Phyre$^2$

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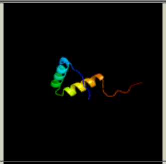
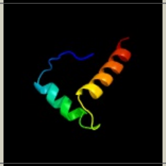
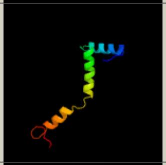
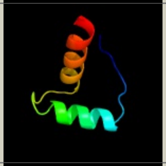
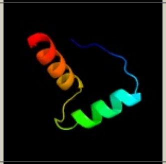
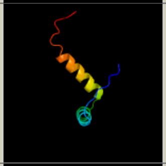
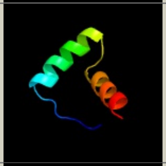
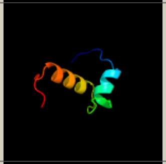
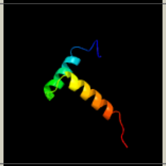
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2871_(-)_3183148_3183405 |
| Date | Wed Aug 7 12:50:54 BST 2019 |
| Unique Job ID | ba943b1ea2457b55 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c5x3tA_ | Alignment |  | 96.4 | 31 | **PDB header:**antitoxin/toxin<br>**Chain:** A: **PDB Molecule:**antitoxin vapb26;<br>**PDBTitle:** vapbc from mycobacterium tuberculosis |
| 2 | c2bj3D_ | Alignment |  | 94.6 | 17 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**nickel responsive regulator;<br>**PDBTitle:** nikr-apo |
| 3 | d2bsqe1 | Alignment |  | 94.2 | 16 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Trafficking protein A-like |
| 4 | c1q5vB_ | Alignment |  | 93.7 | 28 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**nickel responsive regulator;<br>**PDBTitle:** apo-nikr |
| 5 | d2bj7a1 | Alignment |  | 93.7 | 18 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 6 | c2ca9B_ | Alignment |  | 93.2 | 18 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**putative nickel-responsive regulator;<br>**PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation |
| 7 | c2k5jB_ | Alignment |  | 92.6 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein yiif;<br>**PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1 |
| 8 | d1p94a_ | Alignment |  | 92.5 | 30 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 9 | c6a7vU_ | Alignment |  | 92.5 | 39 | **PDB header:**toxin/antitoxin<br>**Chain:** U: **PDB Molecule:**antitoxin vapb11;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex |
| 10 | c2h1oH_ | Alignment |  | 90.8 | 12 | **PDB header:**gene regulation/dna complex<br>**Chain:** H: **PDB Molecule:**trafficking protein a;<br>**PDBTitle:** structure of fitab bound to ir36 dna fragment |
| 11 | d2hzaa1 | Alignment |  | 90.1 | 28 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |

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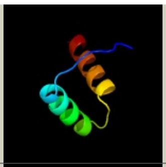
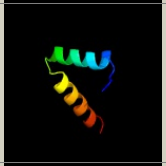
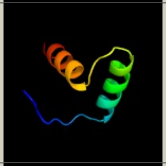
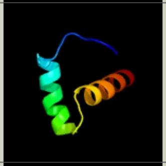
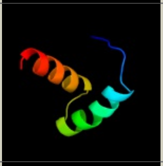
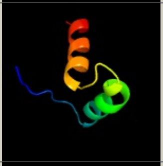
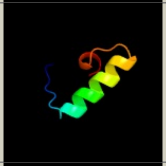
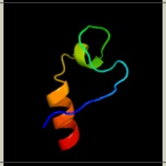
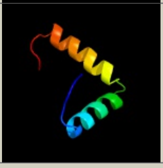
|---|---|---|---|---|---|---|
| 12 | d2hzab1 | Alignment |  | 88.3 | 28 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 13 | c2kelB_ | Alignment |  | 85.5 | 21 | **PDB header:**transcription repressor<br>**Chain:** B: **PDB Molecule:**uncharacterized protein 56b;<br>**PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1 |
| 14 | c6g1nB_ | Alignment |  | 85.0 | 23 | **PDB header:**antitoxin<br>**Chain:** B: **PDB Molecule:**antitoxin hicb;<br>**PDBTitle:** crystal structure of the burkholderia pseudomallei antitoxin hicb |
| 15 | c4a1qB_ | Alignment |  | 84.8 | 26 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**orf e73;<br>**PDBTitle:** solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park |
| 16 | c4aaiB_ | Alignment |  | 84.8 | 26 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**orf e73;<br>**PDBTitle:** thermostable protein from hyperthermophilic virus ssv-rh |
| 17 | c4p7dA_ | Alignment |  | 81.5 | 13 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**antitoxin hicb3;<br>**PDBTitle:** antitoxin hicb3 crystal structure |
| 18 | c3kk4B_ | Alignment |  | 81.1 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein bp1543;<br>**PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i |
| 19 | c5yrzC_ | Alignment |  | 77.4 | 19 | **PDB header:**antitoxin/hydrolase<br>**Chain:** C: **PDB Molecule:**hicb;<br>**PDBTitle:** toxin-antitoxin complex from streptococcus pneumoniae |
| 20 | c2k29A_ | Alignment |  | 72.5 | 24 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**antitoxin relb;<br>**PDBTitle:** structure of the dbd domain of e. coli antitoxin relb |
| 21 | c6iyaD_ | Alignment | not modelled | 69.6 | 16 | **PDB header:**antitoxin<br>**Chain:** D: **PDB Molecule:**transcriptional regulator copg family;<br>**PDBTitle:** structure of the dna binding domain of antitoxin copaso |
| 22 | c4hv0B_ | Alignment | not modelled | 69.3 | 19 | **PDB header:**transcription, viral protein<br>**Chain:** B: **PDB Molecule:**avtr;<br>**PDBTitle:** structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus |
| 23 | d2cpga_ | Alignment | not modelled | 67.8 | 18 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 24 | c1ea4K_ | Alignment | not modelled | 67.7 | 18 | **PDB header:**gene regulation/dna<br>**Chain:** K: **PDB Molecule:**transcriptional repressor copg;<br>**PDBTitle:** transcriptional repressor copg/22bp dsdna complex |
| 25 | d1mnta_ | Alignment | not modelled | 64.3 | 26 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**Arc/Mnt-like phage repressors |
| 26 | c2an7A_ | Alignment | not modelled | 62.9 | 34 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**protein pard;<br>**PDBTitle:** solution structure of the bacterial antidote pard |
| 27 | c2k6lA_ | Alignment | not modelled | 52.6 | 29 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** the solution structure of xacb0070 from xanthonomas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors |
| 28 | c6ajnF_ | Alignment | not modelled | 47.5 | 18 | **PDB header:**toxin<br>**Chain:** F: **PDB Molecule:**duf1778 domain-containing protein;<br>**PDBTitle:** crystal structure of atatr bound with accoa |
| | | | | | | **Fold:**Ribbon-helix-helix |

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| 29 | d1y9ba1 | Alignment | not modelled | 45.5 | 21 | **Superfamily:**Ribbon-helix-helix<br>**Family:**VCA0319-like |
| 30 | c1xrxD_ | Alignment | not modelled | 40.9 | 38 | **PDB header:**replication inhibitor<br>**Chain:** D: **PDB Molecule:**seqa protein;<br>**PDBTitle:** crystal structure of a dna-binding protein |
| 31 | d1xrxa1 | Alignment | not modelled | 40.9 | 38 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**SeqA N-terminal domain-like |
| 32 | c2rbfB_ | Alignment | not modelled | 39.4 | 22 | **PDB header:**oxidoreductase/dna<br>**Chain:** B: **PDB Molecule:**bifunctional protein puta;<br>**PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2) |
| 33 | c3kxeD_ | Alignment | not modelled | 39.3 | 15 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**antitoxin protein pard-1;<br>**PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex |
| 34 | c4fxeB_ | Alignment | not modelled | 37.9 | 24 | **PDB header:**toxin/toxin inhibitor<br>**Chain:** B: **PDB Molecule:**antitoxin relb;<br>**PDBTitle:** crystal structure of the intact e. coli relbe toxin-antitoxin complex |
| 35 | c1u9pA_ | Alignment | not modelled | 37.2 | 21 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**parc;<br>**PDBTitle:** permuted single-chain arc |
| 36 | c2mdvB_ | Alignment | not modelled | 31.8 | 19 | **PDB header:**de novo protein<br>**Chain:** B: **PDB Molecule:**designed protein;<br>**PDBTitle:** nmr structure of beta alpha alpha 38 |
| 37 | d1q9ja2 | Alignment | not modelled | 30.7 | 13 | **Fold:**CoA-dependent acyltransferases<br>**Superfamily:**CoA-dependent acyltransferases<br>**Family:**NRPS condensation domain (amide synthase) |
| 38 | c6bwqB_ | Alignment | not modelled | 30.5 | 16 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel<br>**PDBTitle:** larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp |
| 39 | c6gtsC_ | Alignment | not modelled | 29.7 | 13 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**duf1778 domain-containing protein;<br>**PDBTitle:** structure of the atat-atar complex bound dna |
| 40 | c4pg8B_ | Alignment | not modelled | 26.8 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of s. aureus homoserine dehydrogenase at ph8.5 |
| 41 | c4q2uM_ | Alignment | not modelled | 26.6 | 21 | **PDB header:**toxin/toxin repressor<br>**Chain:** M: **PDB Molecule:**antitoxin dinj;<br>**PDBTitle:** crystal structure of the e. coli dinj-yafq toxin-antitoxin complex |
| 42 | d1rkta2 | Alignment | not modelled | 25.1 | 18 | **Fold:**Tetracyclin repressor-like, C-terminal domain<br>**Superfamily:**Tetracyclin repressor-like, C-terminal domain<br>**Family:**Tetracyclin repressor-like, C-terminal domain |
