# Phyre²

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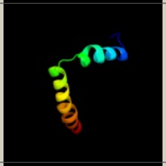
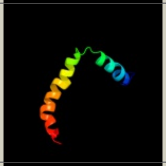
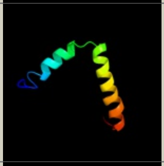
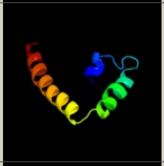
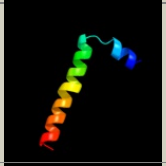
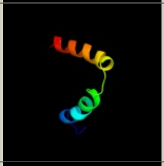
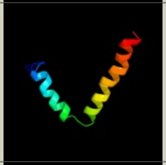
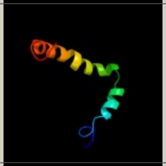
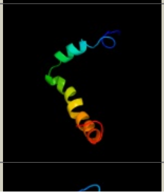
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ADV7 |
| Date | Thu Jan 5 11:21:56 GMT 2012 |
| Unique Job ID | 589724252b18bfbd |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2qguA_ | Alignment |  | 100.0 | 25 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**probable signal peptide protein;<br>**PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89 |
| 2 | c2co9A_ | Alignment |  | 86.7 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox;<br>**PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse |
| 3 | d1k99a_ | Alignment |  | 86.5 | 21 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 4 | d1j46a_ | Alignment |  | 84.2 | 20 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 5 | d1v63a_ | Alignment |  | 84.2 | 18 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 6 | d1v8ga1 | Alignment |  | 83.5 | 13 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 7 | c3fghA_ | Alignment |  | 83.3 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial;<br>**PDBTitle:** human mitochondrial transcription factor a box b |
| 8 | c2yulA_ | Alignment |  | 83.0 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor sox-17;<br>**PDBTitle:** solution structure of the hmg box of human transcription2 factor sox-17 |
| 9 | c2crjA_ | Alignment |  | 82.9 | 22 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin-<br>**PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2 |
| 10 | c1hmfA_ | Alignment |  | 82.8 | 21 | **PDB header:**dna-binding<br>**Chain:** A: **PDB Molecule:**high mobility group protein fragment-b;<br>**PDBTitle:** structure of the hmg box motif in the b-domain of hmg1 |
| 11 | d1hmfa_ | Alignment |  | 82.8 | 21 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |

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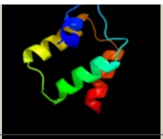
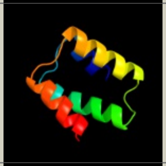
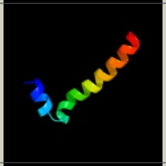
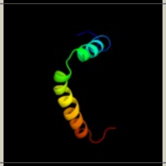
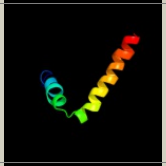
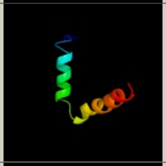
| 12 | d1khda1 | Alignment |  | 81.8 | 10 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 13 | d2lefa_ | Alignment |  | 81.7 | 13 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 14 | d2tpta1 | Alignment |  | 81.6 | 15 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 15 | d1uoua1 | Alignment |  | 81.0 | 10 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 16 | c2eqzA_ | Alignment |  | 80.4 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**high mobility group protein b3;<br>**PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3 |
| 17 | c3u2bC_ | Alignment |  | 80.3 | 13 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**transcription factor sox-4;<br>**PDBTitle:** structure of the sox4 hmg domain bound to dna |
| 18 | d1lwma_ | Alignment |  | 79.9 | 27 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 19 | c2e6oA_ | Alignment |  | 79.4 | 16 | **PDB header:**transcription, cell cycle<br>**Chain:** A: **PDB Molecule:**hmg box-containing protein 1;<br>**PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1 |
| 20 | d1ckta_ | Alignment |  | 79.3 | 12 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 21 | c2cs1A_ | Alignment | not modelled | 78.7 | 13 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**pms1 protein homolog 1;<br>**PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein |
| 22 | d1vqqa1 | Alignment | not modelled | 77.7 | 9 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain |
| 23 | d1brwa1 | Alignment | not modelled | 77.6 | 13 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 24 | d2gzka2 | Alignment | not modelled | 77.4 | 19 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 25 | d3cnxa1 | Alignment | not modelled | 77.3 | 11 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**SAV4671-like |
| 26 | c2d7lA_ | Alignment | not modelled | 76.4 | 5 | **PDB header:**gene regulation, dna binding protein<br>**Chain:** A: **PDB Molecule:**wd repeat and hmg-box dna binding protein 1;<br>**PDBTitle:** solution structure of the hmg box domain from human wd2 repeat and hmg-box dna binding protein 1 |
| 27 | d1gt0d_ | Alignment | not modelled | 76.3 | 13 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 28 | d1o17a1 | Alignment | not modelled | 74.6 | 13 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |

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| 29 | c1hrzA_ | Alignment | not modelled | 74.6 | 21 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**human sry;<br>**PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multi-dimensional heteronuclear-edited and-filtered nmr |
| 30 | c1hryA_ | Alignment | not modelled | 74.4 | 21 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**human sry;<br>**PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multid-dimensional heteronuclear-edited and-filtered nmr |
| 31 | d1j3xa_ | Alignment | not modelled | 74.0 | 4 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 32 | c1j3xA_ | Alignment | not modelled | 74.0 | 4 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**high mobility group protein 2;<br>**PDBTitle:** solution structure of the n-terminal domain of the hmgb2 |
| 33 | c3tq6B_ | Alignment | not modelled | 73.7 | 11 | **PDB header:**transcription/dna<br>**Chain:** B: **PDB Molecule:**transcription factor a, mitochondrial;<br>**PDBTitle:** crystal structure of human mitochondrial transcription factor a, tfam2 or mttfa, bound to the light strand promoter lsp |
| 34 | c3k7cC_ | Alignment | not modelled | 73.3 | 12 | **PDB header:**protein binding<br>**Chain:** C: **PDB Molecule:**putative ntf2-like transpeptidase;<br>**PDBTitle:** crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution |
| 35 | c3epvB_ | Alignment | not modelled | 72.9 | 11 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr;<br>**PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms |
| 36 | d1aaba_ | Alignment | not modelled | 70.0 | 11 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 37 | c1aabA_ | Alignment | not modelled | 70.0 | 11 | **PDB header:**dna-binding<br>**Chain:** A: **PDB Molecule:**high mobility group protein;<br>**PDBTitle:** nmr structure of rat hmg1 hmga fragment |
| 38 | c1khdD_ | Alignment | not modelled | 69.5 | 10 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase;<br>**PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum) |
| 39 | d1i11a_ | Alignment | not modelled | 68.5 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 40 | d1j3da_ | Alignment | not modelled | 67.5 | 23 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 41 | d1hsma_ | Alignment | not modelled | 66.0 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 42 | c1wz6A_ | Alignment | not modelled | 65.3 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**hmg-box transcription factor bbx;<br>**PDBTitle:** solution structure of the hmg_box domain of murine bobby2 sox homolog |
| 43 | d1v64a_ | Alignment | not modelled | 64.8 | 20 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 44 | c1brwB_ | Alignment | not modelled | 64.0 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase);<br>**PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation |
| 45 | c3qzcA_ | Alignment | not modelled | 63.5 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**periplasmic protein cpxp;<br>**PDBTitle:** structure of the periplasmic stress response protein cpxp |
| 46 | c1wx2A_ | Alignment | not modelled | 62.7 | 12 | **PDB header:**oxidoreductase/metal transport<br>**Chain:** A: **PDB Molecule:**tyrosinase;<br>**PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of hydrogenperoxide |
| 47 | c1v8gB_ | Alignment | not modelled | 61.9 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase;<br>**PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8 |
| 48 | d1lnla1 | Alignment | not modelled | 61.8 | 24 | **Fold:**Di-copper centre-containing domain<br>**Superfamily:**Di-copper centre-containing domain<br>**Family:**Hemocyanin middle domain |
| 49 | c1wxlA_ | Alignment | not modelled | 61.1 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**single-strand recognition protein;<br>**PDBTitle:** solution structure of the hmg-box domain in the ssrp12 subunit of fact |
| 50 | d1wgfa_ | Alignment | not modelled | 60.5 | 13 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 51 | c3h5qA_ | Alignment | not modelled | 59.6 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase;<br>**PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus |
| 52 | c3l6wB_ | Alignment | not modelled | 59.6 | 14 | **PDB header:**oxygen binding<br>**Chain:** B: **PDB Molecule:**hemocyanin 1;<br>**PDBTitle:** structure of the collar functional unit (klh1-h) of keyhole2 limpet hemocyanin |
| 53 | c3oeoD_ | Alignment | not modelled | 59.3 | 15 | **PDB header:**signaling protein<br>**Chain:** D: **PDB Molecule:**spheroplast protein y;<br>**PDBTitle:** the crystal structure e. coli spy |
| 54 | c1otpA_ | Alignment | not modelled | 59.3 | 14 | **PDB header:**phosphorylase<br>**Chain:** A: **PDB Molecule:**thymidine phosphorylase;<br>**PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine |

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| | | | | | | phosphorylase |
| 55 | c1vquB_ | Alignment | not modelled | 59.2 | 10 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2;<br>**PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution |
| 56 | c2j0fC_ | Alignment | not modelled | 58.8 | 10 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**thymidine phosphorylase;<br>**PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design |
| 57 | d1js8a1 | Alignment | not modelled | 57.5 | 19 | **Fold:**Di-copper centre-containing domain<br>**Superfamily:**Di-copper centre-containing domain<br>**Family:**Hemocyanin middle domain |
| 58 | c1lnlB_ | Alignment | not modelled | 56.7 | 24 | **PDB header:**oxygen storage/transport<br>**Chain:** B: **PDB Molecule:**hemocyanin;<br>**PDBTitle:** structure of deoxygenated hemocyanin from rapana thomasiana |
| 59 | c2bpqB_ | Alignment | not modelled | 56.6 | 11 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase;<br>**PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure) |
| 60 | c3gwrA_ | Alignment | not modelled | 55.4 | 11 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**putative calcium/calmodulin-dependent protein kinase type<br>**PDBTitle:** crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution |
| 61 | c1js8A_ | Alignment | not modelled | 54.2 | 17 | **PDB header:**oxygen storage/transport<br>**Chain:** A: **PDB Molecule:**hemocyanin;<br>**PDBTitle:** structure of a functional unit from octopus hemocyanin |
| 62 | c3o39A_ | Alignment | not modelled | 54.1 | 15 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**periplasmic protein related to spheroblast formation;<br>**PDBTitle:** crystal structure of spy |
| 63 | d3bb9a1 | Alignment | not modelled | 53.8 | 15 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**SO0125-like |
| 64 | c3npyB_ | Alignment | not modelled | 53.4 | 4 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**tyrosinase;<br>**PDBTitle:** crystal structure of tyrosinase from bacillus megaterium soaked in2 cuso4 |
| 65 | c2yrqA_ | Alignment | not modelled | 50.4 | 22 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**high mobility group protein b1;<br>**PDBTitle:** solution structure of the tandem hmg box domain from human2 high mobility group protein b1 |
| 66 | c1o17A_ | Alignment | not modelled | 49.8 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase;<br>**PDBTitle:** anthranilate phosphoribosyl-transferase (trpd) |
| 67 | c3ke7A_ | Alignment | not modelled | 48.5 | 5 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative ketosteroid isomerase;<br>**PDBTitle:** crystal structure of putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution |
| 68 | c3evyB_ | Alignment | not modelled | 48.4 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative type i restriction enzyme r protein;<br>**PDBTitle:** crystal structure of a fragment of a putative type i2 restriction enzyme r protein from bacteroides fragilis |
| 69 | c2gzkA_ | Alignment | not modelled | 47.5 | 20 | **PDB header:**dna/structural protein<br>**Chain:** A: **PDB Molecule:**sex-determining region on y / hmgb1;<br>**PDBTitle:** structure of a complex of tandem hmg boxes and dna |
| 70 | c1ye9E_ | Alignment | not modelled | 44.5 | 20 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**catalase hpii;<br>**PDBTitle:** crystal structure of proteolytically truncated catalase2 hpii from e. coli |
| 71 | c3itfA_ | Alignment | not modelled | 44.4 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp;<br>**PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein |
| 72 | c3qk9B_ | Alignment | not modelled | 43.0 | 9 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase subunit<br>**PDBTitle:** yeast tim44 c-terminal domain complexed with cymal-3 |
| 73 | c3bqsB_ | Alignment | not modelled | 42.7 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form |
| 74 | d2r4ia1 | Alignment | not modelled | 41.3 | 15 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**CHU142-like |
| 75 | d3cu3a1 | Alignment | not modelled | 37.9 | 9 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**BaiE/LinA-like |
| 76 | c3dukD_ | Alignment | not modelled | 35.6 | 16 | **PDB header:**unknown function<br>**Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function;<br>**PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution |
| 77 | c2dsjA_ | Alignment | not modelled | 35.1 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase;<br>**PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8 |
| 78 | c2lhjA_ | Alignment | not modelled | 34.7 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**high mobility group protein homolog nhp1; |

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| | | | | | | **PDBTitle:** nmr structure of the high mobility group protein-like protein nhp12 from babesia bovis t2bo (baboa.00841.a) |
| 79 | c3fkaD_ | Alignment | not modelled | 30.4 | 16 | **PDB header:**unknown function<br>**Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein;<br>**PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution |
| 80 | d2cw9a1 | Alignment | not modelled | 30.0 | 10 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**TIM44-like |
| 81 | c3m20A_ | Alignment | not modelled | 26.4 | 8 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative;<br>**PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution |
| 82 | d2owpa1 | Alignment | not modelled | 26.1 | 9 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**BxeB1374-like |
| 83 | c3kspA_ | Alignment | not modelled | 24.6 | 13 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent kinase ii association domain;<br>**PDBTitle:** crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution |
| 84 | c2ia5C_ | Alignment | not modelled | 24.5 | 11 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**polynucleotide kinase;<br>**PDBTitle:** t4 polynucleotide kinase/phosphatase with bound sulfate and2 magnesium. |
| 85 | d1c07a_ | Alignment | not modelled | 23.4 | 22 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Eps15 homology domain (EH domain) |
| 86 | c3robC_ | Alignment | not modelled | 23.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**uncharacterized conserved protein;<br>**PDBTitle:** the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776 |
| 87 | d1ueab_ | Alignment | not modelled | 21.5 | 20 | **Fold:**OB-fold<br>**Superfamily:**TIMP-like<br>**Family:**Tissue inhibitor of metalloproteinases, TIMP |
| 88 | c3a16C_ | Alignment | not modelled | 21.4 | 24 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**aldoxime dehydratase;<br>**PDBTitle:** crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime |
| 89 | d1w8ia_ | Alignment | not modelled | 21.4 | 38 | **Fold:**PIN domain-like<br>**Superfamily:**PIN domain-like<br>**Family:**PIN domain |
| 90 | c2kgrA_ | Alignment | not modelled | 21.0 | 17 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**intersectin-1;<br>**PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a |
| 91 | d2juza1 | Alignment | not modelled | 20.0 | 21 | **Fold:**YejL-like<br>**Superfamily:**YejL-like<br>**Family:**YejL-like |
| 92 | d1otfa_ | Alignment | not modelled | 19.0 | 16 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**4-oxalocrotonate tautomerase-like |
| 93 | c3ry0A_ | Alignment | not modelled | 18.9 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative tautomerase;<br>**PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway |
| 94 | d2gxfa1 | Alignment | not modelled | 18.8 | 17 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**YybH-like |
| 95 | d1gyxa_ | Alignment | not modelled | 18.6 | 14 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**4-oxalocrotonate tautomerase-like |
| 96 | d1bjpa_ | Alignment | not modelled | 18.3 | 12 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**4-oxalocrotonate tautomerase-like |
| 97 | d1qrva_ | Alignment | not modelled | 18.1 | 20 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 98 | c3chtA_ | Alignment | not modelled | 17.8 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**p-aminobenzoate n-oxygenase;<br>**PDBTitle:** crystal structure of di-iron aurf with partially bound ligand |
| 99 | c3ej6D_ | Alignment | not modelled | 17.7 | 20 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**catalase-3;<br>**PDBTitle:** neurospora crassa catalase-3 crystal structure |