# Phyre$^2$

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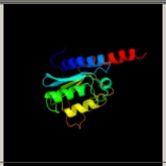
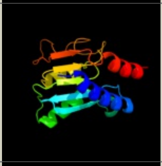
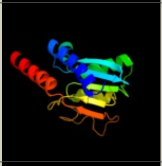
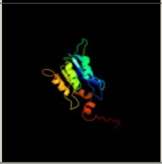
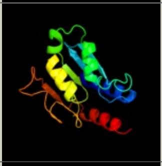
| Email | l.a.kelley@imperial.ac.uk |
| Description | P68398 |
| Date | Thu Jan 5 12:11:02 GMT 2012 |
| Unique Job ID | b0836fb5cf88052e |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1z3aa1 | Alignment |  | 100.0 | 100 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 2 | c2nx8A_ | Alignment |  | 100.0 | 37 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**trna-specific adenosine deaminase;<br>**PDBTitle:** the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes |
| 3 | d2b3ja1 | Alignment |  | 100.0 | 44 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 4 | c3ocqA_ | Alignment |  | 100.0 | 92 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative cytosine/adenosine deaminase;<br>**PDBTitle:** crystal structure of trna-specific adenosine deaminase from salmonella2 enterica |
| 5 | d1wwra1 | Alignment |  | 100.0 | 41 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 6 | c2o7pA_ | Alignment |  | 100.0 | 34 | **PDB header:**hydrolase, oxidoreductase<br>**Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd;<br>**PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain |
| 7 | c2d5nB_ | Alignment |  | 100.0 | 38 | **PDB header:**hydrolase, oxidoreductase<br>**Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribd;<br>**PDBTitle:** crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis |
| 8 | c2hxvA_ | Alignment |  | 100.0 | 34 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5-<br>**PDBTitle:** crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution |
| 9 | d2g84a1 | Alignment |  | 100.0 | 31 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 10 | c3dh1D_ | Alignment |  | 100.0 | 34 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**trna-specific adenosine deaminase 2;<br>**PDBTitle:** crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2 |
| 11 | d2a8na1 | Alignment |  | 100.0 | 42 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |

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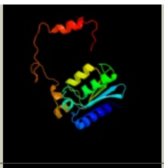
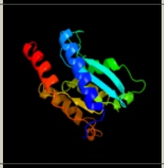
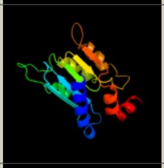
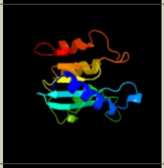
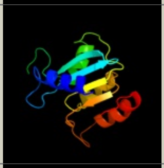
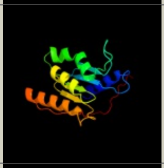
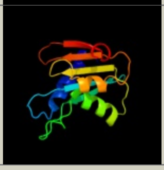
| 12 | d1wkqa_ | Alignment |  | 100.0 | 29 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 13 | d1p6oa_ | Alignment |  | 100.0 | 29 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 14 | d2hxva2 | Alignment |  | 100.0 | 26 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 15 | d2b3za2 | Alignment |  | 100.0 | 40 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 16 | d1vq2a_ | Alignment |  | 100.0 | 27 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 17 | c2hvwC_ | Alignment |  | 100.0 | 29 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**deoxycytidylate deaminase;<br>**PDBTitle:** crystal structure of dcmp deaminase from streptococcus2 mutans |
| 18 | c2w4lC_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**deoxycytidylate deaminase;<br>**PDBTitle:** human dcmp deaminase |
| 19 | d1uwza_ | Alignment |  | 98.3 | 16 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 20 | d2d30a1 | Alignment |  | 98.3 | 17 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 21 | d1r5ta_ | Alignment | not modelled | 98.2 | 18 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 22 | d1mq0a_ | Alignment | not modelled | 98.2 | 17 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 23 | d2fr5a1 | Alignment | not modelled | 98.2 | 18 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 24 | c3dmoD_ | Alignment | not modelled | 98.2 | 22 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**cytidine deaminase;<br>**PDBTitle:** 1.6 a crystal structure of cytidine deaminase from2 burkholderia pseudomallei |
| 25 | c3ijfX_ | Alignment | not modelled | 98.1 | 17 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**cytidine deaminase;<br>**PDBTitle:** crystal structure of cytidine deaminase from mycobacterium2 tuberculosis |
| 26 | c3r2nC_ | Alignment | not modelled | 98.0 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**cytidine deaminase;<br>**PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae |
| 27 | c3b8fB_ | Alignment | not modelled | 98.0 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative blasticidin s deaminase;<br>**PDBTitle:** crystal structure of the cytidine deaminase from bacillus anthracis |
| 28 | d1alna1 | Alignment | not modelled | 97.8 | 23 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| | | | | | | **Fold:**Cytidine deaminase-like |

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| 29 | d2z3ga1 | Alignment | not modelled | 97.8 | 13 | **Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 30 | c3oj6C_ | Alignment | not modelled | 97.7 | 10 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**blasticidin-s deaminase;<br>**PDBTitle:** crystal structure of blasticidin s deaminase from coccidioides immitis |
| 31 | d1alna2 | Alignment | not modelled | 97.6 | 15 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 32 | c1alnA_ | Alignment | not modelled | 97.5 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytidine deaminase;<br>**PDBTitle:** crystal structure of cytidine deaminase complexed with 3-deazacytidine |
| 33 | c3g8qA_ | Alignment | not modelled | 97.0 | 25 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump<br>**PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea |
| 34 | c2nytB_ | Alignment | not modelled | 93.6 | 28 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2;<br>**PDBTitle:** the apobec2 crystal structure and functional implications2 for aid |
| 35 | c2kboA_ | Alignment | not modelled | 92.0 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dna dc->du-editing enzyme apobec-3g;<br>**PDBTitle:** structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g |
| 36 | c3gxgA_ | Alignment | not modelled | 51.0 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative phosphatase (duf442);<br>**PDBTitle:** crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution |
| 37 | d1zbfa1 | Alignment | not modelled | 49.7 | 21 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Ribonuclease H |
| 38 | c3e9jC_ | Alignment | not modelled | 42.9 | 71 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**thiol/disulfide oxidoreductase dsbb;<br>**PDBTitle:** structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb |
| 39 | d2hi7b1 | Alignment | not modelled | 42.9 | 71 | **Fold:**Bromodomain-like<br>**Superfamily:**DsbB-like<br>**Family:**DsbB-like |
| 40 | d2b0va1 | Alignment | not modelled | 30.6 | 14 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**MutT-like |
| 41 | c3dkuB_ | Alignment | not modelled | 27.7 | 11 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative phosphohydrolase;<br>**PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1 |
| 42 | c3ggmB_ | Alignment | not modelled | 24.8 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein bt9727_2919;<br>**PDBTitle:** crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b |
| 43 | c2lk2A_ | Alignment | not modelled | 20.9 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**homeobox protein tgif1;<br>**PDBTitle:** solution nmr structure of homeobox domain (171-248) of human homeobox2 protein tgif1, northeast structural genomics consortium target3 hr4411b |
| 44 | c3rh7A_ | Alignment | not modelled | 15.7 | 32 | **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 |
| 45 | c3o8sA_ | Alignment | not modelled | 15.3 | 9 | **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 |
| 46 | c3nznA_ | Alignment | not modelled | 14.6 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glutaredoxin;<br>**PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1 |
| 47 | c3q4iA_ | Alignment | not modelled | 13.7 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein);<br>**PDBTitle:** crystal structure of cdp-chase in complex with gd3+ |
| 48 | c3d2oB_ | Alignment | not modelled | 13.5 | 18 | **PDB header:**hydrolase, biosynthetic protein<br>**Chain:** B: **PDB Molecule:**upf0343 protein ngo0387;<br>**PDBTitle:** crystal structure of manganese-metallated gtp cyclohydrolase2 type ib |
| 49 | d1j9ba_ | Alignment | not modelled | 13.2 | 17 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**ArsC-like |
| 50 | c2imrA_ | Alignment | not modelled | 13.0 | 36 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein dr_0824;<br>**PDBTitle:** crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans |
| 51 | d1ttza_ | Alignment | not modelled | 12.3 | 40 | **Fold:**Thioredoxin fold<br>**Superfamily:**Thioredoxin-like<br>**Family:**Thioltransferase |
| 52 | d2fb5a1 | Alignment | not modelled | 11.7 | 29 | **Fold:**YojJ-like<br>**Superfamily:**YojJ-like<br>**Family:**YojJ-like |
| 53 | c3ld0Q_ | Alignment | not modelled | 11.6 | 63 | **PDB header:**gene regulation<br>**Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa;<br>**PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions |
|  |  |  |  |  |  | **Fold:**LuxS/MPP-like metallohydrolase |

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| 54 | d1hr6a1 | Alignment | not modelled | 11.4 | 13 | **Superfamily:**LuxS/MPP-like metallohydrolase<br>**Family:**MPP-like |
| 55 | c3ipzA_ | Alignment | not modelled | 10.7 | 15 | **PDB header:**electron transport, oxidoreductase<br>**Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic;<br>**PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp |
| 56 | d1xdpa4 | Alignment | not modelled | 10.6 | 16 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 57 | d2o8ra4 | Alignment | not modelled | 10.4 | 16 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 58 | c4a1oB_ | Alignment | not modelled | 9.7 | 21 | **PDB header:**transferase-hydrolase<br>**Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution. |
| 59 | c2oodA_ | Alignment | not modelled | 9.7 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**blr3880 protein;<br>**PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum |
| 60 | c2klxA_ | Alignment | not modelled | 9.6 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glutaredoxin;<br>**PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston |
| 61 | c2r5rA_ | Alignment | not modelled | 9.3 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0343 protein ne1163;<br>**PDBTitle:** the crystal structure of duf198 from nitrosomonas europaea2 atcc 19718 |
| 62 | d1zcza2 | Alignment | not modelled | 9.0 | 16 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC |
| 63 | c2dmnA_ | Alignment | not modelled | 8.4 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**homeobox protein tgif2lx;<br>**PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein tgif2lx |
| 64 | d1nuia2 | Alignment | not modelled | 8.4 | 27 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**DNA primase zinc finger |
| 65 | c2pq1B_ | Alignment | not modelled | 8.0 | 29 | **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 |
| 66 | c2kq2A_ | Alignment | not modelled | 7.6 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ribonuclease h-related protein;<br>**PDBTitle:** solution nmr structure of the apo form of a ribonuclease h2 domain of protein dsy1790 from desulfitobacterium3 hafniense, northeast structural genomics target dhr1a |
| 67 | d2drpa2 | Alignment | not modelled | 7.2 | 60 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 68 | c2khpA_ | Alignment | not modelled | 7.0 | 32 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**glutaredoxin;<br>**PDBTitle:** solution structure of glutaredoxin from brucella melitensis |
| 69 | c3hstD_ | Alignment | not modelled | 6.9 | 15 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**protein rv2228c/mt2287;<br>**PDBTitle:** n-terminal rnase h domain of rv2228c from mycobacterium tuberculosis2 as a fusion protein with maltose binding protein |
| 70 | d1i1qb_ | Alignment | not modelled | 6.8 | 29 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 71 | d2akla2 | Alignment | not modelled | 6.4 | 56 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**PhnA zinc-binding domain |
| 72 | c2bx9J_ | Alignment | not modelled | 5.7 | 57 | **PDB header:**transcription regulation<br>**Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory<br>**PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions |
| 73 | c2xzn5_ | Alignment | not modelled | 5.7 | 70 | **PDB header:**ribosome<br>**Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |
| 74 | d1vdda_ | Alignment | not modelled | 5.5 | 21 | **Fold:**Recombination protein RecR<br>**Superfamily:**Recombination protein RecR<br>**Family:**Recombination protein RecR |
| 75 | d2r5yb1 | Alignment | not modelled | 5.4 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Homeodomain |
| 76 | d2baia1 | Alignment | not modelled | 5.3 | 44 | **Fold:**Viral leader polypeptide zinc finger<br>**Superfamily:**Viral leader polypeptide zinc finger<br>**Family:**Viral leader polypeptide zinc finger |
| 77 | d1k61a_ | Alignment | not modelled | 5.3 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Homeodomain |
| 78 | d1du6a_ | Alignment | not modelled | 5.2 | 9 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Homeodomain |

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| 79 | c2o8rA_ | Alignment | not modelled | 5.1 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis |