# Phyre$^2$

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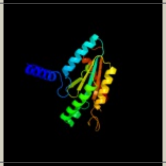
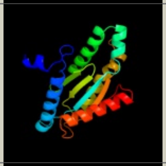
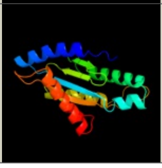
| Description | P0AAP1 |
| Date | Thu Jan 5 11:13:24 GMT 2012 |
| Unique Job ID | 992dd48c0956d666 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1w25B_ | Alignment |  | 100.0 | 28 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein;<br>**PDBTitle:** response regulator pled in complex with c-digmp |
| 2 | c3ezuA_ | Alignment |  | 100.0 | 27 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**ggdef domain protein;<br>**PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution |
| 3 | c3breA_ | Alignment |  | 100.0 | 35 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**probable two-component response regulator;<br>**PDBTitle:** crystal structure of p.aeruginosa pa3702 |
| 4 | c3i5cA_ | Alignment |  | 100.0 | 35 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response<br>**PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa |
| 5 | c3ignA_ | Alignment |  | 100.0 | 38 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diguanylate cyclase;<br>**PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a |
| 6 | c3i5aA_ | Alignment |  | 100.0 | 32 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein;<br>**PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae |
| 7 | c3hvaA_ | Alignment |  | 100.0 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein fimx;<br>**PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa |
| 8 | c3i5bA_ | Alignment |  | 100.0 | 35 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**wspr response regulator;<br>**PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa |
| 9 | c3iclA_ | Alignment |  | 100.0 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**eal/ggdef domain protein;<br>**PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c |
| 10 | c3qyyB_ | Alignment |  | 100.0 | 32 | **PDB header:**signaling protein/inhibitor<br>**Chain:** B: **PDB Molecule:**response regulator;<br>**PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5 )-cyclic di-gmp |
| 11 | d1w25a3 | Alignment |  | 100.0 | 33 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**GGDEF domain |

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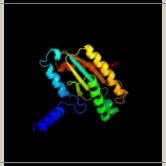
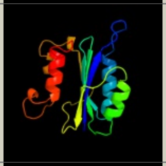
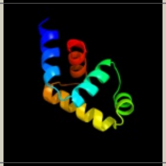
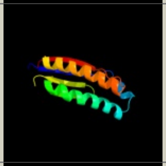
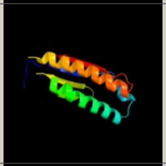
| 12 | c3mtkA_ | Alignment |  | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase;<br>**PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c |
| 13 | c3pjwA_ | Alignment |  | 99.9 | 25 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein;<br>**PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23 |
| 14 | c3hvwA_ | Alignment |  | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc);<br>**PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c |
| 15 | c3gfzB_ | Alignment |  | 99.4 | 14 | **PDB header:**hydrolase, signaling protein<br>**Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1;<br>**PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex |
| 16 | c3p7nB_ | Alignment |  | 98.2 | 8 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**sensor histidine kinase;<br>**PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis |
| 17 | c2qv6D_ | Alignment |  | 96.0 | 18 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii;<br>**PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions |
| 18 | c1cjkA_ | Alignment |  | 95.0 | 13 | **PDB header:**lyase/lyase/signaling protein<br>**Chain:** A: **PDB Molecule:**adenylate cyclase, type v;<br>**PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn |
| 19 | d1azsa_ | Alignment |  | 94.8 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**Adenylyl and guanylyl cyclase catalytic domain |
| 20 | c3mr7B_ | Alignment |  | 94.7 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold<br>**PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi |
| 21 | d1wc1a_ | Alignment | not modelled | 94.0 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**Adenylyl and guanylyl cyclase catalytic domain |
| 22 | c2w01C_ | Alignment | not modelled | 93.9 | 14 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**adenylate cyclase;<br>**PDBTitle:** crystal structure of the guanylyl cyclase cya2 |
