Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0C066
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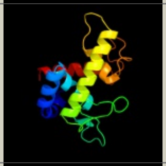
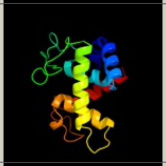
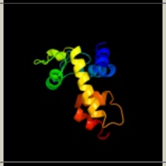
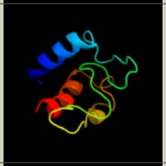
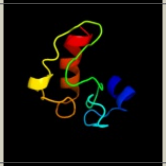
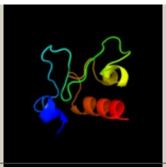
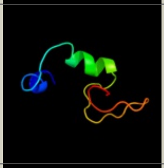
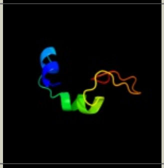
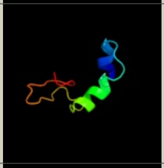
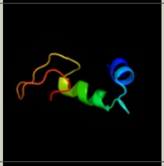
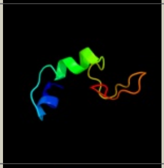
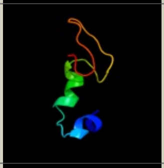
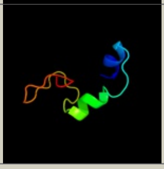
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y8pA_	Alignment		100.0	37	**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	29	**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	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
4	c3mgwA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
5	c3gxkB_	Alignment		100.0	24	**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
6	d1gbsa_	Alignment		100.0	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
7	c3bkhA_	Alignment		99.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
8	d1qusa_	Alignment		99.0	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
9	c1xsfA_	Alignment		97.3	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	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
11	c3ct5A_	Alignment		96.9	23	**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

12	c3eo5A_	Alignment		96.6	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
13	c2fbdB_	Alignment		96.5	25	**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.
14	d1gd6a_	Alignment		96.4	32	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
15	d1hhla_	Alignment		96.2	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
16	d1iiza_	Alignment		96.2	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
17	d2vb1a1	Alignment		96.2	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
18	d1ghla_	Alignment		96.1	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
19	d1jsea_	Alignment		95.8	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
20	d1lmqa_	Alignment		95.8	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
21	c3csqC_	Alignment	not modelled	95.7	21	**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
22	c2goiC_	Alignment	not modelled	95.6	25	**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
23	d1qqya_	Alignment	not modelled	95.5	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
24	c2z2fA_	Alignment	not modelled	95.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme c-2; **PDBTitle:** x-ray crystal structure of bovine stomach lysozyme
25	d1juga_	Alignment	not modelled	95.4	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
26	d1lsga1	Alignment	not modelled	95.3	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
27	c3fi7A_	Alignment	not modelled	95.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
28	d1ivma_	Alignment	not modelled	94.8	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
29	c2zycA_	Alignment	not modelled	94.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj;

		Alignment				**PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
30	d2nwdx1	Alignment	not modelled	94.5	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
31	d2eqla_	Alignment	not modelled	93.5	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
32	d1f6sa_	Alignment	not modelled	93.5	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
33	d1b9oa_	Alignment	not modelled	93.1	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
34	d1hfxa_	Alignment	not modelled	92.3	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
35	d1yroa1	Alignment	not modelled	92.3	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
36	d1fkqa_	Alignment	not modelled	92.2	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
37	d1alca_	Alignment	not modelled	91.5	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
38	d1nvma1	Alignment	not modelled	37.3	30	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
39	d3efxd1	Alignment	not modelled	22.9	15	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
40	c3lxuX_	Alignment	not modelled	18.7	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**tripeptidyl-peptidase 2; **PDBTitle:** crystal structure of tripeptidyl peptidase 2 (tpp ii)
41	d157la_	Alignment	not modelled	11.5	12	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
42	d1t8fa_	Alignment	not modelled	11.3	9	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
43	c1mgtA_	Alignment	not modelled	11.1	28	**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
44	d1jwya1	Alignment	not modelled	9.2	23	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
45	d1jtma_	Alignment	not modelled	9.0	10	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
46	d176la_	Alignment	not modelled	8.7	10	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
47	d189la_	Alignment	not modelled	8.6	10	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
48	c2dbtA_	Alignment	not modelled	8.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase c; **PDBTitle:** crystal structure of chitinase c from streptomyces griseus2 hut6037
49	d2cvza1	Alignment	not modelled	8.4	22	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
50	d2fp1a1	Alignment	not modelled	8.1	14	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Secreted chorismate mutase-like
51	c2cooA_	Alignment	not modelled	7.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
52	d1mgta1	Alignment	not modelled	6.7	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain **Family:**Methylated DNA-protein cysteine methyltransferase, C-terminal domain
53	d191la_	Alignment	not modelled	6.4	10	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
54	c1fi4A_	Alignment	not modelled	5.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
						PDB header:kinase

55	c1umwB_	Alignment	not modelled	5.8	40	**Chain:** B: **PDB Molecule:**serine/threonine-protein kinase plk; **PDBTitle:** structure of a human plk1 polo-box domain/phosphopeptide2 complex
56	c3hbhA_	Alignment	not modelled	5.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class iv chitinase chia4-pa2; **PDBTitle:** class iv chitinase structure from picea abies at 2.25a
57	c2eq9C_	Alignment	not modelled	5.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
58	d2cyua1	Alignment	not modelled	5.4	24	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
59	c2cjlA_	Alignment	not modelled	5.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted chitinase; **PDBTitle:** crystal structure and enzymatic properties of a bacterial2 family 19 chitinase reveal differences with plant enzymes
60	d1w4ha1	Alignment	not modelled	5.1	24	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex