Phyre^2

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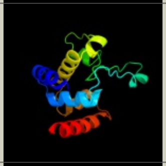
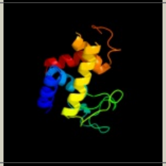
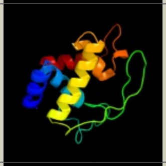
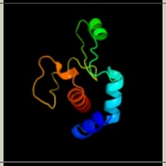
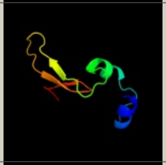
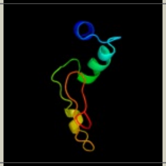
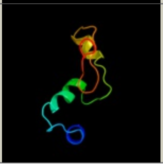
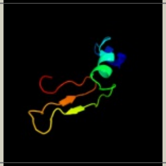
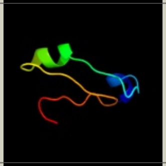
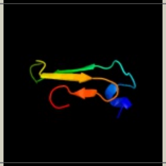
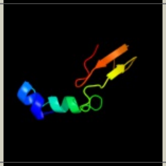
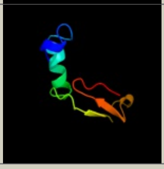
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	d1qsaa2	Alignment		100.0	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
3	c2y8pA_	Alignment		100.0	21	**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
4	c3mgwA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
5	c3gxkB_	Alignment		99.9	19	**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		99.9	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
7	c3bkhA_	Alignment		98.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
8	d1qusa_	Alignment		98.4	13	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
9	d1gd6a_	Alignment		98.0	34	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
10	d1iiza_	Alignment		97.9	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
11	c2fbdB_	Alignment		97.9	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.

12	d1hhla_	Alignment		97.7	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
13	d2vb1a1	Alignment		97.7	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
14	d1ghla_	Alignment		97.6	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
15	d1lsga1	Alignment		97.6	36	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
16	d2eqla_	Alignment		97.5	35	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
17	d1jsea_	Alignment		97.4	36	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
18	c2goiC_	Alignment		97.4	15	**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
19	d1lmqa_	Alignment		97.4	33	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
20	d1juga_	Alignment		97.3	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
21	d1qqya_	Alignment	not modelled	97.3	32	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
22	c2z2fA_	Alignment	not modelled	97.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme c-2; **PDBTitle:** x-ray crystal structure of bovine stomach lysozyme
23	d1ivma_	Alignment	not modelled	97.2	26	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
24	c3ct5A_	Alignment	not modelled	96.9	13	**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
25	d2nwdx1	Alignment	not modelled	96.9	35	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
26	d1b9oa_	Alignment	not modelled	96.7	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
27	d1fkqa_	Alignment	not modelled	96.7	45	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
28	d1f6sa_	Alignment	not modelled	96.7	41	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
29	d1yroa1	Alignment	not modelled	96.6	34	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like

						Family:C-type lysozyme
30	d1hfxa_	Alignment	not modelled	96.6	34	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
31	d1alca_	Alignment	not modelled	96.5	31	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
32	c1xsfA_	Alignment	not modelled	96.4	15	**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
33	d1xsfa1	Alignment	not modelled	95.9	15	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
34	c3fi7A_	Alignment	not modelled	94.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
35	c2zycA_	Alignment	not modelled	93.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
36	c3eo5A_	Alignment	not modelled	93.7	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
37	c2dqaA_	Alignment	not modelled	90.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of tapes japonica lysozyme
38	c3ab6A_	Alignment	not modelled	87.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of nag3 bound lysozyme from meretrix lusoria
39	c3csqC_	Alignment	not modelled	81.8	14	**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
40	c3aq8A_	Alignment	not modelled	45.4	19	**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
41	d1idra_	Alignment	not modelled	45.4	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
42	d1dlwa_	Alignment	not modelled	43.2	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
43	c1dlyA_	Alignment	not modelled	40.7	13	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
44	d1dlya_	Alignment	not modelled	40.7	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
45	c3k1tA_	Alignment	not modelled	36.4	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
46	c2bmmA_	Alignment	not modelled	28.2	8	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca; **PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca
47	d1nvma1	Alignment	not modelled	18.0	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
48	c2kscA_	Alignment	not modelled	17.6	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cyanoglobin; **PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin
49	c2xykB_	Alignment	not modelled	16.1	15	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**2-on-2 hemoglobin; **PDBTitle:** group ii 2-on-2 hemoglobin from the plant pathogen2 agrobacterium tumefaciens
50	c2k53A_	Alignment	not modelled	14.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
51	c2yusA_	Alignment	not modelled	13.7	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
52	d2coba1	Alignment	not modelled	13.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
53	d1ux8a_	Alignment	not modelled	13.3	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
54	c2k5eA_	Alignment	not modelled	13.1	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3

						structural genomics consortium (nesg) target gsr195
55	d1bw6a_	Alignment	not modelled	12.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
56	d2ahra1	Alignment	not modelled	12.6	14	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
57	d1yt3a2	Alignment	not modelled	12.1	17	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
58	d1t56a2	Alignment	not modelled	11.4	12	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
59	d1s69a_	Alignment	not modelled	10.9	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
60	d1yqga1	Alignment	not modelled	8.5	13	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
61	d2jn6a1	Alignment	not modelled	7.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
62	d1i36a1	Alignment	not modelled	7.0	13	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Conserved hypothetical protein MTH1747
63	c2rn7A_	Alignment	not modelled	6.8	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
64	c2elkA_	Alignment	not modelled	6.8	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**spcc24b10.08c protein; **PDBTitle:** solution structure of the sant domain of fission yeast2 spcc24b10.08c protein
65	d1qdva_	Alignment	not modelled	6.6	6	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
66	d1t1da_	Alignment	not modelled	6.5	10	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
67	d1hlva1	Alignment	not modelled	6.2	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
68	d2cvza1	Alignment	not modelled	6.2	7	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
69	d1riqa1	Alignment	not modelled	6.0	24	**Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
70	c1yx5A_	Alignment	not modelled	5.8	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
71	c3hbhA_	Alignment	not modelled	5.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class iv chitinase chia4-pa2; **PDBTitle:** class iv chitinase structure from picea abies at 2.25a
72	d1ynja1	Alignment	not modelled	5.7	18	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
73	d1wj9a2	Alignment	not modelled	5.3	20	**Fold:**Ferredoxin-like **Superfamily:**CRISPR-associated protein **Family:**CRISPR-associated protein
74	d1smya1	Alignment	not modelled	5.2	23	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain