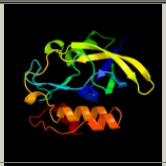
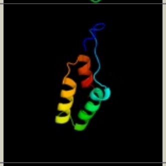
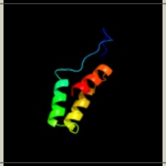
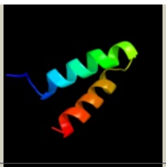
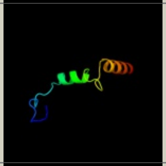
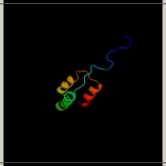
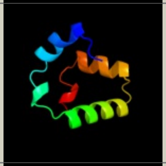
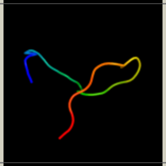
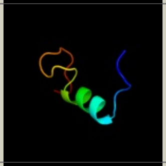
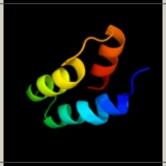
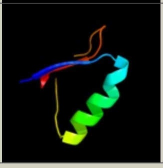
# Phyre²

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P39163 |
| Date | Thu Jan 5 11:58:18 GMT 2012 |
| Unique Job ID | a344c022454339fd |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2rbhA_ | Alignment |  | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gamma-glutamyl cyclotransferase;<br>**PDBTitle:** gamma-glutamyl cyclotransferase |
| 2 | c2qikA_ | Alignment |  | 99.7 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0131 protein ykqa;<br>**PDBTitle:** crystal structure of ykqa from bacillus subtilis. northeast2 structural genomics target sr631 |
| 3 | c2g0qA_ | Alignment |  | 98.9 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**at5g39720.1 protein;<br>**PDBTitle:** solution structure of at5g39720.1 from arabidopsis thaliana |
| 4 | c2jqvA_ | Alignment |  | 98.6 | 16 | **PDB header:**structural genomics<br>**Chain:** A: **PDB Molecule:**aig2 protein-like;<br>**PDBTitle:** solution structure at3g28950.1 from arabidopsis thaliana |
| 5 | d1xhsa_ | Alignment |  | 98.5 | 19 | **Fold:**Gamma-glutamyl cyclotransferase-like<br>**Superfamily:**Gamma-glutamyl cyclotransferase-like<br>**Family:**Gamma-glutamyl cyclotransferase-like |
| 6 | c3jubA_ | Alignment |  | 98.2 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**aig2-like domain-containing protein 1;<br>**PDBTitle:** human gamma-glutamylamine cyclotransferase |
| 7 | d1vkba_ | Alignment |  | 98.1 | 23 | **Fold:**Gamma-glutamyl cyclotransferase-like<br>**Superfamily:**Gamma-glutamyl cyclotransferase-like<br>**Family:**Gamma-glutamyl cyclotransferase-like |
| 8 | d1v30a_ | Alignment |  | 97.3 | 19 | **Fold:**Gamma-glutamyl cyclotransferase-like<br>**Superfamily:**Gamma-glutamyl cyclotransferase-like<br>**Family:**Gamma-glutamyl cyclotransferase-like |
| 9 | c2x8qA_ | Alignment |  | 55.1 | 10 | **PDB header:**virus<br>**Chain:** A: **PDB Molecule:**capsid protein p27;<br>**PDBTitle:** cryo-em 3d model of the icosahedral particle2 composed of rous sarcoma virus capsid protein pentamers |
| 10 | d1em9a_ | Alignment |  | 54.9 | 10 | **Fold:**Retrovirus capsid protein, N-terminal core domain<br>**Superfamily:**Retrovirus capsid protein, N-terminal core domain<br>**Family:**Retrovirus capsid protein, N-terminal core domain |
| 11 | c2kgfA_ | Alignment |  | 47.3 | 16 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**capsid protein p27;<br>**PDBTitle:** n-terminal domain of capsid protein from the mason-pfizer2 monkey virus |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c2c2zB_ | Alignment |  | 44.8 | 21 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**caspase-8 p10 subunit;<br>**PDBTitle:** crystal structure of caspase-8 in complex with aza-peptide michael2 acceptor inhibitor |
| 13 | c3edyA_ | Alignment |  | 36.5 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1;<br>**PDBTitle:** crystal structure of the precursor form of human tripeptidyl-peptidase2 1 |
| 14 | d1p7na_ | Alignment |  | 35.6 | 11 | **Fold:**Retrovirus capsid protein, N-terminal core domain<br>**Superfamily:**Retrovirus capsid protein, N-terminal core domain<br>**Family:**Retrovirus capsid protein, N-terminal core domain |
| 15 | c3ee6A_ | Alignment |  | 35.4 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1;<br>**PDBTitle:** crystal structure analysis of tripeptidyl peptidase -i |
| 16 | c3m66A_ | Alignment |  | 34.5 | 7 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**mterf domain-containing protein 1, mitochondrial;<br>**PDBTitle:** crystal structure of human mitochondrial transcription termination2 factor 3 |
| 17 | d1bdsa_ | Alignment |  | 33.9 | 35 | **Fold:**Defensin-like<br>**Superfamily:**Defensin-like<br>**Family:**Defensin |
| 18 | d1gk8i_ | Alignment |  | 28.4 | 21 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 19 | d1d1da2 | Alignment |  | 26.5 | 10 | **Fold:**Retrovirus capsid protein, N-terminal core domain<br>**Superfamily:**Retrovirus capsid protein, N-terminal core domain<br>**Family:**Retrovirus capsid protein, N-terminal core domain |
| 20 | d2cvea2 | Alignment |  | 24.4 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**EF-G C-terminal domain-like<br>**Family:**YigZ C-terminal domain-like |
| 21 | d2plga1 | Alignment | not modelled | 22.5 | 44 | **Fold:**Secretion chaperone-like<br>**Superfamily:**Type III secretory system chaperone-like<br>**Family:**Tll0839-like |
| 22 | d1mpga1 | Alignment | not modelled | 22.2 | 21 | **Fold:**DNA-glycosylase<br>**Superfamily:**DNA-glycosylase<br>**Family:**DNA repair glycosylase, 2 C-terminal domains |
| 23 | d1fp2a1 | Alignment | not modelled | 22.1 | 10 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Plant O-methyltransferase, N-terminal domain |
| 24 | d1wdds_ | Alignment | not modelled | 21.7 | 21 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 25 | c2v4xA_ | Alignment | not modelled | 21.5 | 8 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**capsid protein p27;<br>**PDBTitle:** crystal structure of jaagsiekte sheep retrovirus capsid n-2 terminal domain |
| 26 | d2v6ai1 | Alignment | not modelled | 20.6 | 21 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 27 | c2dwuA_ | Alignment | not modelled | 20.1 | 16 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis |
| 28 | d1no5a_ | Alignment | not modelled | 20.1 | 25 | **Fold:**Nucleotidyltransferase<br>**Superfamily:**Nucleotidyltransferase<br>**Family:**Catalytic subunit of bi-partite nucleotidyltransferase |
| 29 | d8ruci_ | Alignment | not modelled | 19.1 | 21 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | **Family:**RuBisCO, small subunit |
| 30 | c2jfoB_ | Alignment | not modelled | 19.0 | 16 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate |
| 31 | d1uzdc1 | Alignment | not modelled | 18.7 | 21 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 32 | c1mpgB_ | Alignment | not modelled | 18.4 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii;<br>**PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli |
| 33 | d1ej7s_ | Alignment | not modelled | 18.2 | 21 | **Fold:**RuBisCO, small subunit<br>**Superfamily:**RuBisCO, small subunit<br>**Family:**RuBisCO, small subunit |
| 34 | c2qljB_ | Alignment | not modelled | 17.6 | 23 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**caspase-7;<br>**PDBTitle:** crystal structure of caspase-7 with inhibitor ac-wehd-cho |
| 35 | c3c7bA_ | Alignment | not modelled | 17.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha;<br>**PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus |
| 36 | d1t1ea2 | Alignment | not modelled | 16.3 | 10 | **Fold:**Ferredoxin-like<br>**Superfamily:**Protease propeptides/inhibitors<br>**Family:**Subtilase propeptides/inhibitors |
| 37 | d1mm0a_ | Alignment | not modelled | 15.9 | 56 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**Scorpion toxin-like<br>**Family:**Insect defensins |
| 38 | c1b74A_ | Alignment | not modelled | 15.6 | 24 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** glutamate racemase from aquifex pyrophilus |
| 39 | c3lehA_ | Alignment | not modelled | 15.4 | 32 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative hydroxymethylglutaryl-coa synthase;<br>**PDBTitle:** the crystal structure of smu.943c from streptococcus mutans ua159 |
| 40 | d1p17b_ | Alignment | not modelled | 15.0 | 33 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 41 | c3hfrA_ | Alignment | not modelled | 14.9 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes |
| 42 | c1kmcB_ | Alignment | not modelled | 14.6 | 23 | **PDB header:**apoptosis/hydrolase<br>**Chain:** B: **PDB Molecule:**caspase-7;<br>**PDBTitle:** crystal structure of the caspase-7 / xiap-bir2 complex |
| 43 | c3degC_ | Alignment | not modelled | 14.5 | 16 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**gtp-binding protein lepa;<br>**PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp |
| 44 | d1ucva_ | Alignment | not modelled | 14.2 | 13 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 45 | c3nwuB_ | Alignment | not modelled | 14.1 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**serine protease htra1;<br>**PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity |
| 46 | d1pzma_ | Alignment | not modelled | 14.1 | 33 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 47 | c2p2cD_ | Alignment | not modelled | 14.0 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**caspase-2;<br>**PDBTitle:** inhibition of caspase-2 by a designed ankyrin repeat2 protein (darpin) |
| 48 | d2ibna1 | Alignment | not modelled | 13.9 | 29 | **Fold:**HD-domain/PDEase-like<br>**Superfamily:**HD-domain/PDEase-like<br>**Family:**MioX-like |
| 49 | c2ohoA_ | Alignment | not modelled | 13.8 | 27 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** structural basis for glutamate racemase inhibitor |
| 50 | c3kopB_ | Alignment | not modelled | 13.3 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution |
| 51 | d1tc1a_ | Alignment | not modelled | 13.3 | 33 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 52 | c3d0wD_ | Alignment | not modelled | 13.3 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**yflh protein;<br>**PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326 |
| 53 | d1riqa1 | Alignment | not modelled | 12.8 | 21 | **Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)<br>**Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)<br>**Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) |
| 54 | c2ywtA_ | Alignment | not modelled | 12.2 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase;<br>**PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 55 | c3my3A_ | Alignment | not modelled | 12.1 | 4 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**mterf domain-containing protein 1, mitochondrial;<br>**PDBTitle:** crystal structure of human mitochondrial transcription termination2 factor 3 |
| 56 | d1y88a1 | Alignment | not modelled | 11.8 | 14 | **Fold:**SAM domain-like<br>**Superfamily:**Rad51 N-terminal domain-like<br>**Family:**Hypothetical protein AF1548, C-terminal domain |
| 57 | d2qf3a1 | Alignment | not modelled | 11.6 | 13 | **Fold:**Trypsin-like serine proteases<br>**Superfamily:**Trypsin-like serine proteases<br>**Family:**Prokaryotic proteases |
| 58 | c2v4wB_ | Alignment | not modelled | 11.5 | 32 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase,<br>**PDBTitle:** crystal structure of human mitochondrial 3-hydroxy-3-2 methylglutaryl-coenzyme a synthase 2 (hmgcs2) |
| 59 | c3n6sA_ | Alignment | not modelled | 11.4 | 14 | **PDB header:**transcription, replication/dna<br>**Chain:** A: **PDB Molecule:**transcription termination factor, mitochondrial;<br>**PDBTitle:** crystal structure of human mitochondrial mterf in complex with a 15-2 mer dna encompassing the trnaleu(uur) binding sequence |
| 60 | c3kb8A_ | Alignment | not modelled | 10.9 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase;<br>**PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp |
| 61 | c1ru7B_ | Alignment | not modelled | 10.8 | 28 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**hemagglutinin;<br>**PDBTitle:** 1934 human h1 hemagglutinin |
| 62 | c2c1eB_ | Alignment | not modelled | 10.8 | 17 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**caspase-3 subunit p12;<br>**PDBTitle:** crystal structures of caspase-3 in complex with aza-peptide michael2 acceptor inhibitors. |
| 63 | d1g9sa_ | Alignment | not modelled | 10.8 | 33 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 64 | c2dl0A_ | Alignment | not modelled | 10.7 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1;<br>**PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1 |
| 65 | c1x9eB_ | Alignment | not modelled | 10.6 | 27 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**hmg-coa synthase;<br>**PDBTitle:** crystal structure of hmg-coa synthase from enterococcus2 faecalis |
| 66 | c2jfzB_ | Alignment | not modelled | 10.5 | 16 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor |
| 67 | c3bt6B_ | Alignment | not modelled | 10.4 | 25 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**influenza b hemagglutinin (ha);<br>**PDBTitle:** crystal structure of influenza b virus hemagglutinin |
| 68 | c3o7mD_ | Alignment | not modelled | 10.4 | 50 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase;<br>**PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor' |
| 69 | c2h51B_ | Alignment | not modelled | 10.3 | 6 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**caspase-1;<br>**PDBTitle:** crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk) |
| 70 | c2gzmB_ | Alignment | not modelled | 10.0 | 16 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis |
| 71 | c3outC_ | Alignment | not modelled | 9.9 | 19 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**glutamate racemase;<br>**PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate. |
| 72 | d1fp1d1 | Alignment | not modelled | 9.7 | 16 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Plant O-methyltransferase, N-terminal domain |
| 73 | d1pgw21 | Alignment | not modelled | 9.6 | 40 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Positive stranded ssRNA viruses<br>**Family:**Comoviridae-like VP |
| 74 | d1pgl21 | Alignment | not modelled | 9.5 | 40 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Positive stranded ssRNA viruses<br>**Family:**Comoviridae-like VP |
| 75 | d1ny721 | Alignment | not modelled | 9.5 | 40 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Positive stranded ssRNA viruses<br>**Family:**Comoviridae-like VP |
| 76 | c2jbhA_ | Alignment | not modelled | 9.3 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1;<br>**PDBTitle:** human phosphoribosyl transferase domain containing 1 |
| 77 | d1hgxa_ | Alignment | not modelled | 9.3 | 50 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 78 | d1ccwa_ | Alignment | not modelled | 9.2 | 10 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| | | | | | | **PDB header:**viral protein |

| | | | | | | |
|---|---|---|---|---|---|---|
| 79 | c2wrhl_ | Alignment | not modelled | 9.2 | 28 | **Chain:** I: **PDB Molecule:**hemagglutinin ha2 chain;<br>**PDBTitle:** structure of h1 duck albert hemagglutinin with human2 receptor |
| 80 | c1hgeD_ | Alignment | not modelled | 9.1 | 22 | **PDB header:**viral protein<br>**Chain:** D: **PDB Molecule:**hemagglutinin, (g135r), ha1 chain;<br>**PDBTitle:** binding of influenza virus hemagglutinin to analogs of its cell-2 surface receptor, sialic acid: analysis by proton nuclear magnetic3 resonance spectroscopy and x-ray crystallography |
| 81 | c3s5oA_ | Alignment | not modelled | 9.1 | 12 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial;<br>**PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate |
| 82 | c3m5gD_ | Alignment | not modelled | 9.1 | 28 | **PDB header:**viral protein<br>**Chain:** D: **PDB Molecule:**hemagglutinin;<br>**PDBTitle:** crystal structure of a h7 influenza virus hemagglutinin |
| 83 | c1jsdB_ | Alignment | not modelled | 9.1 | 31 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**haemagglutinin (ha2 chain);<br>**PDBTitle:** crystal structure of swine h9 haemagglutinin |
| 84 | c3sirD_ | Alignment | not modelled | 9.1 | 23 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**caspase;<br>**PDBTitle:** crystal structure of drice |
| 85 | d1zs4a1 | Alignment | not modelled | 9.1 | 26 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Bacteriophage CII protein |
| 86 | c2ja9A_ | Alignment | not modelled | 8.9 | 8 | **PDB header:**rna-binding protein<br>**Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40;<br>**PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40 |
| 87 | c2p8uB_ | Alignment | not modelled | 8.8 | 45 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, cytoplasmic;<br>**PDBTitle:** crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i |
| 88 | d1f1ja_ | Alignment | not modelled | 8.6 | 23 | **Fold:**Caspase-like<br>**Superfamily:**Caspase-like<br>**Family:**Caspase catalytic domain |
| 89 | c2d9xA_ | Alignment | not modelled | 8.5 | 17 | **PDB header:**lipid transport<br>**Chain:** A: **PDB Molecule:**oxysterol binding protein-related protein 11;<br>**PDBTitle:** solution structure of the ph domain of oxysterol binding2 protein-related protein 11 from human |
| 90 | d1nu0a_ | Alignment | not modelled | 8.4 | 35 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Ribonuclease H-like<br>**Family:**Putative Holliday junction resolvase RuvX |
| 91 | d1o5ka_ | Alignment | not modelled | 8.3 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class I aldolase |
| 92 | c2rq5A_ | Alignment | not modelled | 8.3 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**protein jumonji;<br>**PDBTitle:** solution structure of the at-rich interaction domain (arid)2 of jumonji/jarid2 |
| 93 | c3nziA_ | Alignment | not modelled | 8.3 | 21 | **PDB header:**hydrolase/hydrolase substrate<br>**Chain:** A: **PDB Molecule:**serine protease htra1;<br>**PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity |
| 94 | c3h9xB_ | Alignment | not modelled | 8.3 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein pspto_3016;<br>**PDBTitle:** crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293 |
| 95 | c2funB_ | Alignment | not modelled | 8.2 | 24 | **PDB header:**apoptosis/hydrolase<br>**Chain:** B: **PDB Molecule:**caspase-8;<br>**PDBTitle:** alternative p35-caspase-8 complex |
| 96 | c1htmB_ | Alignment | not modelled | 8.2 | 22 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain;<br>**PDBTitle:** structure of influenza haemagglutinin at the ph of membrane2 fusion |
| 97 | d2ia7a1 | Alignment | not modelled | 7.9 | 20 | **Fold:**gpW/gp25-like<br>**Superfamily:**gpW/gp25-like<br>**Family:**gpW/gp25-like |
| 98 | c3n7qA_ | Alignment | not modelled | 7.9 | 14 | **PDB header:**transcription, replication/dna<br>**Chain:** A: **PDB Molecule:**transcription termination factor, mitochondrial;<br>**PDBTitle:** crystal structure of human mitochondrial mterf fragment (aa 99-399) in2 complex with a 12-mer dna encompassing the trnaleu(uur) binding3 sequence |
| 99 | c1yfzA_ | Alignment | not modelled | 7.9 | 33 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase;<br>**PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis |