan-binding domain 1; <b>PDBTitle:</b> crystal structure of burkholderia ap3 phage endolysin