Phyre2

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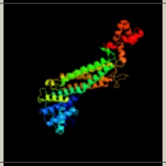
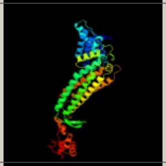
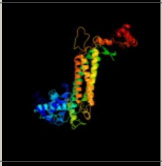
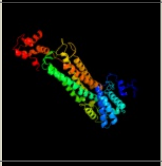
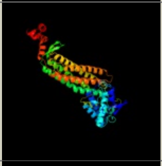
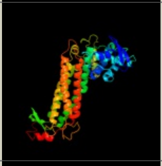
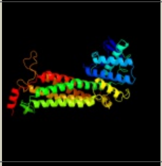
| Email | l.a.kelley@imperial.ac.uk |
| Description | P05042 |
| Date | Thu Jan 5 10:58:37 GMT 2012 |
| Unique Job ID | e72b0832986c4c85 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1j3ua_ | Alignment |  | 100.0 | 41 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 2 | d1vdka_ | Alignment |  | 100.0 | 58 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 3 | c1yfmA_ | Alignment |  | 100.0 | 59 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**fumarase;<br>**PDBTitle:** recombinant yeast fumarase |
| 4 | d1yfma_ | Alignment |  | 100.0 | 59 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 5 | d1fuoa_ | Alignment |  | 100.0 | 100 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 6 | d1jswa_ | Alignment |  | 100.0 | 40 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 7 | c3no9C_ | Alignment |  | 100.0 | 48 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**fumarate hydratase class ii;<br>**PDBTitle:** crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis |
| 8 | c3ocfB_ | Alignment |  | 100.0 | 45 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**fumarate lyase:delta crystallin;<br>**PDBTitle:** crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form |
| 9 | c3e04C_ | Alignment |  | 100.0 | 59 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**fumarate hydratase;<br>**PDBTitle:** crystal structure of human fumarate hydratase |
| 10 | c3gtdB_ | Alignment |  | 100.0 | 56 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**fumarate hydratase class ii;<br>**PDBTitle:** 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii |
| 11 | d1jswc_ | Alignment |  | 100.0 | 41 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |

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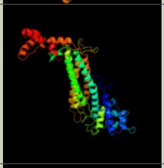
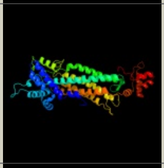
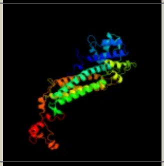
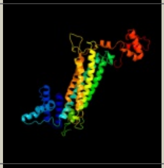
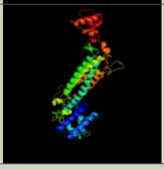
|---|---|---|---|---|---|---|
| 12 | c3r6yG_ | Alignment |  | 100.0 | 41 | **PDB header:**lyase<br>**Chain:** G: **PDB Molecule:**aspartase;<br>**PDBTitle:** crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1 |
| 13 | c2pfmA_ | Alignment |  | 100.0 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**adenylosuccinate lyase;<br>**PDBTitle:** crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis |
| 14 | d1tj7a_ | Alignment |  | 100.0 | 20 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 15 | d1re5a_ | Alignment |  | 100.0 | 24 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 16 | d1q5na_ | Alignment |  | 100.0 | 22 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 17 | c2e9fC_ | Alignment |  | 100.0 | 24 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**argininosuccinate lyase;<br>**PDBTitle:** crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine |
| 18 | d1c3ca_ | Alignment |  | 100.0 | 20 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 19 | d1i0aa_ | Alignment |  | 100.0 | 21 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 20 | d1tjva_ | Alignment |  | 100.0 | 21 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 21 | d1hy0a_ | Alignment | not modelled | 100.0 | 20 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 22 | d1k62a_ | Alignment | not modelled | 100.0 | 20 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 23 | c3c8tA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**fumarate lyase;<br>**PDBTitle:** crystal structure of fumarate lyase from mesorhizobium sp. bnc1 |
| 24 | c3bhgA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**adenylosuccinate lyase;<br>**PDBTitle:** crystal structure of adenylosuccinate lyase from legionella2 pneumophila |
| 25 | c2vd6B_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**adenylosuccinate lyase;<br>**PDBTitle:** human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate. |
| 26 | c2qgaC_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**adenylosuccinate lyase;<br>**PDBTitle:** plasmodium vivax adenylosuccinate lyase pv003765 with amp bound |
| 27 | c2ptsA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**adenylosuccinate lyase;<br>**PDBTitle:** crystal structure of wild type escherichia coli adenylosuccinate lyase |
