



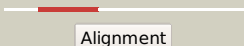

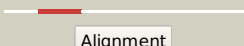

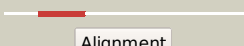

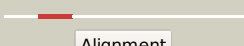
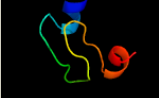
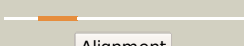









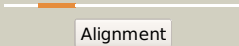




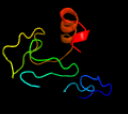
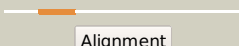

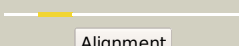
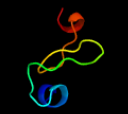
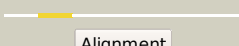

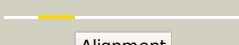


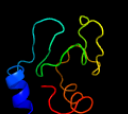



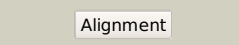

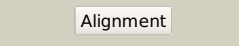






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0867c_(rpfA)_964315_965538
Date	Fri Jul 26 01:50:45 BST 2019
Unique Job ID	f5aa8999c06c7c44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1xsfA_</a>	 Alignment		100.0	48	<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
2	<a href="#">c5e27B_</a>	 Alignment		100.0	44	<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
3	<a href="#">c3eo5A_</a>	 Alignment		100.0	44	<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
4	<a href="#">d1xsfal</a>	 Alignment		100.0	56	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> RPF-like
5	<a href="#">c4ow1A_</a>	 Alignment		100.0	59	<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
6	<a href="#">c3bkhA_</a>	 Alignment		94.6	24	<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
7	<a href="#">c2fbdB_</a>	 Alignment		88.3	21	<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.
8	<a href="#">d1iiza_</a>	 Alignment		87.3	16	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
9	<a href="#">d1hfxa_</a>	 Alignment		85.4	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
10	<a href="#">d1yroal</a>	 Alignment		85.2	24	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
11	<a href="#">d1fkqa_</a>	 Alignment		84.7	23	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme

12	<a href="#">c2z2fA_</a>	 Alignment		84.6	24	<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
13	<a href="#">d1b9oa_</a>	 Alignment		84.0	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
14	<a href="#">d1f6sa_</a>	 Alignment		82.0	20	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
15	<a href="#">d1alca_</a>	 Alignment		80.9	17	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
16	<a href="#">d1qsaa2</a>	 Alignment		79.0	29	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Bacterial muramidase, catalytic domain
17	<a href="#">c3w6dB_</a>	 Alignment		78.7	21	<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
18	<a href="#">d1jsea_</a>	 Alignment		78.4	24	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
19	<a href="#">d1lsga1</a>	 Alignment		77.4	25	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
20	<a href="#">c2y8pA_</a>	 Alignment		74.0	30	<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
21	<a href="#">c4cfoB_</a>	 Alignment	not modelled	73.1	20	<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.
22	<a href="#">c3gxB_</a>	 Alignment	not modelled	70.5	21	<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
23	<a href="#">d1gbsa_</a>	 Alignment	not modelled	69.9	24	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> G-type lysozyme
24	<a href="#">c2goiC_</a>	 Alignment	not modelled	66.6	22	<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
25	<a href="#">d1qqya_</a>	 Alignment	not modelled	65.7	22	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
26	<a href="#">c4oz9A_</a>	 Alignment	not modelled	60.8	24	<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
27	<a href="#">d1gd6a_</a>	 Alignment	not modelled	60.6	22	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
28	<a href="#">d1eh9a2</a>	 Alignment	not modelled	57.3	31	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain

						Family:alpha-Amylases, C-terminal beta-sheet domain
29	<a href="#">d2vb1a1</a>	Alignment	not modelled	54.0	32	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
30	<a href="#">d1ghla_</a>	Alignment	not modelled	54.0	32	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
31	<a href="#">c3mgwA_</a>	Alignment	not modelled	52.9	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
32	<a href="#">d1lmqa_</a>	Alignment	not modelled	50.5	24	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
33	<a href="#">d1hhla_</a>	Alignment	not modelled	48.4	29	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
34	<a href="#">d1juga_</a>	Alignment	not modelled	48.2	29	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
35	<a href="#">d2eqla_</a>	Alignment	not modelled	44.7	22	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
36	<a href="#">d1ivma_</a>	Alignment	not modelled	36.4	30	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
37	<a href="#">d2nwdx1</a>	Alignment	not modelled	36.2	32	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
38	<a href="#">c4nooA_</a>	Alignment	not modelled	32.3	50	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> svrg protein; <b>PDBTitle:</b> molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
39	<a href="#">c4xp8A_</a>	Alignment	not modelled	27.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> etga protein; <b>PDBTitle:</b> structure of etga d60n mutant
40	<a href="#">c6cfcA_</a>	Alignment	not modelled	13.7	26	<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
41	<a href="#">c5bq9B_</a>	Alignment	not modelled	12.0	55	<b>PDB header:</b> unknown function, structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein lpg1496 legionella2 pneumophila subsp. pneumophila
42	<a href="#">d1kula_</a>	Alignment	not modelled	10.8	21	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain
43	<a href="#">c2jnza_</a>	Alignment	not modelled	6.9	14	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> phl p 3 allergen; <b>PDBTitle:</b> solution structure of phl p 3, a major allergen from2 timothy grass pollen
44	<a href="#">c3ct5A_</a>	Alignment	not modelled	6.6	29	<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
45	<a href="#">c6fcqA_</a>	Alignment	not modelled	6.0	23	<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
46	<a href="#">c2gyaZ_</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l32; <b>PDBTitle:</b> structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
47	<a href="#">c5j9hA_</a>	Alignment	not modelled	5.3	20	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)