Phyre$^2$

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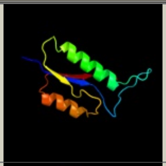
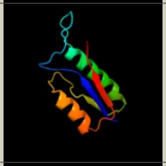
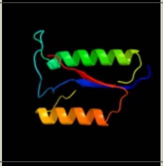
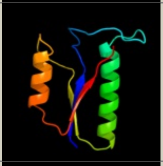
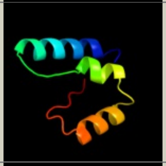
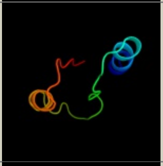
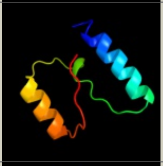
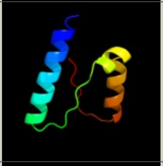
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q1PH25 |
| Date | Thu Jan 5 12:33:27 GMT 2012 |
| Unique Job ID | fa4e939289b68800 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3ne8A_ | Alignment |  | 99.9 | 51 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase;<br>**PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1 |
| 2 | d1jwqa_ | Alignment |  | 99.9 | 47 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**N-acetylmuramoyl-L-alanine amidase-like |
| 3 | c3czxA_ | Alignment |  | 99.9 | 28 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative n-acetylmuramoyl-l-alanine amidase;<br>**PDBTitle:** the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis |
| 4 | c3qayC_ | Alignment |  | 99.8 | 15 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**endolysin;<br>**PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile |
| 5 | c1xovA_ | Alignment |  | 99.8 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ply protein;<br>**PDBTitle:** the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa |
| 6 | d1xova2 | Alignment |  | 99.8 | 18 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**N-acetylmuramoyl-L-alanine amidase-like |
| 7 | d1nyra1 | Alignment |  | 85.2 | 10 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 8 | d2g4ca1 | Alignment |  | 82.5 | 9 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 9 | d1g5ha1 | Alignment |  | 81.5 | 10 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 10 | d1nj1a1 | Alignment |  | 77.6 | 24 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 11 | d1wu7a1 | Alignment |  | 77.1 | 20 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |

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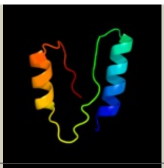
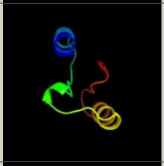
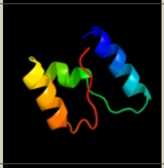
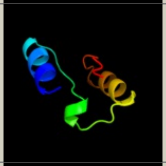
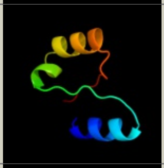
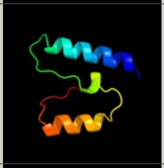
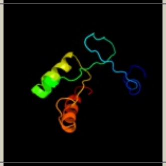
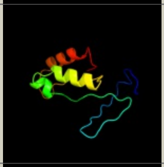
|---|---|---|---|---|---|---|
| 12 | d1qf6a1 | Alignment |  | 75.7 | 8 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 13 | c1y80A_ | Alignment |  | 70.9 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**predicted cobalamin binding protein;<br>**PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica |
| 14 | d1qe0a1 | Alignment |  | 70.0 | 22 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 15 | d1ccwa_ | Alignment |  | 69.2 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 16 | d3bula2 | Alignment |  | 69.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 17 | c1nj2A_ | Alignment |  | 67.0 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**proline-trna synthetase;<br>**PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus |
| 18 | c1u83A_ | Alignment |  | 64.2 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**phosphosulfolactate synthase;<br>**PDBTitle:** psl synthase from bacillus subtilis |
| 19 | d1u83a_ | Alignment |  | 64.2 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA<br>**Family:**(2r)-phospho-3-sulfolactate synthase ComA |
| 20 | c1fyfB_ | Alignment |  | 62.9 | 8 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**threonyl-trna synthetase;<br>**PDBTitle:** crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog |
| 21 | c1g5hA_ | Alignment | not modelled | 62.2 | 10 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**mitochondrial dna polymerase accessory subunit;<br>**PDBTitle:** crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma |
| 22 | c2yxbA_ | Alignment | not modelled | 59.0 | 26 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase;<br>**PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix |
| 23 | c3netB_ | Alignment | not modelled | 58.5 | 19 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**histidyl-trna synthetase;<br>**PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120 |
| 24 | d1nj8a1 | Alignment | not modelled | 58.3 | 16 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 25 | d1fmfa_ | Alignment | not modelled | 57.0 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 26 | c2vefB_ | Alignment | not modelled | 55.9 | 35 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dihydropteroate synthase;<br>**PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae |
| 27 | c2i4lC_ | Alignment | not modelled | 54.6 | 17 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**proline-trna ligase;<br>**PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase |
| 28 | c2qvpC_ | Alignment | not modelled | 53.4 | 20 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative metallopeptidase (sama_0725) from2 shewanella amazonensis sb2b at 2.00 a |

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| | | | | | | resolution |
| 29 | c1vmeB_ | Alignment | not modelled | 53.0 | 17 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**flavoprotein;<br>**PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution |
| 30 | c2hqbA_ | Alignment | not modelled | 51.3 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional activator of comk gene;<br>**PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans |
| 31 | c2j3mA_ | Alignment | not modelled | 50.3 | 10 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**prolyl-trna synthetase;<br>**PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol |
| 32 | c3rfqC_ | Alignment | not modelled | 50.2 | 18 | **PDB header:**biosynthetic protein<br>**Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2;<br>**PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum |
| 33 | c3hriF_ | Alignment | not modelled | 49.1 | 18 | **PDB header:**ligase<br>**Chain:** F: **PDB Molecule:**histidyl-trna synthetase;<br>**PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei |
| 34 | c3i3wB_ | Alignment | not modelled | 48.0 | 30 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**phosphoglucosamine mutase;<br>**PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis |
| 35 | c2an1D_ | Alignment | not modelled | 47.8 | 16 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**putative kinase;<br>**PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2 |
| 36 | c1bmtB_ | Alignment | not modelled | 46.1 | 17 | **PDB header:**methyltransferase<br>**Chain:** B: **PDB Molecule:**methionine synthase;<br>**PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase |
| 37 | c3b2yB_ | Alignment | not modelled | 45.1 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**metallopeptidase containing co-catalytic metalloactive<br>**PDBTitle:** crystal structure of a putative metallopeptidase (sden_2526) from2 shewanella denitrificans os217 at 1.74 a resolution |
| 38 | c1ggmB_ | Alignment | not modelled | 44.9 | 13 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase);<br>**PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate |
| 39 | d2naca2 | Alignment | not modelled | 43.7 | 24 | **Fold:**Flavodoxin-like<br>**Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like<br>**Family:**Formate/glycerate dehydrogenases, substrate-binding domain |
| 40 | c1wu7A_ | Alignment | not modelled | 43.6 | 20 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**histidyl-trna synthetase;<br>**PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum |
| 41 | c2fuvB_ | Alignment | not modelled | 42.4 | 25 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**phosphoglucomutase;<br>**PDBTitle:** phosphoglucomutase from salmonella typhimurium. |
| 42 | c3ezxA_ | Alignment | not modelled | 39.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1;<br>**PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein |
| 43 | c1atiA_ | Alignment | not modelled | 38.7 | 13 | **PDB header:**protein biosynthesis<br>**Chain:** A: **PDB Molecule:**glycyl-trna synthetase;<br>**PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus |
| 44 | c2gx8B_ | Alignment | not modelled | 36.6 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**nif3-related protein;<br>**PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3 |
| 45 | c3ikmC_ | Alignment | not modelled | 36.2 | 7 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**dna polymerase subunit gamma-2;<br>**PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme |
| 46 | d1hc7a1 | Alignment | not modelled | 36.1 | 15 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 47 | c2is8A_ | Alignment | not modelled | 36.0 | 13 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab;<br>**PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8 |
