# Phyre$^2$

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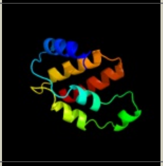
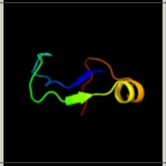
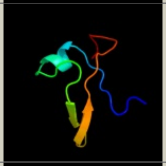
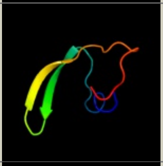
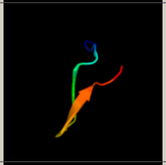
| Description | P77504 |
| Date | Thu Jan 5 12:30:05 GMT 2012 |
| Unique Job ID | 07352cab8308d1f3 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3ftjA_ | Alignment |  | 99.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**macrolide export atp-binding/permease protein<br>**PDBTitle:** crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans |
| 2 | c3is6A_ | Alignment |  | 98.7 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**putative permease protein, abc transporter;<br>**PDBTitle:** the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a |
| 3 | c2a8vA_ | Alignment |  | 81.8 | 27 | **PDB header:**protein/rna<br>**Chain:** A: **PDB Molecule:**rna binding domain of rho transcription<br>**PDBTitle:** rho transcription termination factor/rna complex |
| 4 | c1ciiA_ | Alignment |  | 81.1 | 15 | **PDB header:**transmembrane protein<br>**Chain:** A: **PDB Molecule:**colicin ia;<br>**PDBTitle:** colicin ia |
| 5 | d1a62a2 | Alignment |  | 80.0 | 27 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 6 | d1e32a1 | Alignment |  | 73.6 | 16 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Cdc48 N-terminal domain-like |
| 7 | d1cz5a1 | Alignment |  | 64.6 | 18 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Cdc48 N-terminal domain-like |
| 8 | d2d6fa1 | Alignment |  | 64.1 | 15 | **Fold:**Sm-like fold<br>**Superfamily:**GatD N-terminal domain-like<br>**Family:**GatD N-terminal domain-like |
| 9 | d2f9ha1 | Alignment |  | 63.7 | 26 | **Fold:**PTSIIA/GutA-like<br>**Superfamily:**PTSIIA/GutA-like<br>**Family:**PTSIIA/GutA-like |
| 10 | c1cz5A_ | Alignment |  | 59.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**vcp-like atpase;<br>**PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma) |
| 11 | d1udxa3 | Alignment |  | 55.1 | 13 | **Fold:**Obg GTP-binding protein C-terminal domain<br>**Superfamily:**Obg GTP-binding protein C-terminal domain<br>**Family:**Obg GTP-binding protein C-terminal domain |

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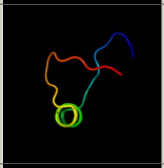
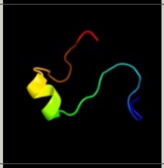
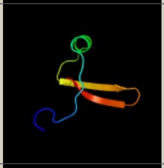
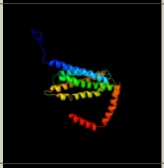
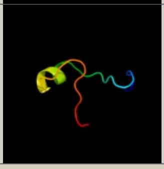
| 12 | d1zq1a1 | Alignment |  | 54.3 | 11 | **Fold:**Sm-like fold<br>**Superfamily:**GatD N-terminal domain-like<br>**Family:**GatD N-terminal domain-like |
| 13 | d1ylea1 | Alignment |  | 51.2 | 15 | **Fold:**Acyl-CoA N-acyltransferases (Nat)<br>**Superfamily:**Acyl-CoA N-acyltransferases (Nat)<br>**Family:**AstA-like |
| 14 | c2pjhB_ | Alignment |  | 48.2 | 15 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase;<br>**PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex |
| 15 | c3k07A_ | Alignment |  | 43.4 | 14 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cation efflux system protein cusa;<br>**PDBTitle:** crystal structure of cusa |
| 16 | c1wlfA_ | Alignment |  | 39.9 | 17 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1;<br>**PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain |
| 17 | d2jioa1 | Alignment |  | 39.0 | 17 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 18 | c1oy8A_ | Alignment |  | 37.7 | 12 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**acriflavine resistance protein b;<br>**PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump |
| 19 | c2fhdA_ | Alignment |  | 35.7 | 12 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2;<br>**PDBTitle:** crystal structure of crb2 tandem tudor domains |
| 20 | c2yujA_ | Alignment |  | 32.5 | 24 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like;<br>**PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1 |
| 21 | c1zc1A_ | Alignment | not modelled | 32.3 | 21 | **PDB header:**protein turnover<br>**Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1;<br>**PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites |
| 22 | d1ub4c_ | Alignment | not modelled | 32.0 | 32 | **Fold:**Double-split beta-barrel<br>**Superfamily:**AbrB/MazE/MraZ-like<br>**Family:**Kis/Peml addiction antidote |
| 23 | d1ogya1 | Alignment | not modelled | 30.5 | 17 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 24 | c3l0oB_ | Alignment | not modelled | 29.1 | 30 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**transcription termination factor rho;<br>**PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima |
| 25 | c1xpuB_ | Alignment | not modelled | 28.9 | 27 | **PDB header:**transcription/rna<br>**Chain:** B: **PDB Molecule:**rho transcription termination factor;<br>**PDBTitle:** structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb) |
| 26 | d1g8ka1 | Alignment | not modelled | 28.7 | 27 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 27 | d1h0ha1 | Alignment | not modelled | 28.2 | 24 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 28 | c2glwA_ | Alignment | not modelled | 25.0 | 35 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**92aa long hypothetical protein;<br>**PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii |

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| 29 | d1vlfm1 | Alignment | not modelled | 24.4 | 12 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 30 | d2iv2x1 | Alignment | not modelled | 23.8 | 12 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 31 | d1rqpa1 | Alignment | not modelled | 23.7 | 27 | **Fold:**Bacterial fluorinating enzyme, C-terminal domain<br>**Superfamily:**Bacterial fluorinating enzyme, C-terminal domain<br>**Family:**Bacterial fluorinating enzyme, C-terminal domain |
| 32 | d1kqfa1 | Alignment | not modelled | 23.6 | 26 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 33 | d1mvfd_ | Alignment | not modelled | 23.5 | 16 | **Fold:**Double-split beta-barrel<br>**Superfamily:**AbrB/MazE/MraZ-like<br>**Family:**Kis/PemI addiction antidote |
| 34 | d1tmoa1 | Alignment | not modelled | 22.8 | 21 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 35 | d1y5ia1 | Alignment | not modelled | 21.4 | 22 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 36 | c1zq1B_ | Alignment | not modelled | 21.2 | 13 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d;<br>**PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi |
| 37 | c2cw5B_ | Alignment | not modelled | 20.6 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**bacterial fluorinating enzyme homolog;<br>**PDBTitle:** crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8 |
| 38 | c3ltiA_ | Alignment | not modelled | 20.4 | 13 | **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 |
| 39 | c2iv2X_ | Alignment | not modelled | 19.2 | 13 | **PDB header:**oxidoreductase<br>**Chain:** X: **PDB Molecule:**formate dehydrogenase h;<br>**PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli |
| 40 | c2p4vA_ | Alignment | not modelled | 18.0 | 19 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation factor greb;<br>**PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution |
| 41 | d1eu1a1 | Alignment | not modelled | 17.8 | 10 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 42 | c2zbvC_ | Alignment | not modelled | 17.0 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**uncharacterized conserved protein;<br>**PDBTitle:** crystal structure of uncharacterized conserved protein from thermotoga2 maritima |
| 43 | c2q6oB_ | Alignment | not modelled | 16.4 | 23 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** sall-y70t with sam and cl |
| 44 | c2w1tB_ | Alignment | not modelled | 16.1 | 17 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**stage v sporulation protein t;<br>**PDBTitle:** crystal structure of b. subtilis spovt |
| 45 | d1dmra1 | Alignment | not modelled | 15.7 | 18 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain |
| 46 | c2f4nA_ | Alignment | not modelled | 15.5 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein mj1651;<br>**PDBTitle:** crystal structure of protein mj1651 from methanococcus2 jannaschii dsm 2661, pfam duf62 |
| 47 | c3cfuA_ | Alignment | not modelled | 14.9 | 14 | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha;<br>**PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562 |
| 48 | c2d6fA_ | Alignment | not modelled | 14.8 | 15 | **PDB header:**ligase/rna<br>**Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d;<br>**PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln) |
| 49 | c1eu1A_ | Alignment | not modelled | 14.3 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase;<br>**PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments. |
| 50 | c1wu8B_ | Alignment | not modelled | 14.1 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein ph0463;<br>**PDBTitle:** crystal structure of project ph0463 from pyrococcus horikoshii ot3 |
| 51 | c2ki8A_ | Alignment | not modelled | 14.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase,<br>**PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7 |
| 52 | d1dzfa2 | Alignment | not modelled | 14.0 | 28 | **Fold:**RPB5-like RNA polymerase subunit<br>**Superfamily:**RPB5-like RNA polymerase subunit<br>**Family:**RPB5 |
| | | | | | | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; |

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| 53 | c2v45A_ | Alignment | not modelled | 14.0 | 17 | **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand |
| 54 | d1guta_ | Alignment | not modelled | 13.7 | 14 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
| 55 | d2vbua1 | Alignment | not modelled | 13.7 | 32 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin kinase-like<br>**Family:**CTP-dependent riboflavin kinase-like |
| 56 | d1hmja_ | Alignment | not modelled | 13.2 | 17 | **Fold:**RPB5-like RNA polymerase subunit<br>**Superfamily:**RPB5-like RNA polymerase subunit<br>**Family:**RPB5 |
| 57 | c2nyaF_ | Alignment | not modelled | 13.2 | 19 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**periplasmic nitrate reductase;<br>**PDBTitle:** crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli |
| 58 | d1h9ma1 | Alignment | not modelled | 12.5 | 14 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 59 | d1fr3a_ | Alignment | not modelled | 12.4 | 23 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
| 60 | c1rqrA_ | Alignment | not modelled | 12.2 | 27 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**5'-fluoro-5'-deoxyadenosine synthase;<br>**PDBTitle:** crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex |
| 61 | c3pjyB_ | Alignment | not modelled | 12.0 | 21 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**hypothetical signal peptide protein;<br>**PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution |
| 62 | c1g8jC_ | Alignment | not modelled | 11.9 | 27 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**arsenite oxidase;<br>**PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis |
| 63 | c2cwbA_ | Alignment | not modelled | 11.9 | 16 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g<br>**PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin |
| 64 | d1h9ma2 | Alignment | not modelled | 11.8 | 23 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 65 | d2f23a2 | Alignment | not modelled | 11.8 | 18 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**GreA transcript cleavage factor, C-terminal domain |
| 66 | c1h0hA_ | Alignment | not modelled | 11.7 | 24 | **PDB header:**dehydrogenase<br>**Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit);<br>**PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas |
| 67 | c2etnA_ | Alignment | not modelled | 11.6 | 16 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor<br>**PDBTitle:** crystal structure of thermus aquaticus gfh1 |
| 68 | c2kncA_ | Alignment | not modelled | 11.5 | 20 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-iib;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 69 | d1p9ka_ | Alignment | not modelled | 11.5 | 11 | **Fold:**Alpha-L RNA-binding motif<br>**Superfamily:**Alpha-L RNA-binding motif<br>**Family:**YbcJ-like |
| 70 | d1dgsa2 | Alignment | not modelled | 11.4 | 15 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**DNA ligase/mRNA capping enzyme postcatalytic domain |
| 71 | c2l66B_ | Alignment | not modelled | 11.4 | 20 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family;<br>**PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea. |
| 72 | c3m7aA_ | Alignment | not modelled | 11.3 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution |
| 73 | c2ivfA_ | Alignment | not modelled | 11.3 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit;<br>**PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 74 | c2e7zA_ | Alignment | not modelled | 11.2 | 8 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**acetylene hydratase ahy;<br>**PDBTitle:** acetylene hydratase from pelobacter acetylenicus |
| 75 | d2d9ra1 | Alignment | not modelled | 11.2 | 21 | **Fold:**Double-split beta-barrel<br>**Superfamily:**AF2212/PG0164-like<br>**Family:**PG0164-like |
| 76 | c3h43F_ | Alignment | not modelled | 11.1 | 10 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase;<br>**PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii |
| 77 | c2dahA_ | Alignment | not modelled | 11.1 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ubiquilin-3;<br>**PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3 |
| 78 | c1tmoA_ | Alignment | not modelled | 10.9 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase;<br>**PDBTitle:** trimethylamine n-oxide reductase from shewanella |

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| 79 | d2dnaa1 | Alignment | not modelled | 10.8 | 8 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 80 | d1k0ha_ | Alignment | not modelled | 10.7 | 20 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**gpFII-like |
| 81 | d2bwba1 | Alignment | not modelled | 10.7 | 8 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 82 | c2fugC_ | Alignment | not modelled | 10.5 | 16 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3;<br>**PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 83 | c3l53F_ | Alignment | not modelled | 10.4 | 28 | **PDB header:**structural genomics, unknown function<br>**Chain:** F: **PDB Molecule:**putative fumarylacetoacetate isomerase/hydrolase;<br>**PDBTitle:** crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica |
| 84 | c2zpmA_ | Alignment | not modelled | 10.4 | 33 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**regulator of sigma e protease;<br>**PDBTitle:** crystal structure analysis of pdz domain b |
| 85 | c2wg6L_ | Alignment | not modelled | 10.4 | 17 | **PDB header:**transcription,hydrolase<br>**Chain:** L: **PDB Molecule:**general control protein gcn4,<br>**PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant |
| 86 | c1wr1B_ | Alignment | not modelled | 10.4 | 8 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2;<br>**PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin |
| 87 | c1h5nC_ | Alignment | not modelled | 10.3 | 18 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**dmso reductase;<br>**PDBTitle:** dmso reductase modified by the presence of dms and air |
| 88 | d4ubpc1 | Alignment | not modelled | 10.2 | 21 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**alpha-Subunit of urease |
| 89 | c2ro5B_ | Alignment | not modelled | 9.9 | 22 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**stage v sporulation protein t;<br>**PDBTitle:** rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt |
| 90 | c2k29A_ | Alignment | not modelled | 9.8 | 7 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**antitoxin relb;<br>**PDBTitle:** structure of the dbd domain of e. coli antitoxin relb |
| 91 | c1kqgA_ | Alignment | not modelled | 9.8 | 27 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit;<br>**PDBTitle:** formate dehydrogenase n from e. coli |
| 92 | c2kncB_ | Alignment | not modelled | 9.7 | 15 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 93 | d2cqaa1 | Alignment | not modelled | 9.7 | 28 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**TIP49 domain |
| 94 | d2etna2 | Alignment | not modelled | 9.7 | 16 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**GreA transcript cleavage factor, C-terminal domain |
| 95 | d2daha1 | Alignment | not modelled | 9.6 | 12 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| 96 | c1ogyA_ | Alignment | not modelled | 9.6 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**periplasmic nitrate reductase;<br>**PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides |
| 97 | d1h9ra1 | Alignment | not modelled | 9.5 | 24 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 98 | c1vlfQ_ | Alignment | not modelled | 9.5 | 12 | **PDB header:**oxidoreductase<br>**Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit;<br>**PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene |
| 99 | d2cu3a1 | Alignment | not modelled | 9.4 | 17 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |