

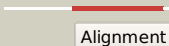
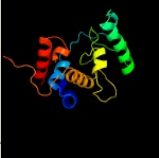
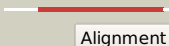


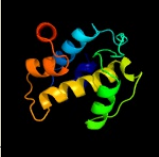







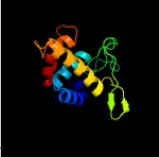





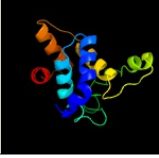


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1230c_(-)_1372968_1374203
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	b6817d2d29e4fb28

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5anzA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: soluble lytic transglycosylase b3; PDBTitle: crystal structure of sltb3 from pseudomonas aeruginosa.
2	d1qusa_	 Alignment		100.0	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
3	c4anrA_	 Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
4	d1qsaa2	 Alignment		99.1	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
5	c3gxkB_	 Alignment		99.0	19	PDB header: hydrolase Chain: B: PDB Molecule: goose-type lysozyme 1; PDBTitle: 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
6	c3w6dB_	 Alignment		99.0	21	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme-like chitinolytic enzyme; PDBTitle: crystal structure of catalytic domain of chitinase from ralstonia sp.2 a-471 (e141q) in complex with tetrasaccharide
7	c4oz9A_	 Alignment		98.9	23	PDB header: lyase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
8	d1qbsa_	 Alignment		98.9	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme
9	c4cfoB_	 Alignment		98.8	25	PDB header: hydrolase Chain: B: PDB Molecule: mltc; PDBTitle: structure of lytic transglycosylase mltc from escherichia2 coli in complex with tetrasaccharide at 2.9 a resolution.
10	c2y8pA_	 Alignment		98.7	26	PDB header: lyase Chain: A: PDB Molecule: endo-type membrane-bound lytic murein transglycosylase a; PDBTitle: crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
11	c3mgwA_	 Alignment		98.6	18	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme g; PDBTitle: thermodynamics and structure of a salmon cold-active goose-type2 lysozyme

12	c1slyA_	Alignment		97.7	27	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
13	c6fcqA_	Alignment		97.5	29	PDB header: lyase Chain: A: PDB Molecule: soluble lytic murein transglycosylase; PDBTitle: the x-ray structure of lytic transglycosylase slt inactive mutant2 e503q from pseudomonas aeruginosa in complex with bulgecin a
14	c6cfcA_	Alignment		95.3	17	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of soluble lytic transglycosylase cj0843 of2 campylobacter jejuni in complex with bulgecin a
15	c4xp8A_	Alignment		94.2	15	PDB header: hydrolase Chain: A: PDB Molecule: etga protein; PDBTitle: structure of etga d60n mutant
16	c4fdyA_	Alignment		82.0	12	PDB header: hydrolase Chain: A: PDB Molecule: similar to lipoprotein, nlp/p60 family; PDBTitle: crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
17	c4hpeA_	Alignment		73.2	20	PDB header: hydrolase Chain: A: PDB Molecule: putative cell wall hydrolase tn916-like,ctn1-orf17; PDBTitle: crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution
18	c3bkhA_	Alignment		63.2	30	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
19	c1xsfA_	Alignment		58.9	35	PDB header: cell cycle, hydrolase Chain: A: PDB Molecule: probable resuscitation-promoting factor rpfb; PDBTitle: solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
20	d1xsfal	Alignment		57.6	35	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: RPF-like
21	c5e27B_	Alignment	not modelled	57.0	35	PDB header: cell adhesion Chain: B: PDB Molecule: resuscitation-promoting factor rpfb; PDBTitle: the structure of resuscitation promoting factor b from m. tuberculosis2 reveals unexpected ubiquitin-like domains
22	c4ow1A_	Alignment	not modelled	54.6	35	PDB header: hydrolase Chain: A: PDB Molecule: resuscitation-promoting factor rpfc; PDBTitle: crystal structure of resuscitation promoting factor c
23	c3eo5A_	Alignment	not modelled	34.7	35	PDB header: cell adhesion Chain: A: PDB Molecule: resuscitation-promoting factor rpfb; PDBTitle: crystal structure of the resuscitation promoting factor rpfb
24	c4uyqB_	Alignment	not modelled	19.5	24	PDB header: cell adhesion/protein binding Chain: B: PDB Molecule: cellulosomal scaffoldin adaptor protein b; PDBTitle: high resolution structure of the third cohesin scac in complex with2 the scab dockerin with a mutation in the c-terminal helix (in to si)3 from acetivibrio cellulolyticus displaying a type i interaction.
25	c5yanB_	Alignment	not modelled	19.2	67	PDB header: structural protein Chain: B: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
26	c3p0dD_	Alignment	not modelled	17.6	25	PDB header: hydrolase Chain: D: PDB Molecule: glycoside hydrolase family 9; PDBTitle: crystal structure of a multimodular ternary protein complex from2 clostridium thermocellum
27	d1twla_	Alignment	not modelled	16.2	36	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
28	c5wrtB_	Alignment	not modelled	11.9	50	PDB header: hydrolase Chain: B: PDB Molecule: soluble inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase

						from toxoplasma2 gondii.
29	c4nl6C_	Alignment	not modelled	11.2	20	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
30	d1dvoa_	Alignment	not modelled	10.5	17	Fold: FinO-like Superfamily: FinO-like Family: FinO-like
31	c4qdnA_	Alignment	not modelled	10.2	11	PDB header: hydrolase Chain: A: PDB Molecule: flagellar protein flgJ [peptidoglycan hydrolase]; PDBTitle: crystal structure of the endo-beta-n-acetylglucosaminidase from2 thermotoga maritima
32	c3d63B_	Alignment	not modelled	9.8	55	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei
33	c3ld3A_	Alignment	not modelled	9.1	73	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution
34	c1ygzC_	Alignment	not modelled	8.9	45	PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from helicobacter2 pylori
35	c5nb9A_	Alignment	not modelled	8.6	28	PDB header: rna Chain: A: PDB Molecule: rna chaperone proq; PDBTitle: structure of the n-terminal domain of the escherichia coli proq rna2 binding protein
36	c1pdlC_	Alignment	not modelled	7.2	14	PDB header: hydrolase Chain: C: PDB Molecule: tail-associated lysozyme; PDBTitle: fitting of gp5 in the cryoem reconstruction of the bacteriophage t42 baseplate
37	d2hxja1	Alignment	not modelled	6.1	14	Fold: FinO-like Superfamily: FinO-like Family: FinO-like
38	c3emjL_	Alignment	not modelled	5.8	45	PDB header: hydrolase Chain: L: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form)
39	c5m2oB_	Alignment	not modelled	5.7	12	PDB header: protein binding Chain: B: PDB Molecule: group i dockerin; PDBTitle: r. flavefaciens' third scab cohesin in complex with a group 1 dockerin
40	c2zuxA_	Alignment	not modelled	5.5	18	PDB header: lyase Chain: A: PDB Molecule: yesw protein; PDBTitle: crystal structure of rhamnogalacturonan lyase yesw2 complexed with rhamnose
41	c3lo0A_	Alignment	not modelled	5.5	73	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
42	c5yanD_	Alignment	not modelled	5.4	60	PDB header: structural protein Chain: D: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer