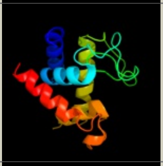
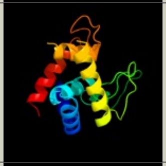
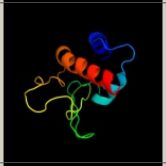
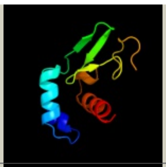
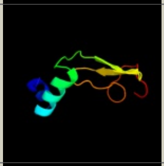
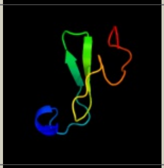
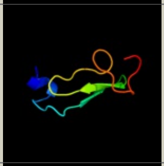
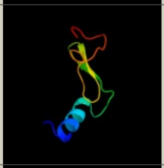
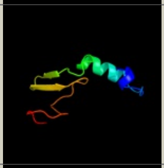
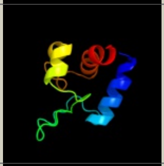
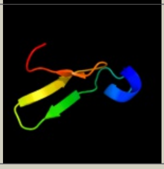
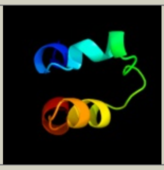
Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P47737 |
| Date | Thu Jan 5 12:04:42 GMT 2012 |
| Unique Job ID | af17990781f5bf73 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1slyA_ | Alignment |  | 100.0 | 22 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase;<br>**PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a |
| 2 | c2y8pA_ | Alignment |  | 100.0 | 24 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a;<br>**PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli |
| 3 | d1qsaa2 | Alignment |  | 100.0 | 23 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Bacterial muramidase, catalytic domain |
| 4 | c3mgwA_ | Alignment |  | 100.0 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lysozyme g;<br>**PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme |
| 5 | d1gbsa_ | Alignment |  | 100.0 | 24 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**G-type lysozyme |
| 6 | c3gxkB_ | Alignment |  | 99.9 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**goose-type lysozyme 1;<br>**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 | c3bkhA_ | Alignment |  | 98.8 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lytic transglycosylase;<br>**PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 |
| 8 | d1qusa_ | Alignment |  | 98.7 | 22 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Bacterial muramidase, catalytic domain |
| 9 | d1gd6a_ | Alignment |  | 98.4 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 10 | d1iiza_ | Alignment |  | 98.2 | 20 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 11 | c2fbdB_ | Alignment |  | 98.2 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**lysozyme 1;<br>**PDBTitle:** the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang. |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | d1hhla_ | Alignment |  | 97.9 | 16 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 13 | d2vb1a1 | Alignment |  | 97.8 | 17 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 14 | d1lsga1 | Alignment |  | 97.8 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 15 | d1jsea_ | Alignment |  | 97.7 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 16 | d1ghla_ | Alignment |  | 97.7 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 17 | d1lmqa_ | Alignment |  | 97.6 | 20 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 18 | c2goiC_ | Alignment |  | 97.6 | 14 | **PDB header:**cell adhesion, sugar binding protein<br>**Chain:** C: **PDB Molecule:**sperm lysozyme-like protein 1;<br>**PDBTitle:** crystal structure of mouse sperm c-type lysozyme-like2 protein 1 |
| 19 | c1xsfA_ | Alignment |  | 97.5 | 18 | **PDB header:**cell cycle, hydrolase<br>**Chain:** A: **PDB Molecule:**probable resuscitation-promoting factor rpfb;<br>**PDBTitle:** solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis |
| 20 | d2eqla_ | Alignment |  | 97.4 | 24 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 21 | d1juga_ | Alignment | not modelled | 97.4 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 22 | c2z2fA_ | Alignment | not modelled | 97.3 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lysozyme c-2;<br>**PDBTitle:** x-ray crystal structure of bovine stomach lysozyme |
| 23 | d1qqya_ | Alignment | not modelled | 97.2 | 17 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 24 | d1b9oa_ | Alignment | not modelled | 97.2 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 25 | d1xsfa1 | Alignment | not modelled | 97.2 | 18 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**RPF-like |
| 26 | d1fkqa_ | Alignment | not modelled | 97.0 | 20 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 27 | d2nwdx1 | Alignment | not modelled | 97.0 | 19 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 28 | d1yroa1 | Alignment | not modelled | 97.0 | 23 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 29 | d1f6sa_ | Alignment | not modelled | 96.9 | 25 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  |  |  |  | **Family:**C-type lysozyme |
| 30 | d1ivma_ | Alignment | not modelled | 96.9 | 24 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 31 | d1alca_ | Alignment | not modelled | 96.8 | 21 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 32 | d1hfxa_ | Alignment | not modelled | 96.8 | 26 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**C-type lysozyme |
| 33 | c3eo5A_ | Alignment | not modelled | 96.5 | 17 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb;<br>**PDBTitle:** crystal structure of the resuscitation promoting factor rpfb |
| 34 | c3fi7A_ | Alignment | not modelled | 95.6 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lmo1076 protein;<br>**PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain |
| 35 | c3ct5A_ | Alignment | not modelled | 95.3 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**morphogenesis protein 1;<br>**PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail |
| 36 | c2zycA_ | Alignment | not modelled | 94.6 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj;<br>**PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1 |
| 37 | c3ab6A_ | Alignment | not modelled | 91.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lysozyme;<br>**PDBTitle:** crystal structure of nag3 bound lysozyme from meretrix lusoria |
| 38 | c2dqaA_ | Alignment | not modelled | 88.5 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lysozyme;<br>**PDBTitle:** crystal structure of tapes japonica lysozyme |
| 39 | c3csqC_ | Alignment | not modelled | 88.0 | 18 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**morphogenesis protein 1;<br>**PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail |
| 40 | c2k5eA_ | Alignment |  | 52.9 | 5 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195 |
| 41 | d1idra_ | Alignment | not modelled | 49.1 | 8 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Truncated hemoglobin |
| 42 | c3aq8A_ | Alignment | not modelled | 48.6 | 5 | **PDB header:**oxygen binding<br>**Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin;<br>**PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form |
| 43 | c3k1tA_ | Alignment | not modelled | 48.1 | 26 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha;<br>**PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution |
| 44 | d1dlwa_ | Alignment | not modelled | 46.4 | 8 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Truncated hemoglobin |
| 45 | d1nvma1 | Alignment | not modelled | 44.1 | 13 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**post-HMGL domain-like<br>**Family:**DmpG/LeuA communication domain-like |
| 46 | c2k53A_ | Alignment | not modelled | 43.5 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**a3dk08 protein;<br>**PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9 |
| 47 | c2bmmA_ | Alignment | not modelled | 41.7 | 10 | **PDB header:**oxygen storage/transport<br>**Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca;<br>**PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca |
| 48 | c1dlyA_ | Alignment | not modelled | 38.0 | 5 | **PDB header:**oxygen storage/transport<br>**Chain:** A: **PDB Molecule:**hemoglobin;<br>**PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos |
| 49 | d1dlya_ | Alignment | not modelled | 38.0 | 5 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Truncated hemoglobin |
| 50 | d1xqoa_ | Alignment | not modelled | 24.6 | 19 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**AgoG-like |
| 51 | c2kscA_ | Alignment | not modelled | 19.6 | 10 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**cyanoglobin;<br>**PDBTitle:** solution structure of synechococcus sp. pcc 7002 hemoglobin |
| 52 | d2coba1 | Alignment | not modelled | 19.4 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Psq domain |
| 53 | d1xg7a_ | Alignment | not modelled | 19.2 | 15 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**AgoG-like |
| 54 | d1bw6a_ | Alignment | not modelled | 18.8 | 25 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | **Family:**Centromere-binding |
| 55 | d1s69a_ | Alignment | not modelled | 14.1 | 7 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Truncated hemoglobin |
| 56 | c2xykB_ | Alignment | not modelled | 14.0 | 21 | **PDB header:**oxygen storage/transport<br>**Chain:** B: **PDB Molecule:**2-on-2 hemoglobin;<br>**PDBTitle:** group ii 2-on-2 hemoglobin from the plant pathogen2 agrobacterium tumefaciens |
| 57 | d1sdia_ | Alignment | not modelled | 13.7 | 13 | **Fold:**YcfC-like<br>**Superfamily:**YcfC-like<br>**Family:**YcfC-like |
| 58 | c2yusA_ | Alignment | not modelled | 13.6 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin-<br>**PDBTitle:** solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1 |
| 59 | d1ux8a_ | Alignment | not modelled | 13.3 | 7 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Truncated hemoglobin |
| 60 | d1i3ja_ | Alignment | not modelled | 9.7 | 32 | **Fold:**DNA-binding domain of intron-encoded endonucleases<br>**Superfamily:**DNA-binding domain of intron-encoded endonucleases<br>**Family:**DNA-binding domain of intron-encoded endonucleases |
| 61 | d2jn6a1 | Alignment | not modelled | 9.7 | 19 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Cgl2762-like |
| 62 | d1yt3a2 | Alignment | not modelled | 9.5 | 18 | **Fold:**SAM domain-like<br>**Superfamily:**HRDC-like<br>**Family:**RNase D C-terminal domains |
| 63 | d1r2aa_ | Alignment | not modelled | 9.4 | 17 | **Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit<br>**Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit<br>**Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit |
| 64 | d1vpda1 | Alignment | not modelled | 9.0 | 19 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain |
| 65 | c2gloA_ | Alignment | not modelled | 7.6 | 21 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**brinker cg9653-pa;<br>**PDBTitle:** solution structure of the brinker dna binding domain in2 complex with the omb enhancer |
| 66 | d1qdva_ | Alignment | not modelled | 7.3 | 21 | **Fold:**POZ domain<br>**Superfamily:**POZ domain<br>**Family:**Tetramerization domain of potassium channels |
| 67 | c1yx5A_ | Alignment | not modelled | 7.2 | 42 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4;<br>**PDBTitle:** solution structure of s5a uim-1/ubiquitin complex |
| 68 | c2z39A_ | Alignment | not modelled | 7.2 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**chitinase;<br>**PDBTitle:** crystal structure of brassica juncea chitinase catalytic2 module glu234ala mutant (bjchi3-e234a) |
| 69 | c2rn7A_ | Alignment | not modelled | 7.1 | 18 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**is629 orfa;<br>**PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125 |
| 70 | d2cvza1 | Alignment | not modelled | 7.1 | 5 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain |
| 71 | d3cuma1 | Alignment | not modelled | 7.0 | 9 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain |
| 72 | c1hlvA_ | Alignment | not modelled | 6.6 | 23 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**major centromere autoantigen b;<br>**PDBTitle:** crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna |
| 73 | d1vkeb_ | Alignment | not modelled | 6.3 | 2 | **Fold:**AhpD-like<br>**Superfamily:**AhpD-like<br>**Family:**CMD-like |
| 74 | d1t1da_ | Alignment | not modelled | 6.1 | 17 | **Fold:**POZ domain<br>**Superfamily:**POZ domain<br>**Family:**Tetramerization domain of potassium channels |
| 75 | c2elhA_ | Alignment | not modelled | 5.6 | 25 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**cg11849-pa;<br>**PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa |
| 76 | d1riqa1 | Alignment | not modelled | 5.4 | 27 | **Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)<br>**Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)<br>**Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) |
| 77 | d1i36a1 | Alignment | not modelled | 5.1 | 18 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Conserved hypothetical protein MTH1747 |