| 48 | c1c4gB_ | Alignment | not modelled | 35.0 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate<br>**PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex |
| 49 | c1qf6A_ | Alignment | not modelled | 34.7 | 8 | **PDB header:**ligase/rna<br>**Chain:** A: **PDB Molecule:**threonyl-trna synthetase;<br>**PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna |
| 50 | c4a26B_ | Alignment | not modelled | 33.7 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic;<br>**PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase |
| 51 | d1atia1 | Alignment | not modelled | 33.0 | 14 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 52 | c2pjkA_ | Alignment | not modelled | 31.3 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor<br>**PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii |

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|---|---|---|---|---|---|---|
| 53 | c3hlyA_ | Alignment | not modelled | 30.8 | 9 | **PDB header:**flavoprotein<br>**Chain:** A: **PDB Molecule:**flavodoxin-like domain;<br>**PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d. |
| 54 | d2a5la1 | Alignment | not modelled | 30.5 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**WrbA-like |
| 55 | d1vmea1 | Alignment | not modelled | 28.8 | 11 | **Fold:**Flavodoxin-like<br>**Superfamily:**Flavoproteins<br>**Family:**Flavodoxin-related |
| 56 | c3a32A_ | Alignment | not modelled | 28.3 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**probable threonyl-trna synthetase 1;<br>**PDBTitle:** crystal structure of putative threonyl-trna synthetase2 thrrs-1 from aeropyrum pernix |
| 57 | d2g2ca1 | Alignment | not modelled | 28.0 | 9 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MogA-like |
| 58 | c2pmfA_ | Alignment | not modelled | 27.4 | 18 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**glycyl-trna synthetase;<br>**PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant |
| 59 | c1nyqA_ | Alignment | not modelled | 27.4 | 11 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1;<br>**PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate |
| 60 | d1a9xa3 | Alignment | not modelled | 27.0 | 25 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 61 | d2gx8a1 | Alignment | not modelled | 26.4 | 21 | **Fold:**NIF3 (NGG1p interacting factor 3)-like<br>**Superfamily:**NIF3 (NGG1p interacting factor 3)-like<br>**Family:**NIF3 (NGG1p interacting factor 3)-like |
| 62 | d1kmma1 | Alignment | not modelled | 26.4 | 18 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 63 | c1qe0B_ | Alignment | not modelled | 26.3 | 22 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**histidyl-trna synthetase;<br>**PDBTitle:** crystal structure of apo s. aureus histidyl-trna synthetase |
| 64 | d1kjna_ | Alignment | not modelled | 26.3 | 15 | **Fold:**Hypothetical protein MTH777 (MT0777)<br>**Superfamily:**Hypothetical protein MTH777 (MT0777)<br>**Family:**Hypothetical protein MTH777 (MT0777) |
| 65 | d1h4vb1 | Alignment | not modelled | 25.9 | 21 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**Class II aaRS ABD-related<br>**Family:**Anticodon-binding domain of Class II aaRS |
| 66 | c1nj8C_ | Alignment | not modelled | 25.7 | 16 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**proline-trna synthetase;<br>**PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii |
| 67 | d1vkha_ | Alignment | not modelled | 25.6 | 12 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Putative serine hydrolase Ydr428c |
| 68 | c2g4rB_ | Alignment | not modelled | 25.4 | 16 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein;<br>**PDBTitle:** anomalous substructure of moga |
| 69 | d7reqa2 | Alignment | not modelled | 24.9 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 70 | c2i2xD_ | Alignment | not modelled | 24.6 | 15 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**methyltransferase 1;<br>**PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri |
| 71 | d1mkza_ | Alignment | not modelled | 24.4 | 7 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MogA-like |
| 72 | c3fniA_ | Alignment | not modelled | 24.3 | 9 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3;<br>**PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a |
| 73 | d1xi8a3 | Alignment | not modelled | 24.2 | 11 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MoeA central domain-like |
| 74 | d1xhfa1 | Alignment | not modelled | 24.1 | 19 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 75 | d2f7wa1 | Alignment | not modelled | 24.0 | 9 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MogA-like |
| 76 | d1p5dx2 | Alignment | not modelled | 23.7 | 21 | **Fold:**Phosphoglucomutase, first 3 domains<br>**Superfamily:**Phosphoglucomutase, first 3 domains<br>**Family:**Phosphoglucomutase, first 3 domains |
| 77 | d1kfia2 | Alignment | not modelled | 23.3 | 29 | **Fold:**Phosphoglucomutase, first 3 domains<br>**Superfamily:**Phosphoglucomutase, first 3 domains<br>**Family:**Phosphoglucomutase, first 3 domains |
| 78 | d2fywa1 | Alignment | not modelled | 23.0 | 29 | **Fold:**NIF3 (NGG1p interacting factor 3)-like<br>**Superfamily:**NIF3 (NGG1p interacting factor 3)-like<br>**Family:**NIF3 (NGG1p interacting factor 3)-like |
| 79 | c2ilaD_ | Alignment | not modelled | 22.9 | 16 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene |

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| 79 | c2jfaD_ | Alignment | not modelled | 22.9 | 16 | **PDBTitle:** crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase -semet3 protein |
| 80 | c3c3mA_ | Alignment | not modelled | 22.6 | 17 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**response regulator receiver protein;<br>**PDBTitle:** crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1 |
| 81 | c3maxB_ | Alignment | not modelled | 22.5 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**histone deacetylase 2;<br>**PDBTitle:** crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide |
| 82 | d1qnaa1 | Alignment | not modelled | 21.6 | 19 | **Fold:**TBP-like<br>**Superfamily:**TATA-box binding protein-like<br>**Family:**TATA-box binding protein (TBP), C-terminal domain |
| 83 | d1b74a1 | Alignment | not modelled | 21.6 | 27 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/glutamate racemase<br>**Family:**Aspartate/glutamate racemase |
| 84 | d1iowa1 | Alignment | not modelled | 21.3 | 35 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**D-Alanine ligase N-terminal domain |
| 85 | d2pl1a1 | Alignment | not modelled | 21.2 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**CheY-like<br>**Family:**CheY-related |
| 86 | d1xrsb1 | Alignment | not modelled | 20.9 | 24 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 87 | c2vavL_ | Alignment | not modelled | 20.5 | 13 | **PDB header:**transferase<br>**Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c<br>**PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak) |
| 88 | c2nydB_ | Alignment | not modelled | 20.4 | 12 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**upf0135 protein sa1388;<br>**PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388 |
| 89 | d1y5ea1 | Alignment | not modelled | 20.0 | 11 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MogA-like |
| 90 | d1uz5a3 | Alignment | not modelled | 19.9 | 14 | **Fold:**Molybdenum cofactor biosynthesis proteins<br>**Superfamily:**Molybdenum cofactor biosynthesis proteins<br>**Family:**MoeA central domain-like |
| 91 | d1qwga_ | Alignment | not modelled | 19.4 | 26 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA<br>**Family:**(2r)-phospho-3-sulfolactate synthase ComA |
| 92 | d1o2da_ | Alignment | not modelled | 19.2 | 13 | **Fold:**Dehydroquinate synthase-like<br>**Superfamily:**Dehydroquinate synthase-like<br>**Family:**Iron-containing alcohol dehydrogenase |
| 93 | c1e5dA_ | Alignment | not modelled | 19.1 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase;<br>**PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas |
| 94 | c1cg2D_ | Alignment | not modelled | 19.1 | 18 | **PDB header:**metallocarboxypeptidase<br>**Chain:** D: **PDB Molecule:**carboxypeptidase g2;<br>**PDBTitle:** carboxypeptidase g2 |
| 95 | d2grea2 | Alignment | not modelled | 18.6 | 9 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**Bacterial dinuclear zinc exopeptidases |
| 96 | c3f6sI_ | Alignment | not modelled | 17.6 | 17 | **PDB header:**electron transport<br>**Chain:** I: **PDB Molecule:**flavodoxin;<br>**PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers |
| 97 | c3k5pA_ | Alignment | not modelled | 17.6 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase;<br>**PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis |
| 98 | d1cg2a1 | Alignment | not modelled | 17.4 | 18 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**Bacterial dinuclear zinc exopeptidases |
| 99 | d1fmta2 | Alignment | not modelled | 17.3 | 13 | **Fold:**Formyltransferase<br>**Superfamily:**Formyltransferase<br>**Family:**Formyltransferase |