| 28 | d1dofa_ | Alignment | not modelled | 100.0 | 21 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |

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| 29 | c1yisA_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**adenylosuccinate lyase;<br>**PDBTitle:** structural genomics of caenorhabditis elegans: adenylosuccinate lyase |
| 30 | c2fenA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**3-carboxy-cis,cis-muconate lactonizing enzyme;<br>**PDBTitle:** 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2 |
| 31 | d1f1oa_ | Alignment | not modelled | 100.0 | 19 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**L-aspartase/fumarase |
| 32 | d1gkma_ | Alignment | not modelled | 52.1 | 19 | **Fold:**L-aspartase-like<br>**Superfamily:**L-aspartase-like<br>**Family:**HAL/PAL-like |
| 33 | c3exmA_ | Alignment | not modelled | 27.1 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphatase sc4828;<br>**PDBTitle:** crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp |
| 34 | c2xgvA_ | Alignment | not modelled | 25.7 | 27 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**psiv capsid n-terminal domain;<br>**PDBTitle:** structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik) |
| 35 | d1lbua1 | Alignment | not modelled | 25.1 | 21 | **Fold:**PGBD-like<br>**Superfamily:**PGBD-like<br>**Family:**Peptidoglycan binding domain, PGBD |
| 36 | d1h8ba_ | Alignment | not modelled | 22.2 | 21 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**EF-hand modules in multidomain proteins |
| 37 | d2ce7a1 | Alignment | not modelled | 20.5 | 21 | **Fold:**FtsH protease domain-like<br>**Superfamily:**FtsH protease domain-like<br>**Family:**FtsH protease domain-like |
| 38 | d1e8ga1 | Alignment | not modelled | 19.8 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**FAD-linked oxidases, C-terminal domain<br>**Family:**Vanillyl-alcohol oxidase-like |
| 39 | c2ctoA_ | Alignment | not modelled | 19.8 | 42 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**novel protein;<br>**PDBTitle:** solution structure of the hmg box like domain from human2 hypothetical protein flj14904 |
| 40 | d1wvfa1 | Alignment | not modelled | 19.3 | 16 | **Fold:**Ferredoxin-like<br>**Superfamily:**FAD-linked oxidases, C-terminal domain<br>**Family:**Vanillyl-alcohol oxidase-like |
| 41 | c2di4B_ | Alignment | not modelled | 19.1 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cell division protein ftsh homolog;<br>**PDBTitle:** crystal structure of the ftsh protease domain |
| 42 | d2di4a1 | Alignment | not modelled | 18.5 | 16 | **Fold:**FtsH protease domain-like<br>**Superfamily:**FtsH protease domain-like<br>**Family:**FtsH protease domain-like |
| 43 | c3bkhA_ | Alignment | not modelled | 16.2 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lytic transglycosylase;<br>**PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 |
| 44 | c3lq9B_ | Alignment | not modelled | 15.7 | 21 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**dna-damage-inducible transcript 4 protein;<br>**PDBTitle:** crystal strucure of human redd1, a hypoxia-induced regulator2 of mtor |
| 45 | c3bbnC_ | Alignment | not modelled | 14.3 | 40 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**ribosomal protein s3;<br>**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. |
| 46 | c2zttA_ | Alignment | not modelled | 12.8 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rna-directed rna polymerase catalytic subunit;<br>**PDBTitle:** crystal structure of rna polymerase pb1-pb2 subunits from2 influenza a virus |
| 47 | d3e9va1 | Alignment | not modelled | 12.7 | 22 | **Fold:**BTG domain-like<br>**Superfamily:**BTG domain-like<br>**Family:**BTG domain-like |
| 48 | c3fbtB_ | Alignment | not modelled | 11.6 | 20 | **PDB header:**oxidoreductase, lyase<br>**Chain:** B: **PDB Molecule:**chorismate mutase and shikimate 5-dehydrogenase<br>**PDBTitle:** crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum |
| 49 | c2ev9B_ | Alignment | not modelled | 11.5 | 29 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase;<br>**PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate |
| 50 | c1byvA_ | Alignment | not modelled | 10.7 | 30 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**protein (calcitonin);<br>**PDBTitle:** glycosylated eel calcitonin |
| 51 | d1nvta2 | Alignment | not modelled | 10.7 | 13 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Shikimate dehydrogenase-like |
| 52 | d1npya2 | Alignment | not modelled | 10.5 | 50 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Shikimate dehydrogenase-like |
| 53 | d1n7ka_ | Alignment | not modelled | 9.8 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 54 | c1htrP_ | Alignment | not modelled | 9.2 | 14 | **PDB header:**aspartyl protease<br>**Chain:** P: **PDB Molecule:**progastricsin (pro segment); |

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| 54 | [illegible] | Alignment | not modelled | 9.2 | 14 | **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution |
| 55 | d1vi2a2 | Alignment | not modelled | 9.2 | 14 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Shikimate dehydrogenase-like |
| 56 | c1lbuA_ | Alignment | not modelled | 8.8 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase;<br>**PDBTitle:** hydrolase metallo (zn) dd-peptidase |
| 57 | d2z15a1 | Alignment | not modelled | 8.4 | 13 | **Fold:**BTG domain-like<br>**Superfamily:**BTG domain-like<br>**Family:**BTG domain-like |
| 58 | c1wjvA_ | Alignment | not modelled | 8.4 | 44 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**cell growth regulating nucleolar protein lyar;<br>**PDBTitle:** solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar |
| 59 | d1wjfa_ | Alignment | not modelled | 8.3 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**N-terminal Zn binding domain of HIV integrase<br>**Family:**N-terminal Zn binding domain of HIV integrase |
| 60 | c3m1eA_ | Alignment | not modelled | 8.2 | 9 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm;<br>**PDBTitle:** crystal structure of benm_dbd |
| 61 | d1k6ya1 | Alignment | not modelled | 8.1 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**N-terminal Zn binding domain of HIV integrase<br>**Family:**N-terminal Zn binding domain of HIV integrase |
| 62 | c1nvtA_ | Alignment | not modelled | 8.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**shikimate 5'-dehydrogenase;<br>**PDBTitle:** crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+ |
| 63 | c3no7A_ | Alignment | not modelled | 7.9 | 19 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**putative plasmid related protein;<br>**PDBTitle:** crystal structure of the centromere-binding protein parb from plasmid2 pcxc100 |
| 64 | d1e0ea_ | Alignment | not modelled | 7.8 | 13 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**N-terminal Zn binding domain of HIV integrase<br>**Family:**N-terminal Zn binding domain of HIV integrase |
| 65 | c1yrlD_ | Alignment | not modelled | 7.8 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**ketol-acid reductoisomerase;<br>**PDBTitle:** escherichia coli ketol-acid reductoisomerase |
| 66 | d1rxqa_ | Alignment | not modelled | 7.5 | 16 | **Fold:**DinB/YfiT-like putative metalloenzymes<br>**Superfamily:**DinB/YfiT-like putative metalloenzymes<br>**Family:**YfiT-like putative metal-dependent hydrolases |
| 67 | d2qalc1 | Alignment | not modelled | 7.1 | 38 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Prokaryotic type KH domain (KH-domain type II)<br>**Family:**Prokaryotic type KH domain (KH-domain type II) |
| 68 | d1p77a2 | Alignment | not modelled | 7.1 | 14 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Shikimate dehydrogenase-like |
| 69 | c3pwzA_ | Alignment | not modelled | 6.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3;<br>**PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida |
| 70 | d2b0ja1 | Alignment | not modelled | 6.8 | 21 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**HMD dimerization domain-like |
| 71 | c2dxbR_ | Alignment | not modelled | 6.7 | 15 | **PDB header:**hydrolase<br>**Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma;<br>**PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers |
| 72 | c3u62A_ | Alignment | not modelled | 6.7 | 29 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**shikimate dehydrogenase;<br>**PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima |
| 73 | d2d28c1 | Alignment | not modelled | 6.6 | 28 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**EspE N-terminal domain-like<br>**Family:**GSPII protein E N-terminal domain-like |
| 74 | d1nyta2 | Alignment | not modelled | 6.6 | 14 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Shikimate dehydrogenase-like |
| 75 | c3pmoA_ | Alignment | not modelled | 6.6 | 9 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase;<br>**PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution |
| 76 | c2nloA_ | Alignment | not modelled | 6.4 | 29 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**shikimate dehydrogenase;<br>**PDBTitle:** crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum |
| 77 | c1p74B_ | Alignment | not modelled | 6.4 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase;<br>**PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae |
| 78 | d1u5ta1 | Alignment | not modelled | 6.3 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Vacuolar sorting protein domain |
| 79 | c2w6aB_ | Alignment | not modelled | 6.3 | 17 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1;<br>**PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain |
| 80 | c3tozA_ | Alignment | not modelled | 6.3 | 27 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**shikimate dehydrogenase;<br>**PDBTitle:** 2.2 angstrom crystal structure of shikimate 5- |

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|  |  |  |  |  |  | dehydrogenase from2 listeria monocytogenes in complex with nad. |
| 81 | c2eggA_ | Alignment | not modelled | 6.3 | 29 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase;<br>**PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus |
| 82 | d2dy1a3 | Alignment | not modelled | 6.3 | 22 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 83 | c1ahuB_ | Alignment | not modelled | 6.1 | 21 | **PDB header:**flavoenzyme<br>**Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase;<br>**PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol |
| 84 | c2dinA_ | Alignment | not modelled | 6.1 | 40 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**cell division cycle 5-like protein;<br>**PDBTitle:** solution structure of the myb_dna-binding domain of human2 cell division cycle 5-like protein |
| 85 | d2uubc1 | Alignment | not modelled | 6.1 | 33 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Prokaryotic type KH domain (KH-domain type II)<br>**Family:**Prokaryotic type KH domain (KH-domain type II) |
| 86 | c2hk8B_ | Alignment | not modelled | 6.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**shikimate dehydrogenase;<br>**PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution |
| 87 | d1ugpa_ | Alignment | not modelled | 6.0 | 38 | **Fold:**Nitrile hydratase alpha chain<br>**Superfamily:**Nitrile hydratase alpha chain<br>**Family:**Nitrile hydratase alpha chain |
| 88 | d1g3pa2 | Alignment | not modelled | 6.0 | 20 | **Fold:**N-terminal domains of the minor coat protein g3p<br>**Superfamily:**N-terminal domains of the minor coat protein g3p<br>**Family:**N-terminal domains of the minor coat protein g3p |
| 89 | c3pgjB_ | Alignment | not modelled | 5.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**shikimate dehydrogenase;<br>**PDBTitle:** 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate |
| 90 | d2nr7a1 | Alignment | not modelled | 5.9 | 23 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**NMB1012-like |
| 91 | c2hinA_ | Alignment | not modelled | 5.8 | 25 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**repressor protein;<br>**PDBTitle:** structure of n15 cro at 1.05 a: an ortholog of lambda cro2 with a completely different but equally effective3 dimerization mechanism |
| 92 | d2bv3a3 | Alignment | not modelled | 5.7 | 25 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 93 | c3iymA_ | Alignment | not modelled | 5.7 | 13 | **PDB header:**virus<br>**Chain:** A: **PDB Molecule:**capsid protein;<br>**PDBTitle:** backbone trace of the capsid protein dimer of a fungal partitivirus2 from electron cryomicroscopy and homology modeling |
| 94 | c2fgyA_ | Alignment | not modelled | 5.6 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carboxysome shell polypeptide;<br>**PDBTitle:** beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca) |
| 95 | c2zmeA_ | Alignment | not modelled | 5.6 | 17 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8;<br>**PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex |
| 96 | c1x5bA_ | Alignment | not modelled | 5.5 | 56 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2;<br>**PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2 |
| 97 | c1npyA_ | Alignment | not modelled | 5.5 | 43 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like<br>**PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607 |
| 98 | c2kheA_ | Alignment | not modelled | 5.4 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**toxin-like protein;<br>**PDBTitle:** solution structure of the bacterial toxin rele from thermus2 thermophilus hb8 |
| 99 | c3hzsA_ | Alignment | not modelled | 5.3 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**monofunctional glycosyltransferase;<br>**PDBTitle:** s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin |