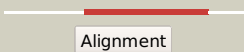

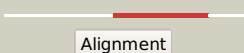
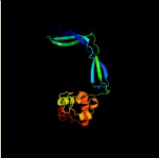




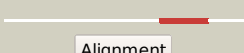


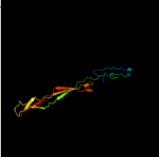
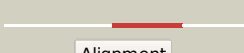
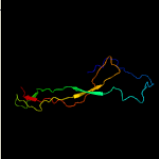

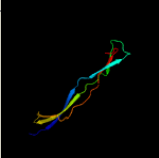

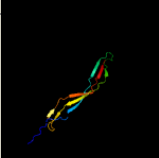

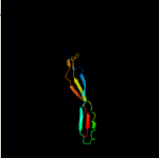




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1009_(rpfB)_1128095_1129183
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	4ed7a6a91268db8f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5e27B_	 Alignment		100.0	100	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
2	c3eo5A_	 Alignment		100.0	96	PDB header: cell adhesion Chain: A: PDB Molecule: resuscitation-promoting factor rpfb; PDBTitle: crystal structure of the resuscitation promoting factor rpfb
3	c1xsfA_	 Alignment		100.0	100	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
4	d1xsfA1	 Alignment		100.0	100	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: RPF-like
5	c4ow1A_	 Alignment		100.0	54	PDB header: hydrolase Chain: A: PDB Molecule: resuscitation-promoting factor rpfC; PDBTitle: crystal structure of resuscitation promoting factor c
6	c3tipA_	 Alignment		99.8	14	PDB header: structural protein Chain: A: PDB Molecule: surface protein g; PDBTitle: crystal structure of staphylococcus aureus sasg e-g52 module
7	c2ltjA_	 Alignment		99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: conformational analysis of strh, the surface-attached exo-beta-d-n-2 acetylglucosaminidase from streptococcus pneumoniae
8	c4fzqC_	 Alignment		99.7	14	PDB header: immune system Chain: C: PDB Molecule: uncharacterized protein conserved in bacteria; PDBTitle: crystal structure of hp0197-g5
9	c4fuoA_	 Alignment		99.6	20	PDB header: membrane protein Chain: A: PDB Molecule: accumulation associated protein; PDBTitle: structural basis for zn2+-dependent intercellular adhesion in2 staphylococcal biofilms
10	c3tiqB_	 Alignment		99.5	13	PDB header: structural protein Chain: B: PDB Molecule: surface protein g; PDBTitle: crystal structure of staphylococcus aureus sasg g51-e-g52 module
11	d1hfxa_	 Alignment		97.6	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme

12	c2fbdB_	Alignment		97.6	24	PDB header: hydrolase Chain: B; PDB Molecule: lysozyme 1; PDBTitle: the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
13	d1yroa1	Alignment		97.6	18	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
14	d1f6sa_	Alignment		97.5	15	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
15	d1fkqa_	Alignment		97.5	18	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
16	d1b9oa_	Alignment		97.5	19	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
17	c2z2fA_	Alignment		97.4	26	PDB header: hydrolase Chain: A; PDB Molecule: lysozyme c-2; PDBTitle: x-ray crystal structure of bovine stomach lysozyme
18	d1alca_	Alignment		97.3	17	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
19	d1iiza_	Alignment		97.3	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
20	d1jsea_	Alignment		97.0	18	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
21	d1hhla_	Alignment	not modelled	97.0	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
22	d1gd6a_	Alignment	not modelled	97.0	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
23	d2vb1a1	Alignment	not modelled	96.9	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
24	d1ghla_	Alignment	not modelled	96.9	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
25	d1ivma_	Alignment	not modelled	96.8	27	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
26	d1lsga1	Alignment	not modelled	96.8	18	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
27	d1qqya_	Alignment	not modelled	96.8	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
28	d2eqla_	Alignment	not modelled	96.7	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
29	d1juga_	Alignment	not modelled	96.6	23	Fold: Lysozyme-like Superfamily: Lysozyme-like