| 43 | c3fmtF_ | Alignment | not modelled | 21.3 | 35 | **PDB header:**replication inhibitor/dna<br>**Chain:** F: **PDB Molecule:**protein seqa;<br>**PDBTitle:** crystal structure of seqa bound to dna |
| 44 | d1vhib_ | Alignment | not modelled | 18.8 | 28 | **Fold:**Ferredoxin-like<br>**Superfamily:**Viral DNA-binding domain<br>**Family:**Viral DNA-binding domain |
| 45 | c3mtjA_ | Alignment | not modelled | 17.1 | 26 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a |
| 46 | c6dzsD_ | Alignment | not modelled | 17.1 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** mycobacterial homoserine dehydrogenase thra in complex with nadp |
| 47 | c1x93B_ | Alignment | not modelled | 16.6 | 17 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**hypothetical protein hp0222;<br>**PDBTitle:** nmr structure of helicobacter pylori hp0222 |
| 48 | c6a6xC_ | Alignment | not modelled | 16.3 | 23 | **PDB header:**toxin<br>**Chain:** C: **PDB Molecule:**antitoxin maze7;<br>**PDBTitle:** the crystal structure of the mtb maze-mazf-mt9 complex |
| 49 | d1x93a1 | Alignment | not modelled | 15.9 | 16 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**CopG-like |
| 50 | c3qoqC_ | Alignment | not modelled | 15.6 | 11 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**alginate and motility regulator z;<br>**PDBTitle:** crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site |
| 51 | c5cegC_ | Alignment | not modelled | 15.4 | 11 | **PDB header:**toxin<br>**Chain:** C: **PDB Molecule:**addiction module antidote protein, copg/arc/metj family;<br>**PDBTitle:** x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum |
| 52 | d1b3ta_ | Alignment | not modelled | 15.3 | 28 | **Fold:**Ferredoxin-like<br>**Superfamily:**Viral DNA-binding domain<br>**Family:**Viral DNA-binding domain |
| 53 | c3do5A_ | Alignment | not modelled | 15.2 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution |
| 54 | d2ve8a1 | Alignment | not modelled | 14.2 | 26 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**FtsK C-terminal domain-like |
| | | | | | | **Fold:**Ribbon-helix-helix |

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| 55 | d1irqa_ | Alignment | not modelled | 14.1 | 24 | **Superfamily:**Ribbon-helix-helix<br>**Family:**Omega transcriptional repressor |
| 56 | c1irqB_ | Alignment | not modelled | 13.9 | 24 | **PDB header:**gene regulation<br>**Chain:** B: **PDB Molecule:**omega transcriptional repressor;<br>**PDBTitle:** crystal structure of omega transcriptional repressor at2 1.5a resolution |
| 57 | d1ebfa2 | Alignment | not modelled | 13.8 | 20 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**Homoserine dehydrogenase-like |
| 58 | c2lxmB_ | Alignment | not modelled | 13.3 | 27 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**charged multivesicular body protein 5;<br>**PDBTitle:** lip5-chmp5 |
| 59 | d1vrpa1 | Alignment | not modelled | 11.8 | 21 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 60 | c3h87D_ | Alignment | not modelled | 11.8 | 18 | **PDB header:**toxin/antitoxin<br>**Chain:** D: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis |
| 61 | c2khvA_ | Alignment | not modelled | 11.7 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**phage integrase;<br>**PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b. |
| 62 | d1puga_ | Alignment | not modelled | 11.7 | 17 | **Fold:**YbaB-like<br>**Superfamily:**YbaB-like<br>**Family:**YbaB-like |
| 63 | d1rfma_ | Alignment | not modelled | 11.6 | 20 | **Fold:**L-sulfolactate dehydrogenase-like<br>**Superfamily:**L-sulfolactate dehydrogenase-like<br>**Family:**L-sulfolactate dehydrogenase-like |
| 64 | c2cw1A_ | Alignment | not modelled | 11.6 | 21 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**sn4m;<br>**PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein |
| 65 | c3opyE_ | Alignment | not modelled | 10.6 | 11 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit;<br>**PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state |
| 66 | c3c8mA_ | Alignment | not modelled | 10.3 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium |
| 67 | d2ay0a1 | Alignment | not modelled | 9.8 | 24 | **Fold:**Ribbon-helix-helix<br>**Superfamily:**Ribbon-helix-helix<br>**Family:**PutA pre-N-terminal region-like |
| 68 | d1u6ra1 | Alignment | not modelled | 9.7 | 29 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 69 | d1crka1 | Alignment | not modelled | 9.7 | 14 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 70 | c3ingA_ | Alignment | not modelled | 9.5 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution |
| 71 | c2ejwB_ | Alignment | not modelled | 9.4 | 33 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**homoserine dehydrogenase;<br>**PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8 |
| 72 | d1i0ea1 | Alignment | not modelled | 9.3 | 36 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 73 | d2g3ba2 | Alignment | not modelled | 9.1 | 21 | **Fold:**Tetracyclin repressor-like, C-terminal domain<br>**Superfamily:**Tetracyclin repressor-like, C-terminal domain<br>**Family:**Tetracyclin repressor-like, C-terminal domain |
| 74 | c3c19A_ | Alignment | not modelled | 9.1 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mk0293;<br>**PDBTitle:** crystal structure of protein mk0293 from methanopyrus kandleri av19 |
| 75 | d1g0wa1 | Alignment | not modelled | 8.7 | 43 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 76 | d2j5pa1 | Alignment | not modelled | 8.7 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**FtsK C-terminal domain-like |
| 77 | c1rrbA_ | Alignment | not modelled | 8.6 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**raf proto-oncogene serine/threonine-protein<br>**PDBTitle:** the ras-binding domain of raf-1 from rat, nmr, 1 structure |
| 78 | c4xb1B_ | Alignment | not modelled | 8.5 | 25 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**319aa long hypothetical homoserine dehydrogenase;<br>**PDBTitle:** hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph |
| 79 | d1m15a1 | Alignment | not modelled | 8.5 | 21 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 80 | d1qh4a1 | Alignment | not modelled | 8.0 | 25 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 81 | c6qeqD_ | Alignment | not modelled | 7.0 | 16 | **PDB header:**dna binding protein<br>**Chain:** D: **PDB Molecule:**pcff; |

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| | | | | | | **PDBTitle:** pcff from enterococcus faecalis pcf10 |
| 82 | d1hwxa2 | Alignment | not modelled | 7.0 | 30 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Aminoacid dehydrogenases |
| 83 | c3i12A_ | Alignment | not modelled | 6.8 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a;<br>**PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 84 | d1qk1a1 | Alignment | not modelled | 6.6 | 18 | **Fold:**Guanido kinase N-terminal domain<br>**Superfamily:**Guanido kinase N-terminal domain<br>**Family:**Guanido kinase N-terminal domain |
| 85 | c6noyB_ | Alignment | not modelled | 6.4 | 33 | **PDB header:**structural protein<br>**Chain:** B: **PDB Molecule:**maintenance of carboxysome positioning b protein, mcsb;<br>**PDBTitle:** structure of cyanothece mcdb |
| 86 | d2outa1 | Alignment | not modelled | 6.4 | 29 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**Rho N-terminal domain-like<br>**Family:**YqbF C-terminal domain-like |
| 87 | c5t81A_ | Alignment | not modelled | 6.0 | 11 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**epob;<br>**PDBTitle:** rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum |
| 88 | d1y88a1 | Alignment | not modelled | 5.8 | 50 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**Hypothetical protein AF1548, C-terminal domain |
| 89 | c3o8oC_ | Alignment | not modelled | 5.4 | 7 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha;<br>**PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae |
| 90 | d1v71a1 | Alignment | not modelled | 5.2 | 23 | **Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 91 | c3d3kD_ | Alignment | not modelled | 5.2 | 17 | **PDB header:**protein binding<br>**Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3;<br>**PDBTitle:** crystal structure of human edc3p |
| 92 | d1gtma2 | Alignment | not modelled | 5.1 | 50 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Aminoacid dehydrogenases |
| 93 | c5k12F_ | Alignment | not modelled | 5.1 | 33 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**glutamate dehydrogenase 1, mitochondrial;<br>**PDBTitle:** cryo-em structure of glutamate dehydrogenase at 1.8 a resolution |