| 23 | c1y10C_ | Alignment | not modelled | 92.5 | 13 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302;<br>**PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state |
| 24 | c1wc6B_ | Alignment | not modelled | 91.0 | 19 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**adenylate cyclase;<br>**PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate |
| 25 | c3uvjC_ | Alignment | not modelled | 90.9 | 19 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3;<br>**PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1. |
| 26 | d1fx2a_ | Alignment | not modelled | 90.4 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**Adenylyl and guanylyl cyclase catalytic domain |
| 27 | c1ybuA_ | Alignment | not modelled | 89.7 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lipj;<br>**PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog. |
| 28 | c2wz1B_ | Alignment | not modelled | 89.5 | 9 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1;<br>**PDBTitle:** structure of the catalytic domain of human soluble2 |

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|  |  |  |  |  |  | guanylate cyclase 1 beta 3. |
| 29 | d1fx4a_ | Alignment | not modelled | 89.0 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**Adenylyl and guanylyl cyclase catalytic domain |
| 30 | c3et6A_ | Alignment | not modelled | 88.4 | 11 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta;<br>**PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase |
| 31 | c1yk9A_ | Alignment | not modelled | 87.2 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**adenylate cyclase;<br>**PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c |
| 32 | c2aq4A_ | Alignment | not modelled | 81.6 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna repair protein rev1;<br>**PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp. |
| 33 | c3gqcB_ | Alignment | not modelled | 76.2 | 22 | **PDB header:**transferase/dna<br>**Chain:** B: **PDB Molecule:**dna repair protein rev1;<br>**PDBTitle:** structure of human rev1-dna-dntp ternary complex |
| 34 | d1azsb_ | Alignment | not modelled | 73.6 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nucleotide cyclase<br>**Family:**Adenylyl and guanylyl cyclase catalytic domain |
| 35 | c3onqB_ | Alignment | not modelled | 67.3 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression;<br>**PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis |
| 36 | d1im4a_ | Alignment | not modelled | 61.1 | 19 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 37 | c1s97D_ | Alignment | not modelled | 57.2 | 16 | **PDB header:**transferase/dna<br>**Chain:** D: **PDB Molecule:**dna polymerase iv;<br>**PDBTitle:** dpo4 with gt mismatch |
| 38 | c1k1qA_ | Alignment | not modelled | 52.1 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dbh protein;<br>**PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus |
| 39 | c1jihA_ | Alignment | not modelled | 46.2 | 22 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**dna polymerase eta;<br>**PDBTitle:** yeast dna polymerase eta |
| 40 | c2oh2B_ | Alignment | not modelled | 39.5 | 20 | **PDB header:**transferase/dna<br>**Chain:** B: **PDB Molecule:**dna polymerase kappa;<br>**PDBTitle:** ternary complex of human dna polymerase |
| 41 | c3mr2A_ | Alignment | not modelled | 38.4 | 22 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase eta;<br>**PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm) |
| 42 | c2r8kB_ | Alignment | not modelled | 36.0 | 20 | **PDB header:**replication, transferase/dna<br>**Chain:** B: **PDB Molecule:**dna polymerase eta;<br>**PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna |
| 43 | d1xxaa_ | Alignment | not modelled | 35.3 | 12 | **Fold:**DCoH-like<br>**Superfamily:**C-terminal domain of arginine repressor<br>**Family:**C-terminal domain of arginine repressor |
| 44 | d1k1sa2 | Alignment | not modelled | 34.6 | 17 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 45 | d1jiha2 | Alignment | not modelled | 34.1 | 12 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 46 | d1gx1a_ | Alignment | not modelled | 33.2 | 17 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**IpsF-like<br>**Family:**IpsF-like |
| 47 | d1jx4a2 | Alignment | not modelled | 29.8 | 15 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 48 | d1w5sa2 | Alignment | not modelled | 29.6 | 12 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Extended AAA-ATPase domain |
| 49 | d1vh8a_ | Alignment | not modelled | 29.5 | 15 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**IpsF-like<br>**Family:**IpsF-like |
| 50 | d1w55a2 | Alignment | not modelled | 24.1 | 13 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**IpsF-like<br>**Family:**IpsF-like |
| 51 | d1j27a_ | Alignment | not modelled | 24.0 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**Hypothetical protein TT1725<br>**Family:**Hypothetical protein TT1725 |
| 52 | d1t0aa_ | Alignment | not modelled | 23.3 | 15 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**IpsF-like<br>**Family:**IpsF-like |
| 53 | c1xaxA_ | Alignment | not modelled | 22.5 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004;<br>**PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae |
| 54 | c3af5A_ | Alignment | not modelled | 21.7 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404;<br>**PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii |
|  |  |  |  |  |  | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hit family hydrolase; |

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| 55 | c3i24B_ | Alignment | not modelled | 21.3 | 18 | **PDBTitle:** crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176 |
| 56 | c2zztA_ | Alignment | not modelled | 20.8 | 16 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein |
| 57 | d1wdia_ | Alignment | not modelled | 20.4 | 25 | **Fold:**QueA-like<br>**Superfamily:**QueA-like<br>**Family:**QueA-like |
| 58 | c3b6nA_ | Alignment | not modelled | 20.3 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate<br>**PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax |
| 59 | c2pmpA_ | Alignment | not modelled | 20.0 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase;<br>**PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana |
| 60 | c2jroA_ | Alignment | not modelled | 19.1 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75 |
| 61 | d1xm5a_ | Alignment | not modelled | 18.5 | 17 | **Fold:**Zincin-like<br>**Superfamily:**Metalloproteases ("zincins"), catalytic domain<br>**Family:**Predicted metal-dependent hydrolase |
| 62 | c3f0gA_ | Alignment | not modelled | 18.5 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase;<br>**PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp |
| 63 | d3bypa1 | Alignment | not modelled | 18.4 | 20 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Cation efflux protein cytoplasmic domain-like<br>**Family:**Cation efflux protein cytoplasmic domain-like |
| 64 | d1oz9a_ | Alignment | not modelled | 18.4 | 15 | **Fold:**Zincin-like<br>**Superfamily:**Metalloproteases ("zincins"), catalytic domain<br>**Family:**Predicted metal-dependent hydrolase |
| 65 | d1iv3a_ | Alignment | not modelled | 18.1 | 18 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**IpsF-like<br>**Family:**IpsF-like |
| 66 | c1qgeE_ | Alignment | not modelled | 17.4 | 23 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**protein (triacylglycerol hydrolase);<br>**PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase |
| 67 | c3v4gA_ | Alignment | not modelled | 17.1 | 18 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**arginine repressor;<br>**PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6 |
| 68 | c3mc6C_ | Alignment | not modelled | 17.0 | 11 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**sphingosine-1-phosphate lyase;<br>**PDBTitle:** crystal structure of scdpl1 |
| 69 | c3oheA_ | Alignment | not modelled | 16.3 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**histidine triad (hit) protein;<br>**PDBTitle:** crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution |
| 70 | d2ox6a1 | Alignment | not modelled | 16.3 | 19 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**YdiL-like |
| 71 | d2o5aa1 | Alignment | not modelled | 15.9 | 11 | **Fold:**Nucleotidyltransferase<br>**Superfamily:**Nucleotidyltransferase<br>**Family:**Iojap/YbeB-like |
| 72 | d1y4ia1 | Alignment | not modelled | 14.6 | 33 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 73 | d2qfia1 | Alignment | not modelled | 14.5 | 13 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Cation efflux protein cytoplasmic domain-like<br>**Family:**Cation efflux protein cytoplasmic domain-like |
| 74 | c1t3nB_ | Alignment | not modelled | 14.1 | 26 | **PDB header:**replication/dna<br>**Chain:** B: **PDB Molecule:**polymerase (dna directed) iota;<br>**PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp |
| 75 | d1n8pa_ | Alignment | not modelled | 13.6 | 35 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**Cystathionine synthase-like |
| 76 | d2phcb2 | Alignment | not modelled | 13.1 | 11 | **Fold:**DCoH-like<br>**Superfamily:**PH0987 N-terminal domain-like<br>**Family:**PH0987 N-terminal domain-like |
| 77 | c3upsA_ | Alignment | not modelled | 12.6 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**iojap-like protein;<br>**PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis |
| 78 | c3l5aA_ | Alignment | not modelled | 12.5 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase;<br>**PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus |
| 79 | c2htfA_ | Alignment | not modelled | 12.4 | 27 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase mu;<br>**PDBTitle:** the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain |
| 80 | d1t94a2 | Alignment | not modelled | 12.2 | 21 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases |

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| | | | | | | **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain |
| 81 | d2fsqa1 | Alignment | not modelled | 12.1 | 12 | **Fold:**LigT-like<br>**Superfamily:**LigT-like<br>**Family:**Atu0111-like |
| 82 | c1t94B_ | Alignment | not modelled | 12.0 | 21 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa;<br>**PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa |
| 83 | d2c0ra1 | Alignment | not modelled | 11.6 | 12 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 84 | c3k30B_ | Alignment | not modelled | 11.4 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**histamine dehydrogenase;<br>**PDBTitle:** histamine dehydrogenase from nocardiodes simplex |
| 85 | c2qfiB_ | Alignment | not modelled | 11.3 | 14 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**ferrous-iron efflux pump fief;<br>**PDBTitle:** structure of the zinc transporter yiip |
| 86 | c3nrdB_ | Alignment | not modelled | 11.2 | 19 | **PDB header:**nucleotide binding protein<br>**Chain:** B: **PDB Molecule:**histidine triad (hit) protein;<br>**PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution |
| 87 | c3l7xA_ | Alignment | not modelled | 11.2 | 16 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle<br>**PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159 |
| 88 | c3nj2B_ | Alignment | not modelled | 11.0 | 10 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**duf269-containing protein;<br>**PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family |
| 89 | d2p5ma1 | Alignment | not modelled | 11.0 | 20 | **Fold:**DCoH-like<br>**Superfamily:**C-terminal domain of arginine repressor<br>**Family:**C-terminal domain of arginine repressor |
| 90 | d1zaka2 | Alignment | not modelled | 10.7 | 43 | **Fold:**Rubredoxin-like<br>**Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain<br>**Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain |
| 91 | c3jurA_ | Alignment | not modelled | 10.7 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase;<br>**PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima |
| 92 | c1x31A_ | Alignment | not modelled | 10.7 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit;<br>**PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96 |
| 93 | c2fllA_ | Alignment | not modelled | 10.6 | 24 | **PDB header:**replication/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase iota;<br>**PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp |
| 94 | c3kmlB_ | Alignment | not modelled | 10.6 | 55 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**coat protein;<br>**PDBTitle:** circular permutant of the tobacco mosaic virus |
| 95 | d1ei7a_ | Alignment | not modelled | 10.6 | 55 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**TMV-like viral coat proteins<br>**Family:**TMV-like viral coat proteins |
| 96 | d1iwga2 | Alignment | not modelled | 10.1 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br>**Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 97 | d1b4ba_ | Alignment | not modelled | 10.1 | 18 | **Fold:**DCoH-like<br>**Superfamily:**C-terminal domain of arginine repressor<br>**Family:**C-terminal domain of arginine repressor |
| 98 | c2uzhB_ | Alignment | not modelled | 10.0 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**2c-methyl-d-erythritol 2,4-cyclodiphosphate<br>**PDBTitle:** mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf) |
| 99 | d1vtmp_ | Alignment | not modelled | 9.9 | 40 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**TMV-like viral coat proteins<br>**Family:**TMV-like viral coat proteins |