						Family: C-type lysozyme
30	d1lmqa_	Alignment	not modelled	96.5	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
31	d2nwdx1	Alignment	not modelled	96.5	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
32	c2goiC_	Alignment	not modelled	96.5	21	PDB header: cell adhesion, sugar binding protein Chain: C: PDB Molecule: sperm lysozyme-like protein 1; PDBTitle: crystal structure of mouse sperm c-type lysozyme-like protein 1
33	d1qsaa2	Alignment	not modelled	96.4	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
34	c3w6dB_	Alignment	not modelled	96.4	13	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
35	c2y8pA_	Alignment	not modelled	96.0	22	PDB header: lyase Chain: A: PDB Molecule: endo-type membrane-bound lytic murein transglycosylase a; PDBTitle: crystal structure of an outer membrane-anchored endolytic 2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
36	c3bkhA_	Alignment	not modelled	95.9	27	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
37	c4cfoB_	Alignment	not modelled	95.9	19	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.
38	d1gbsa_	Alignment	not modelled	94.1	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme
39	c4xp8A_	Alignment	not modelled	93.9	20	PDB header: hydrolase Chain: A: PDB Molecule: etga protein; PDBTitle: structure of etga d60n mutant
40	c4oz9A_	Alignment	not modelled	93.8	19	PDB header: lyase Chain: A: PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
41	c3gxkB_	Alignment	not modelled	93.4	22	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
42	c3mgwA_	Alignment	not modelled	91.1	15	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme g; PDBTitle: thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
43	c6cfcA_	Alignment	not modelled	90.4	15	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
44	d1y7ma2	Alignment	not modelled	90.1	9	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
45	c6fcqA_	Alignment	not modelled	87.1	20	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
46	c4ebzA_	Alignment	not modelled	85.6	15	PDB header: transferase Chain: A: PDB Molecule: chitin elicitor receptor kinase 1; PDBTitle: crystal structure of the ectodomain of a receptor like kinase
47	c1slyA_	Alignment	not modelled	85.2	23	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
48	c5ls2B_	Alignment	not modelled	83.1	9	PDB header: plant protein Chain: B: PDB Molecule: lysm type receptor kinase; PDBTitle: receptor mediated chitin perception in legumes is functionally2 seperable from nod factor perception
49	c5k2IA_	Alignment	not modelled	83.0	16	PDB header: hydrolase Chain: A: PDB Molecule: chitinase, lysozyme; PDBTitle: crystal structure of lysm domain from volvox carteri chitinase
50	c2mkxA_	Alignment	not modelled	82.5	13	PDB header: hydrolase Chain: A: PDB Molecule: autolysin; PDBTitle: solution structure of lysm the peptidoglycan binding domain of2 autolysin atla from enterococcus faecalis
51	d1tygb_	Alignment	not modelled	82.4	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
52	c2ki0A_	Alignment	not modelled	80.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
53	d2cu3a1	Alignment	not modelled	79.1	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
						PDB header: hydrolase

54	c3ct5A_	Alignment	not modelled	78.2	16	Chain: A: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
55	c4pxvC_	Alignment	not modelled	76.0	11	PDB header: sugar binding protein Chain: C: PDB Molecule: chitinase a; PDBTitle: crystal structure of lysm domain from pteris ryukuensis chitinase a
56	c5bumA_	Alignment	not modelled	75.5	12	PDB header: sugar binding protein Chain: A: PDB Molecule: chitinase a; PDBTitle: crystal structure of lysm domain from equisetum arvense chitinase a
57	c5jceA_	Alignment	not modelled	75.3	16	PDB header: sugar binding protein Chain: A: PDB Molecule: chitin elicitor-binding protein; PDBTitle: crystal structure of oscebip complex
58	c3I53F_	Alignment	not modelled	75.0	20	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative fumarylacetoacetate isomerase/hydrolase; PDBTitle: crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
59	c4uz2D_	Alignment	not modelled	74.8	13	PDB header: hydrolase Chain: D: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the n-terminal lysm domains from the putative2 nlpc/p60 d,l endopeptidase from t. thermophilus
60	c2I9yA_	Alignment	not modelled	74.1	13	PDB header: sugar binding protein Chain: A: PDB Molecule: cnvh-lysm lectin; PDBTitle: solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgs_03307)
61	c1tygG_	Alignment	not modelled	73.9	14	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
62	c4b9hA_	Alignment	not modelled	72.9	15	PDB header: sugar binding protein Chain: A: PDB Molecule: extracellular protein 6; PDBTitle: cladospirium fulvum lysm effector ecp6 in complex with a2 beta-1,4-linked n-acetyl-d-glucosamine tetramer: i3c heavy3 atom derivative
63	d1e0ga_	Alignment	not modelled	72.4	11	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
64	c4xcmB_	Alignment	not modelled	65.0	7	PDB header: hydrolase Chain: B: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlpc/p60 d,l endopeptidase from t.2 thermophilus
65	d1qusa_	Alignment	not modelled	64.6	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
66	d1zud2I	Alignment	not modelled	63.0	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/This Family: This
67	c3cwiA_	Alignment	not modelled	62.3	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
68	c1i7oC_	Alignment	not modelled	62.2	17	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
69	c2dfuB_	Alignment	not modelled	56.6	16	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
70	c4anrA_	Alignment	not modelled	53.2	21	PDB header: lyase Chain: A: PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
71	c4s3kA_	Alignment	not modelled	53.0	6	PDB header: hydrolase Chain: A: PDB Molecule: spore germination protein yaah; PDBTitle: crystal structure of the bacillus megaterium qm b1551 spore cortex-2 lytic enzyme slsl
72	d1sawa_	Alignment	not modelled	51.5	17	Fold: FAH Superfamily: FAH Family: FAH
73	c5Ic5G_	Alignment	not modelled	49.0	22	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
74	c2djpA_	Alignment	not modelled	47.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein sb145; PDBTitle: the solution structure of the lysm domain of human2 hypothetical protein sb145
75	d1eh9a2	Alignment	not modelled	44.5	30	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
76	c5anzA_	Alignment	not modelled	44.0	23	PDB header: hydrolase Chain: A: PDB Molecule: soluble lytic transglycosylase b3; PDBTitle: crystal structure of sltb3 from pseudomonas aeruginosa.
77	c6jvwA_	Alignment	not modelled	43.9	13	PDB header: hydrolase Chain: A: PDB Molecule: maleylypyruvate hydrolase; PDBTitle: crystal structure of maleylypyruvate hydrolase from sphingobium sp.2 syk-6 in complex with manganese (ii) ion and pyruvate
78	d3c8ya2	Alignment	not modelled	41.5	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins

79	d1nr9a_	Alignment	not modelled	41.5	16	Fold: FAH Superfamily: FAH Family: FAH
80	c1fuiB_	Alignment	not modelled	40.9	33	PDB header: isomerase Chain: B: PDB Molecule: l-fucose isomerase; PDBTitle: l-fucose isomerase from escherichia coli
81	c4s3jC_	Alignment	not modelled	40.4	16	PDB header: hydrolase Chain: C: PDB Molecule: cortical-lytic enzyme; PDBTitle: crystal structure of the bacillus cereus spore cortex-lytic enzyme2 slel
82	c4nooA_	Alignment	not modelled	40.2	46	PDB header: immune system Chain: A: PDB Molecule: vgrg protein; PDBTitle: molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
83	c5xf9F_	Alignment	not modelled	39.2	17	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
84	c3u7zA_	Alignment	not modelled	37.4	22	PDB header: metal binding protein Chain: A: PDB Molecule: putative metal binding protein rumgna_00854; PDBTitle: crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
85	c1y7mB_	Alignment	not modelled	34.5	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14040; PDBTitle: crystal structure of the b. subtilis ykud protein at 2 a2 resolution
86	c3csqC_	Alignment	not modelled	33.2	17	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
87	c5fimA_	Alignment	not modelled	32.8	5	PDB header: unknown function Chain: A: PDB Molecule: ygau; PDBTitle: the structure of kbp.k from e. coli
88	d1gtta1	Alignment	not modelled	32.2	17	Fold: FAH Superfamily: FAH Family: FAH
89	c5ldxG_	Alignment	not modelled	32.0	24	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
90	c5ldwG_	Alignment	not modelled	32.0	24	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
91	d1nkqa_	Alignment	not modelled	30.0	19	Fold: FAH Superfamily: FAH Family: FAH
92	c5lnk3_	Alignment	not modelled	29.8	22	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
93	c3qdfA_	Alignment	not modelled	29.3	21	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
94	c1wzoC_	Alignment	not modelled	29.2	19	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
95	c4maqB_	Alignment	not modelled	28.9	15	PDB header: hydrolase Chain: B: PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
96	d2fug33	Alignment	not modelled	27.3	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
97	d1gtta2	Alignment	not modelled	26.6	16	Fold: FAH Superfamily: FAH Family: FAH
98	d1sv6a_	Alignment	not modelled	25.8	11	Fold: FAH Superfamily: FAH Family: FAH
99	c3s52A_	Alignment	not modelled	25.7	15	PDB header: hydrolase Chain: A: PDB Molecule: putative fumarylacetoacetate hydrolase family protein; PDBTitle: crystal structure of a putative fumarylacetoacetate hydrolase family2 protein from yersinia pestis co92
100	c3a9rA_	Alignment	not modelled	22.7	32	PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
101	c6gcsA_	Alignment	not modelled	22.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
102	c6iydB_	Alignment	not modelled	22.0	23	PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
103	c5j9hA_	Alignment	not modelled	21.7	25	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)