# Phyre$^2$

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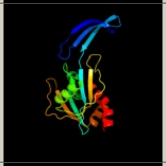
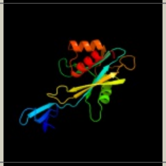
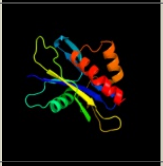
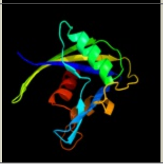
| Email | l.a.kelley@imperial.ac.uk |
| Description | P45799 |
| Date | Thu Jan 5 12:03:47 GMT 2012 |
| Unique Job ID | 9711ecffe67439cd |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1vhza_ | Alignment |  | 100.0 | 99 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 2 | c2yvoA_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of ndx2 in complex with mg2+ and amp from thermus2 thermophilus hb8 |
| 3 | d1g0sa_ | Alignment |  | 100.0 | 20 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 4 | d1viua_ | Alignment |  | 100.0 | 18 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 5 | c3bm4B_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adp-sugar pyrophosphatase;<br>**PDBTitle:** crystal structure of human adp-ribose pyrophosphatase nudt52 in complex with magnesium and ampcpr |
| 6 | d1mqea_ | Alignment |  | 100.0 | 19 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 7 | d1v8ya_ | Alignment |  | 100.0 | 23 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 8 | c2w4eA_ | Alignment |  | 100.0 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans |
| 9 | c3q91D_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase;<br>**PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14) |
| 10 | d1sjya_ | Alignment |  | 99.9 | 15 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 11 | c3dkuB_ | Alignment |  | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative phosphohydrolase;<br>**PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1 |

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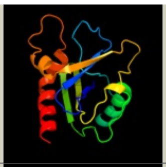
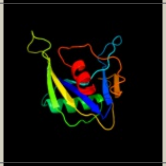
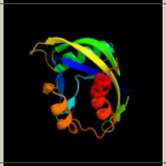
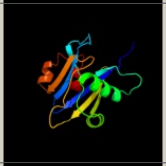
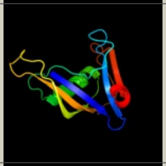
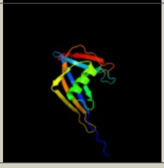
| 12 | c2jvbA_ | Alignment |  | 99.8 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2;<br>**PDBTitle:** solution structure of catalytic domain of ydcp2 |
| 13 | d1vk6a2 | Alignment |  | 99.8 | 15 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**NADH pyrophosphatase |
| 14 | d2b0va1 | Alignment |  | 99.8 | 17 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 15 | c2gb5B_ | Alignment |  | 99.8 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**nadh pyrophosphatase;<br>**PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution |
| 16 | c2r5wA_ | Alignment |  | 99.8 | 15 | **PDB header:**hydrolase, transferase<br>**Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase;<br>**PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis |
| 17 | c3h95A_ | Alignment |  | 99.8 | 20 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6;<br>**PDBTitle:** crystal structure of the nudix domain of nudt6 |
| 18 | c2fvvA_ | Alignment |  | 99.8 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase<br>**PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1 |
| 19 | d2fvva1 | Alignment |  | 99.8 | 12 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 20 | c3cngC_ | Alignment |  | 99.8 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**nudix hydrolase;<br>**PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea |
| 21 | d2o5fa1 | Alignment | not modelled | 99.8 | 13 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**IPP isomerase-like |
| 22 | d2fkba1 | Alignment | not modelled | 99.8 | 14 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**IPP isomerase-like |
| 23 | d1nqza_ | Alignment | not modelled | 99.8 | 21 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 24 | c3gg6A_ | Alignment | not modelled | 99.8 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 18;<br>**PDBTitle:** crystal structure of the nudix domain of human nudt18 |
| 25 | c3gwyA_ | Alignment | not modelled | 99.8 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase;<br>**PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis |
| 26 | c3sonB_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hypothetical nudix hydrolase;<br>**PDBTitle:** crystal structure of a hypothetical nudix hydrolase (lmof2365_2679)2 from listeria monocytogenes (atcc 19115) at 1.70 a resolution |
| 27 | c3id9B_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis |
| 28 | d2fb1a2 | Alignment | not modelled | 99.7 | 14 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**BT0354 N-terminal domain-like |

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| 29 | d2a6ta2 | Alignment | not modelled | 99.7 | 19 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**mRNA decapping enzyme-like |
| 30 | c3hhjA_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mutator mutt protein;<br>**PDBTitle:** crystal structure of mutator mutt from bartonella henselae |
| 31 | c3q4iA_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein);<br>**PDBTitle:** crystal structure of cdp-chase in complex with gd3+ |
| 32 | d1irya_ | Alignment | not modelled | 99.7 | 16 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 33 | c3i9xA_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua |
| 34 | d1vcda1 | Alignment | not modelled | 99.7 | 24 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 35 | c2pq1B_ | Alignment | not modelled | 99.7 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**ap4a hydrolase;<br>**PDBTitle:** crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5 |
| 36 | d1ktga_ | Alignment | not modelled | 99.7 | 20 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 37 | c2kdvA_ | Alignment | not modelled | 99.7 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase;<br>**PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli |
| 38 | c2qkmF_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**spac19a8.12 protein;<br>**PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex |
| 39 | c3o8sA_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**adp-ribose pyrophosphatase;<br>**PDBTitle:** crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution |
| 40 | c3r03B_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**nudix hydrolase;<br>**PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum |
| 41 | c2qjoB_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**transferase, hydrolase<br>**Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase;<br>**PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp. |
| 42 | c3gz8C_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**dna binding protein<br>**Chain:** C: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** cocrystal structure of nudix domain of shewanella oneidensis2 nrtr complexed with adp ribose |
| 43 | d1xsba_ | Alignment | not modelled | 99.7 | 19 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 44 | c3ef5A_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase;<br>**PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp |
| 45 | c3exqA_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nudix family hydrolase;<br>**PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis |
| 46 | c2o1cB_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase;<br>**PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2 pyrophosphohydrolase |
| 47 | d2azwa1 | Alignment | not modelled | 99.7 | 17 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 48 | c3grnB_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**mutt related protein;<br>**PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1 |
| 49 | d1puna_ | Alignment | not modelled | 99.7 | 24 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 50 | c3fjyB_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**probable mutt1 protein;<br>**PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis |
| 51 | d2b06a1 | Alignment | not modelled | 99.7 | 13 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 52 | d1ryaa_ | Alignment | not modelled | 99.7 | 11 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**GDP-mannose mannosyl hydrolase NudD |
| 53 | c3e57A_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein tm1382;<br>**PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase |
| 54 | c3fk9B_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**mutator mutt protein;<br>**PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 |

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|  |  |  |  |  |  | halodurans |
| 55 | c2yyhC_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain;<br>**PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus |
| 56 | d1ppva_ | Alignment | not modelled | 99.7 | 15 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**IPP isomerase-like |
| 57 | d1jkna_ | Alignment | not modelled | 99.7 | 19 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 58 | c2pqvA_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of mutt/nudix family protein from streptococcus2 pneumoniae |
| 59 | c2fb1A_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein;<br>**PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron |
| 60 | c3n77B_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi;<br>**PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2 |
| 61 | c3fcmA_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hydrolase, nudix family;<br>**PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens |
| 62 | c3f6aA_ | Alignment | not modelled | 99.7 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hydrolase, nudix family;<br>**PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens |
| 63 | d1hzta_ | Alignment | not modelled | 99.7 | 15 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**IPP isomerase-like |
| 64 | c3gz6A_ | Alignment | not modelled | 99.7 | 13 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna |
| 65 | d1k2ea_ | Alignment | not modelled | 99.6 | 13 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 66 | c3f13A_ | Alignment | not modelled | 99.6 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative nudix hydrolase family member;<br>**PDBTitle:** crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum |
| 67 | c3edsA_ | Alignment | not modelled | 99.6 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis |
| 68 | d2fmla2 | Alignment | not modelled | 99.6 | 16 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**BT0354 N-terminal domain-like |
| 69 | c3rh7A_ | Alignment | not modelled | 99.5 | 12 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical oxidoreductase;<br>**PDBTitle:** crystal structure of a hypothetical oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution |
| 70 | c2fmlB_ | Alignment | not modelled | 99.5 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of mutt/nudix family protein from enterococcus2 faecalis |
| 71 | d1x51a1 | Alignment | not modelled | 99.4 | 11 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutY C-terminal domain-like |
| 72 | c2i6kA_ | Alignment | not modelled | 99.4 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1;<br>**PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog |
| 73 | c1rrqA_ | Alignment | not modelled | 99.3 | 13 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**muty;<br>**PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair |
| 74 | d1q33a_ | Alignment | not modelled | 99.3 | 19 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 75 | d1u20a1 | Alignment | not modelled | 99.3 | 16 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 76 | c3dupB_ | Alignment | not modelled | 99.3 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**mutt/nudix family protein;<br>**PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170 |
| 77 | d1rrqa2 | Alignment | not modelled | 99.2 | 13 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutY C-terminal domain-like |
| 78 | c2j8qB_ | Alignment | not modelled | 99.2 | 16 | **PDB header:**nuclear protein<br>**Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 5;<br>**PDBTitle:** crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion. |
| 79 | c2pnyA_ | Alignment | not modelled | 99.2 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2;<br>**PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2 |
|  |  |  |  |  |  | **PDB header:**hydrolase |

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| 80 | c3qsjA_ | Alignment | not modelled | 99.2 | 20 | **Chain:** A: **PDB Molecule:**nudix hydrolase;<br>**PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius |
| 81 | c3couA_ | Alignment | not modelled | 98.3 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16;<br>**PDBTitle:** crystal structure of human nudix motif 16 (nudt16) |
| 82 | c3kvhA_ | Alignment | not modelled | 97.9 | 19 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**protein syndesmos;<br>**PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein) |
| 83 | c3p5tE_ | Alignment | not modelled | 95.5 | 16 | **PDB header:**rna binding protein<br>**Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5;<br>**PDBTitle:** cfim25-cfim68 complex |
| 84 | c2k2pA_ | Alignment | not modelled | 21.9 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu1203;<br>**PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183 |
| 85 | d1sb6a_ | Alignment | not modelled | 20.9 | 8 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 86 | d1nc7a_ | Alignment | not modelled | 15.5 | 19 | **Fold:**Hypothetical protein TM1070<br>**Superfamily:**Hypothetical protein TM1070<br>**Family:**Hypothetical protein TM1070 |
| 87 | c3h76A_ | Alignment | not modelled | 14.3 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pqs biosynthetic enzyme;<br>**PDBTitle:** crystal structure of pqsd, a key enzyme in pseudomonas2 aeruginosa quinolone signal biosynthesis pathway |
| 88 | d1ub7a1 | Alignment | not modelled | 12.9 | 10 | **Fold:**Thiolase-like<br>**Superfamily:**Thiolase-like<br>**Family:**Chalcone synthase-like |
| 89 | d1cc8a_ | Alignment | not modelled | 12.7 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 90 | d1aopa2 | Alignment | not modelled | 12.6 | 11 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**Duplicated SiR/NiR-like domains 1 and 3 |
| 91 | c3s3lB_ | Alignment | not modelled | 12.1 | 11 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**cerj;<br>**PDBTitle:** crystal structure of cerj from streptomyces tendae |
| 92 | c3enoB_ | Alignment | not modelled | 10.7 | 8 | **PDB header:**hydrolase/unknown function<br>**Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein endopeptidase;<br>**PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1 |
| 93 | d1bm8a_ | Alignment | not modelled | 9.3 | 24 | **Fold:**DNA-binding domain of Mlu1-box binding protein MBP1<br>**Superfamily:**DNA-binding domain of Mlu1-box binding protein MBP1<br>**Family:**DNA-binding domain of Mlu1-box binding protein MBP1 |
| 94 | c2ii8F_ | Alignment | not modelled | 9.1 | 14 | **PDB header:**signaling protein<br>**Chain:** F: **PDB Molecule:**anabaena sensory rhodopsin transducer protein;<br>**PDBTitle:** anabaena sensory rhodopsin transducer |
| 95 | c2rogA_ | Alignment | not modelled | 9.0 | 28 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**heavy metal binding protein;<br>**PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells |
| 96 | c3h37B_ | Alignment | not modelled | 8.6 | 21 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**trna nucleotidyl transferase-related protein;<br>**PDBTitle:** the structure of cca-adding enzyme apo form i |
| 97 | c2jswA_ | Alignment | not modelled | 8.6 | 33 | **PDB header:**actin-binding protein<br>**Chain:** A: **PDB Molecule:**talin-1;<br>**PDBTitle:** nmr structure of the talin c-terminal actin binding site |
| 98 | c1yg0A_ | Alignment | not modelled | 7.4 | 11 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**cop associated protein;<br>**PDBTitle:** solution structure of apo-copp from helicobacter pylori |
| 99 | d2fug21 | Alignment | not modelled | 7.3 | 12 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**NQO2-like |