Phyre^{2}

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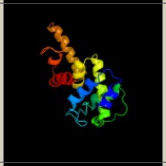
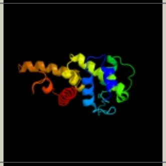
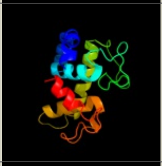
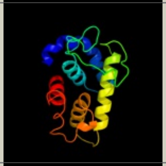
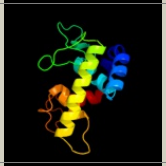
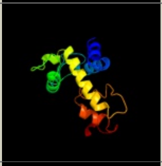
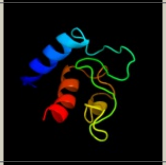
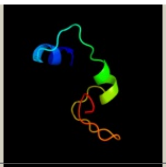
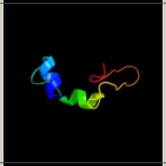
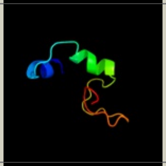
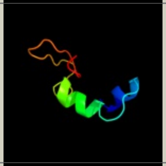
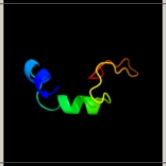
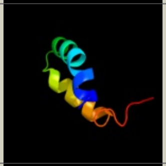
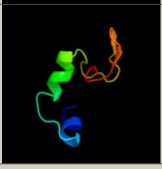
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y8pA_	Alignment		100.0	100	**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
2	c1slyA_	Alignment		100.0	22	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
3	d1qsaa2	Alignment		100.0	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
4	c3mgwA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
5	d1gbsa_	Alignment		100.0	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
6	c3gxkB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
7	d1qusa_	Alignment		99.1	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
8	c3bkhA_	Alignment		99.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
9	c1xsfA_	Alignment		97.4	21	**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
10	d1xsfa1	Alignment		97.2	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
11	c3eo5A_	Alignment		96.6	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb

12	c2fbdB_	Alignment		96.2	32	**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	d1gd6a_	Alignment		96.1	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
14	d1iiza_	Alignment		96.1	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
15	d1hhla_	Alignment		95.6	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
16	d2vb1a1	Alignment		95.6	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
17	d1ghla_	Alignment		95.5	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
18	c3fi7A_	Alignment		95.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
19	c2zycA_	Alignment		95.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
20	d1jsea_	Alignment		95.1	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
21	c3ct5A_	Alignment	not modelled	95.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
22	d1lmqa_	Alignment	not modelled	95.1	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
23	c2goiC_	Alignment	not modelled	95.0	30	**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-like2 protein 1
24	d1qqya_	Alignment	not modelled	94.9	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
25	d1juga_	Alignment	not modelled	94.8	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
26	c2z2fA_	Alignment	not modelled	94.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme c-2; **PDBTitle:** x-ray crystal structure of bovine stomach lysozyme
27	d1lsga1	Alignment	not modelled	94.5	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
28	d1ivma_	Alignment	not modelled	94.5	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
29	d2nwdx1	Alignment	not modelled	93.8	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like

						Family:C-type lysozyme
30	d1f6sa_	Alignment	not modelled	92.5	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
31	d2eqla_	Alignment	not modelled	92.5	34	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
32	d1b9oa_	Alignment	not modelled	92.3	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
33	d1yroa1	Alignment	not modelled	91.9	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
34	d1hfxa_	Alignment	not modelled	91.9	38	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
35	d1fkqa_	Alignment	not modelled	91.3	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
36	d1alca_	Alignment	not modelled	90.3	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
37	c3csqC_	Alignment	not modelled	80.4	18	**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
38	d1nvma1	Alignment	not modelled	34.0	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
39	d1idra_	Alignment	not modelled	29.8	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
40	d1yt3a2	Alignment	not modelled	21.8	4	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
41	d2coba1	Alignment	not modelled	15.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
42	c3aq8A_	Alignment	not modelled	9.2	14	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
43	c2l5qA_	Alignment	not modelled	9.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of bvu_3817 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr159
44	d2cvza1	Alignment	not modelled	8.7	22	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
45	d1dlwa_	Alignment	not modelled	8.3	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
46	c1mgtA_	Alignment	not modelled	7.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (o6-methylguanine-dna methyltransferase); **PDBTitle:** crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
47	d1a5za1	Alignment	not modelled	6.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
48	d2fnoa1	Alignment	not modelled	6.2	32	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
49	d2fp1a1	Alignment	not modelled	5.8	17	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Secreted chorismate mutase-like
50	d1bw6a_	Alignment	not modelled	5.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding