# Phyre2

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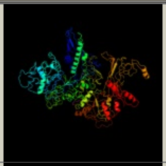
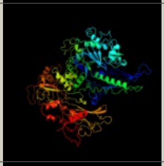
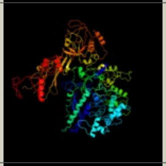
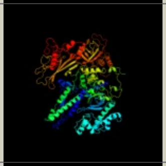
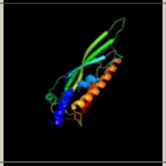
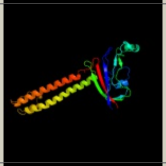
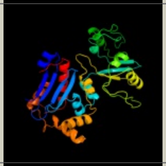
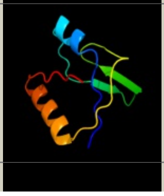
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A8V2 |
| Date | Wed Jan 25 15:20:19 GMT 2012 |
| Unique Job ID | d381a67183fa0e58 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3iydC_ | Alignment |  | 100.0 | 99 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex |
| 2 | d1smyc_ | Alignment |  | 100.0 | 50 | **Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Family:**RNA-polymerase beta |
| 3 | d1ynjc1 | Alignment |  | 100.0 | 50 | **Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Family:**RNA-polymerase beta |
| 4 | c2pmzB_ | Alignment |  | 100.0 | 31 | **PDB header:**translation, transferase<br>**Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit b;<br>**PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus |
| 5 | c3h0gN_ | Alignment |  | 100.0 | 27 | **PDB header:**transcription<br>**Chain:** N: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb2;<br>**PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 6 | d1twfb_ | Alignment |  | 100.0 | 30 | **Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Family:**RNA-polymerase beta |
| 7 | c3mlqD_ | Alignment |  | 100.0 | 54 | **PDB header:**transferase/transcription<br>**Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain |
| 8 | c3mlqB_ | Alignment |  | 100.0 | 59 | **PDB header:**transferase/transcription<br>**Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain |
| 9 | c3tbiB_ | Alignment |  | 100.0 | 100 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain |
| 10 | c3ltiA_ | Alignment |  | 100.0 | 92 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains |
| 11 | c3qqcA_ | Alignment |  | 99.4 | 23 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit b, dna-directed rna<br>**PDBTitle:** crystal structure of archaeal spt4/5 bound to the rnap clamp domain |

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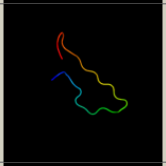
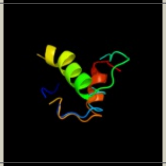
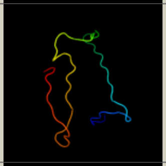
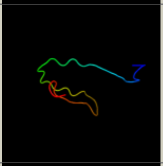
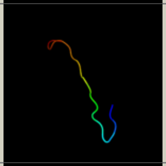
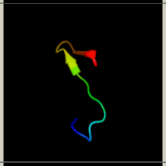
| 12 | c3e7hA_ | Alignment |  | 95.6 | 75 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor |
| 13 | d1r46a1 | Alignment |  | 50.9 | 20 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**alpha-Amylases, C-terminal beta-sheet domain |
| 14 | c1gjjA_ | Alignment |  | 50.3 | 20 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**lap2;<br>**PDBTitle:** n-terminal constant region of the nuclear envelope protein2 lap2 |
| 15 | c2gtiA_ | Alignment |  | 41.6 | 14 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**replicase polyprotein 1ab;<br>**PDBTitle:** mutation of mhv coronavirus non-structural protein nsp15 (f307l) |
| 16 | d1n26a2 | Alignment |  | 30.8 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Fibronectin type III<br>**Family:**Fibronectin type III |
| 17 | d2eyqa5 | Alignment |  | 28.1 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Tandem AAA-ATPase domain |
| 18 | d1gm5a4 | Alignment |  | 27.8 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Tandem AAA-ATPase domain |
| 19 | d1y4oa1 | Alignment |  | 26.6 | 53 | **Fold:**Profilin-like<br>**Superfamily:**Roadblock/LC7 domain<br>**Family:**Roadblock/LC7 domain |
| 20 | d2f3na1 | Alignment |  | 25.7 | 10 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 21 | d1zq1c1 | Alignment | not modelled | 24.5 | 36 | **Fold:**GatB/YqeY motif<br>**Superfamily:**GatB/YqeY motif<br>**Family:**GatB/GatE C-terminal domain-like |
| 22 | c2db3D_ | Alignment | not modelled | 24.0 | 38 | **PDB header:**hydrolase/rna<br>**Chain:** D: **PDB Molecule:**atp-dependent rna helicase vasa;<br>**PDBTitle:** structural basis for rna unwinding by the dead-box protein2 drosophila vasa |
| 23 | d2g7ja1 | Alignment | not modelled | 22.8 | 32 | **Fold:**Secretion chaperone-like<br>**Superfamily:**YgaC/TfoX-N like<br>**Family:**YgaC-like |
| 24 | d1nbwa1 | Alignment | not modelled | 21.4 | 17 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit<br>**Family:**Swiveling domain of dehydratase reactivase alpha subunit |
| 25 | d2gtia2 | Alignment | not modelled | 21.2 | 10 | **Fold:**EndoU-like<br>**Superfamily:**EndoU-like<br>**Family:**Nsp15 C-terminal domain-like |
| 26 | c2c2lD_ | Alignment | not modelled | 20.5 | 19 | **PDB header:**chaperone<br>**Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein;<br>**PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase |
| 27 | d1sy7a1 | Alignment | not modelled | 20.5 | 15 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Catalase, C-terminal domain |
| 28 | c2aujD_ | Alignment | not modelled | 20.4 | 33 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain;<br>**PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert |
| 29 | c3mjhD_ | Alignment | not modelled | 19.3 | 38 | **PDB header:**protein transport<br>**Chain:** D: **PDB Molecule:**early endosome antigen 1;<br>**PDBTitle:** crystal structure of human rab5a in complex with the |

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| | | | | | | c2h2 zinc finger2 of eea1 |
| 30 | c3bxzA_ | Alignment | not modelled | 19.2 | 33 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**preprotein translocase subunit seca;<br>**PDBTitle:** crystal structure of the isolated dead motor domains from2 escherichia coli seca |
| 31 | c3cwiA_ | Alignment | not modelled | 18.9 | 22 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this;<br>**PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137 |
| 32 | d1d02a_ | Alignment | not modelled | 18.7 | 17 | **Fold:**Restriction endonuclease-like<br>**Superfamily:**Restriction endonuclease-like<br>**Family:**Restriction endonuclease MunI |
| 33 | d1ujpa_ | Alignment | not modelled | 18.4 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 34 | c3izbX_ | Alignment | not modelled | 18.3 | 63 | **PDB header:**ribosome<br>**Chain:** X: **PDB Molecule:**40s ribosomal protein rps27 (s27e);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 35 | d1jqna_ | Alignment | not modelled | 18.1 | 29 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Phosphoenolpyruvate carboxylase |
| 36 | d1tf5a4 | Alignment | not modelled | 17.7 | 33 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Tandem AAA-ATPase domain |
| 37 | c3kdeC_ | Alignment | not modelled | 17.6 | 19 | **PDB header:**dna binding protein/dna<br>**Chain:** C: **PDB Molecule:**transposable element p transposase;<br>**PDBTitle:** crystal structure of the thap domain from d. melanogaster p-element2 transposase in complex with its natural dna binding site |
| 38 | c2nu9E_ | Alignment | not modelled | 16.8 | 18 | **PDB header:**ligase<br>**Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain;<br>**PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form |
| 39 | c3bq7A_ | Alignment | not modelled | 16.2 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diacylglycerol kinase delta;<br>**PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g) |
| 40 | c2hsiB_ | Alignment | not modelled | 16.2 | 25 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative peptidase m23;<br>**PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium |
| 41 | d1cf2o2 | Alignment | not modelled | 16.0 | 31 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 42 | c3lvwA_ | Alignment | not modelled | 16.0 | 18 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**glutamate--cysteine ligase;<br>**PDBTitle:** glutathione-inhibited scgcl |
| 43 | c3u5cI_ | Alignment | not modelled | 15.4 | 22 | **PDB header:**ribosome<br>**Chain:** I: **PDB Molecule:**40s ribosomal protein s8-a;<br>**PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution |
| 44 | c2ivfC_ | Alignment | not modelled | 15.3 | 38 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**ethylbenzene dehydrogenase gamma-subunit;<br>**PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 45 | c2bhmE_ | Alignment | not modelled | 15.2 | 24 | **PDB header:**bacterial protein<br>**Chain:** E: **PDB Molecule:**type iv secretion system protein virb8;<br>**PDBTitle:** crystal structure of virb8 from brucella suis |
| 46 | c3iz6X_ | Alignment | not modelled | 15.2 | 75 | **PDB header:**ribosome<br>**Chain:** X: **PDB Molecule:**40s ribosomal protein s27 (s27e);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 47 | c6paxA_ | Alignment | not modelled | 14.3 | 22 | **PDB header:**gene regulation/dna<br>**Chain:** A: **PDB Molecule:**homeobox protein pax-6;<br>**PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions |
| 48 | d2bpa2_ | Alignment | not modelled | 14.1 | 31 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**ssDNA viruses<br>**Family:**Microviridae-like VP |
| 49 | d2d6fc2 | Alignment | not modelled | 13.6 | 46 | **Fold:**DCoH-like<br>**Superfamily:**GAD domain-like<br>**Family:**GAD domain |
| 50 | c2vb0A_ | Alignment | not modelled | 13.4 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**polyprotein 3bcd;<br>**PDBTitle:** crystal structure of coxsackievirus b3 proteinase 3c |
| 51 | d2hz5a1 | Alignment | not modelled | 13.1 | 59 | **Fold:**Profilin-like<br>**Superfamily:**Roadblock/LC7 domain<br>**Family:**Roadblock/LC7 domain |
| 52 | c3eq5G_ | Alignment | not modelled | 12.9 | 18 | **PDB header:**signaling protein<br>**Chain:** G: **PDB Molecule:**ski-like protein;<br>**PDBTitle:** crystal structure of fragment 137 to 238 of the human ski-like protein |
| 53 | c1m1jA_ | Alignment | not modelled | 12.9 | 38 | **PDB header:**blood clotting<br>**Chain:** A: **PDB Molecule:**fibrinogen alpha subunit;<br>**PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands |
| 54 | d2gpra_ | Alignment | not modelled | 12.6 | 17 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |

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| 55 | d1dcza_ | Alignment | not modelled | 12.4 | 27 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 56 | d1flja_ | Alignment | not modelled | 12.2 | 33 | **Fold:**Carbonic anhydrase<br>**Superfamily:**Carbonic anhydrase<br>**Family:**Carbonic anhydrase |
| 57 | d2pxyd2 | Alignment | not modelled | 12.2 | 56 | **Fold:**MHC antigen-recognition domain<br>**Superfamily:**MHC antigen-recognition domain<br>**Family:**MHC antigen-recognition domain |
| 58 | c3dlmA_ | Alignment | not modelled | 12.1 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setdb1;<br>**PDBTitle:** crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1 |
| 59 | c2qm3A_ | Alignment | not modelled | 11.8 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**predicted methyltransferase;<br>**PDBTitle:** crystal structure of a predicted methyltransferase from pyrococcus2 furiosus |
| 60 | d1px5a1 | Alignment | not modelled | 11.7 | 28 | **Fold:**PAP/OAS1 substrate-binding domain<br>**Superfamily:**PAP/OAS1 substrate-binding domain<br>**Family:**2'-5'-oligoadenylate synthetase 1, OAS1, second domain |
| 61 | c2cwpA_ | Alignment | not modelled | 11.7 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**metrs related protein;<br>**PDBTitle:** crystal structure of metrs related protein from pyrococcus horikoshii |
| 62 | c2gu1A_ | Alignment | not modelled | 11.4 | 30 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**zinc peptidase;<br>**PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae |
| 63 | d1lk5a2 | Alignment | not modelled | 11.4 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain<br>**Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain |
| 64 | d1pfva2 | Alignment | not modelled | 11.3 | 40 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain |
| 65 | d2pwwa1 | Alignment | not modelled | 11.2 | 7 | **Fold:**TBP-like<br>**Superfamily:**YugN-like<br>**Family:**YugN-like |
| 66 | d1prtc1 | Alignment | not modelled | 11.1 | 14 | **Fold:**OB-fold<br>**Superfamily:**Bacterial enterotoxins<br>**Family:**Bacterial AB5 toxins, B-subunits |
| 67 | c2f1mA_ | Alignment | not modelled | 11.1 | 20 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**acriflavine resistance protein a;<br>**PDBTitle:** conformational flexibility in the multidrug efflux system protein acra |
| 68 | d1glaf_ | Alignment | not modelled | 10.8 | 20 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |
| 69 | c2oy7A_ | Alignment | not modelled | 10.7 | 13 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer surface protein a;<br>**PDBTitle:** the crystal structure of ospa mutant |
| 70 | d1gjja1 | Alignment | not modelled | 10.5 | 29 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**LEM domain<br>**Family:**LEM domain |
| 71 | c2hxyC_ | Alignment | not modelled | 10.3 | 33 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**probable atp-dependent rna helicase ddx48;<br>**PDBTitle:** crystal structure of human apo-eif4aiii |
| 72 | c2dneA_ | Alignment | not modelled | 10.2 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase<br>**PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase |
| 73 | c2pjmA_ | Alignment | not modelled | 10.2 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a;<br>**PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii |
| 74 | c3nyyA_ | Alignment | not modelled | 10.2 | 32 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm;<br>**PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution |
| 75 | d1m0sa2 | Alignment | not modelled | 10.2 | 19 | **Fold:**Ferredoxin-like<br>**Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain<br>**Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain |
| 76 | d1pk1c1 | Alignment | not modelled | 10.2 | 3 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 77 | d1f46a_ | Alignment | not modelled | 10.1 | 57 | **Fold:**TBP-like<br>**Superfamily:**Cell-division protein ZipA, C-terminal domain<br>**Family:**Cell-division protein ZipA, C-terminal domain |
| 78 | c3ghgD_ | Alignment | not modelled | 10.0 | 29 | **PDB header:**blood clotting<br>**Chain:** D: **PDB Molecule:**fibrinogen alpha chain;<br>**PDBTitle:** crystal structure of human fibrinogen |
| 79 | c1pk1A_ | Alignment | not modelled | 9.9 | 5 | **PDB header:**transcription repression<br>**Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein;<br>**PDBTitle:** hetero sam domain structure of ph and scm. |
| 80 | c1pd7B_ | Alignment | not modelled | 9.9 | 60 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**mad1;<br>**PDBTitle:** extended sid of mad1 bound to the pah2 domain of msin3b |

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| 81 | d1aola_ | Alignment | not modelled | 9.8 | 21 | **Fold:**ENV polyprotein, receptor-binding domain<br>**Superfamily:**ENV polyprotein, receptor-binding domain<br>**Family:**ENV polyprotein, receptor-binding domain |
| 82 | c2jgnB_ | Alignment | not modelled | 9.7 | 24 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx3x;<br>**PDBTitle:** ddx3 helicase domain |
| 83 | c3gekA_ | Alignment | not modelled | 9.7 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative thioesterase yhda;<br>**PDBTitle:** crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113 |
| 84 | d1prtb1 | Alignment | not modelled | 9.7 | 14 | **Fold:**OB-fold<br>**Superfamily:**Bacterial enterotoxins<br>**Family:**Bacterial AB5 toxins, B-subunits |
| 85 | d1luga_ | Alignment | not modelled | 9.6 | 33 | **Fold:**Carbonic anhydrase<br>**Superfamily:**Carbonic anhydrase<br>**Family:**Carbonic anhydrase |
| 86 | d2c4ka1 | Alignment | not modelled | 9.5 | 13 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosylpyrophosphate synthetase-like |
| 87 | c3kizA_ | Alignment | not modelled | 9.5 | 27 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase;<br>**PDBTitle:** crystal structure of putative phosphoribosylformylglycinamidine cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution |
| 88 | c1a1vA_ | Alignment | not modelled | 9.5 | 26 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**protein (ns3 protein);<br>**PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna |
| 89 | d1m5ha1 | Alignment | not modelled | 9.5 | 42 | **Fold:**Ferredoxin-like<br>**Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase<br>**Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase |
| 90 | d2d0oa1 | Alignment | not modelled | 9.4 | 12 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit<br>**Family:**Swiveling domain of dehydratase reactivase alpha subunit |
| 91 | d1u9ya1 | Alignment | not modelled | 9.4 | 20 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosylpyrophosphate synthetase-like |
| 92 | d1ftra1 | Alignment | not modelled | 9.4 | 54 | **Fold:**Ferredoxin-like<br>**Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase<br>**Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase |
| 93 | d1gpra_ | Alignment | not modelled | 9.3 | 25 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |
| 94 | d1vf7a_ | Alignment | not modelled | 9.3 | 27 | **Fold:**HlyD-like secretion proteins<br>**Superfamily:**HlyD-like secretion proteins<br>**Family:**HlyD-like secretion proteins |
| 95 | c2xzm6_ | Alignment | not modelled | 9.2 | 63 | **PDB header:**ribosome<br>**Chain:** 6: **PDB Molecule:**rps27e;<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 1 |
| 96 | d1m5sa1 | Alignment | not modelled | 9.2 | 42 | **Fold:**Ferredoxin-like<br>**Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase<br>**Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase |
| 97 | d1qxfa_ | Alignment | not modelled | 9.2 | 33 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein S27e |
| 98 | c2kkpA_ | Alignment | not modelled | 9.2 | 36 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**phage integrase;<br>**PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171). |
| 99 | c2fyuE_ | Alignment | not modelled | 9.1 | 43 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit,<br>**PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor |