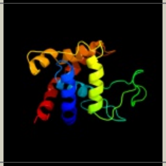
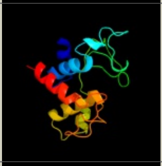
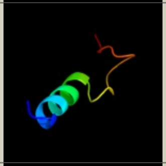
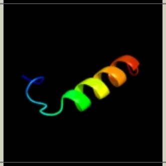
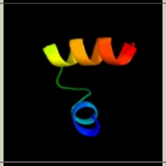
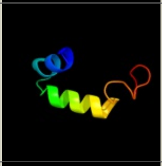
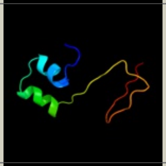
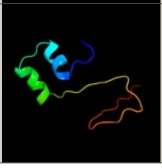
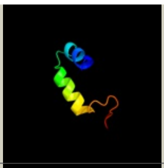
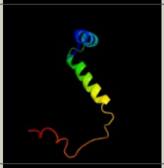
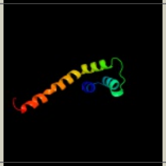
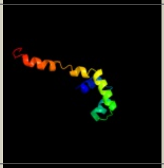
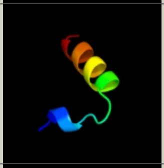
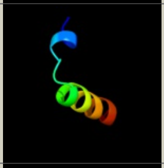
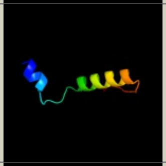
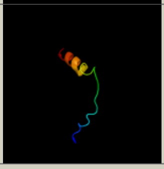
# Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P27297 |
| Date | Thu Jan 5 11:43:43 GMT 2012 |
| Unique Job ID | 0198c00ab246b151 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3fi7A_ | Alignment |  | 100.0 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lmo1076 protein;<br>**PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain |
| 2 | c2zycA_ | Alignment |  | 99.9 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj;<br>**PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1 |
| 3 | d1qsaa2 | Alignment |  | 86.9 | 16 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Bacterial muramidase, catalytic domain |
| 4 | c3gxkB_ | Alignment |  | 71.0 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**goose-type lysozyme 1;<br>**PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9 |
| 5 | d1gbsa_ | Alignment |  | 48.7 | 15 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**G-type lysozyme |
| 6 | c2kiqA_ | Alignment |  | 41.6 | 13 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcription elongation regulator 1;<br>**PDBTitle:** solution structure of the ff domain 2 of human transcription2 elongation factor ca150 |
| 7 | c1u1iC_ | Alignment |  | 38.5 | 24 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**myo-inositol-1-phosphate synthase;<br>**PDBTitle:** myo-inositol phosphate synthase mips from a. fulgidus |
| 8 | c3mgwA_ | Alignment |  | 38.1 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lysozyme g;<br>**PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme |
| 9 | d1qusa_ | Alignment |  | 37.7 | 16 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Bacterial muramidase, catalytic domain |
| 10 | d2hj1a1 | Alignment |  | 29.0 | 14 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**HI0395-like |
| 11 | c2hj1A_ | Alignment |  | 29.0 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c2y8pA_ | Alignment |  | 28.4 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a;<br>**PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli |
| 13 | c2k5jB_ | Alignment |  | 25.0 | 9 | **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 |
| 14 | c2jucA_ | Alignment |  | 24.6 | 30 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**pre-mrna-splicing factor urn1;<br>**PDBTitle:** urn1 ff domain yeast |
| 15 | c3mzvB_ | Alignment |  | 24.2 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**decaprenyl diphosphate synthase;<br>**PDBTitle:** crystal structure of a decaprenyl diphosphate synthase from2 rhodobacter capsulatus |
| 16 | c3oyrB_ | Alignment |  | 21.3 | 7 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**trans-isoprenyl diphosphate synthase;<br>**PDBTitle:** crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate |
| 17 | d1uzca_ | Alignment |  | 20.3 | 19 | **Fold:**Another 3-helical bundle<br>**Superfamily:**FF domain<br>**Family:**FF domain |
| 18 | c2e71A_ | Alignment |  | 19.0 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription elongation regulator 1;<br>**PDBTitle:** solution structure of the second ff domain of human2 transcription factor ca150 |
| 19 | c3frrA_ | Alignment |  | 18.6 | 17 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**uncharacterized protein kiaa0174;<br>**PDBTitle:** structure of human ist1(ntd) - (residues 1-189)(p21) |
| 20 | d1ppje2 | Alignment |  | 17.6 | 27 | **Fold:**Single transmembrane helix<br>**Superfamily:**ISP transmembrane anchor<br>**Family:**ISP transmembrane anchor |
| 21 | d2doea1 | Alignment | not modelled | 16.9 | 17 | **Fold:**Another 3-helical bundle<br>**Superfamily:**FF domain<br>**Family:**FF domain |
| 22 | d2cqna1 | Alignment | not modelled | 15.5 | 17 | **Fold:**Another 3-helical bundle<br>**Superfamily:**FF domain<br>**Family:**FF domain |
| 23 | d1v6ga1 | Alignment | not modelled | 15.4 | 35 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 24 | c3kevA_ | Alignment | not modelled | 15.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**galieria sulfuraria dcun1 domain-containing protein;<br>**PDBTitle:** x-ray crystal structure of a dcun1 domain-containing protein from2 galdieria sulfuraria |
| 25 | d2opoa1 | Alignment | not modelled | 14.9 | 19 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Polcalcin |
| 26 | c3ggzC_ | Alignment | not modelled | 14.1 | 24 | **PDB header:**protein transport, endocytosis<br>**Chain:** C: **PDB Molecule:**increased sodium tolerance protein 1;<br>**PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in2 complex with did2 mim motif |
| 27 | d1p35a_ | Alignment | not modelled | 13.3 | 71 | **Fold:**Baculovirus p35 protein<br>**Superfamily:**Baculovirus p35 protein<br>**Family:**Baculovirus p35 protein |
| 28 | c2ktgA_ | Alignment | not modelled | 12.4 | 10 | **PDB header:**ca-binding protein<br>**Chain:** A: **PDB Molecule:**calmodulin, putative;<br>**PDBTitle:** calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein |

| | | | | | | |
|---|---|---|---|---|---|---|
| 29 | d1t6ca2 | Alignment | not modelled | 11.9 | 18 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**Ppx/GppA phosphatase |
| 30 | d2o5ha1 | Alignment | not modelled | 11.4 | 14 | **Fold:**NMB0513-like<br>**Superfamily:**NMB0513-like<br>**Family:**NMB0513-like |
| 31 | c2ckzC_ | Alignment | not modelled | 11.1 | 22 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**dna-directed rna polymerase iii 18 kd<br>**PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25. |
| 32 | c2doqA_ | Alignment | not modelled | 10.7 | 2 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**cell division control protein 31;<br>**PDBTitle:** crystal structure of sfi1p/cdc31p complex |
| 33 | d1tn4a_ | Alignment | not modelled | 10.5 | 13 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 34 | d1kyqa2 | Alignment | not modelled | 10.3 | 7 | **Fold:**Siroheme synthase middle domains-like<br>**Superfamily:**Siroheme synthase middle domains-like<br>**Family:**Siroheme synthase middle domains-like |
| 35 | d1u6za3 | Alignment | not modelled | 9.8 | 6 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**Ppx/GppA phosphatase |
| 36 | d1avsa_ | Alignment | not modelled | 9.7 | 16 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 37 | c2dimA_ | Alignment | not modelled | 9.7 | 24 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**cell division cycle 5-like protein;<br>**PDBTitle:** solution structure of the myb_dna-binding domain of human2 cell division cycle 5-like protein |
| 38 | c1x41A_ | Alignment | not modelled | 9.4 | 15 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional adaptor 2-like, isoform b;<br>**PDBTitle:** solution structure of the myb-like dna binding domain of2 human transcriptional adaptor 2-like, isoform b |
| 39 | c3bkhA_ | Alignment | not modelled | 9.3 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lytic transglycosylase;<br>**PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 |
| 40 | c1idzA_ | Alignment | not modelled | 9.3 | 25 | **PDB header:**dna-binding protein<br>**Chain:** A: **PDB Molecule:**mouse c-myb dna-binding domain repeat 3;<br>**PDBTitle:** structure of myb transforming protein, nmr, 20 structures |
| 41 | d1bl0a2 | Alignment | not modelled | 9.3 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |
| 42 | d1br1b_ | Alignment | not modelled | 9.0 | 12 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 43 | d2zdra2 | Alignment | not modelled | 9.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**NeuB-like |
| 44 | d1d5ya2 | Alignment | not modelled | 9.0 | 12 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**AraC type transcriptional activator |
| 45 | d1fi6a_ | Alignment | not modelled | 8.9 | 10 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Eps15 homology domain (EH domain) |
| 46 | d1f54a_ | Alignment | not modelled | 8.8 | 11 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 47 | d1mbja_ | Alignment | not modelled | 8.8 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 48 | c1mbjA_ | Alignment | not modelled | 8.8 | 21 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**myb proto-oncogene protein;<br>**PDBTitle:** mouse c-myb dna-binding domain repeat 3 |
| 49 | d1n0ya_ | Alignment | not modelled | 8.6 | 15 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 50 | d2oc6a1 | Alignment | not modelled | 8.5 | 19 | **Fold:**Secretion chaperone-like<br>**Superfamily:**YdhG-like<br>**Family:**YdhG-like |
| 51 | c3ayhA_ | Alignment | not modelled | 8.2 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc9;<br>**PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii |
| 52 | c2kl4A_ | Alignment | not modelled | 8.2 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**bh2032 protein;<br>**PDBTitle:** nmr structure of the protein nb7804a |
| 53 | c2k7bA_ | Alignment | not modelled | 7.2 | 12 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**calcium-binding protein 1;<br>**PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain |
| 54 | d1a04a1 | Alignment | not modelled | 7.2 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**C-terminal effector domain of the bipartite response regulators<br>**Family:**GerE-like (LuxR/UhpA family of transcriptional regulators) |
| 55 | c3ox6C_ | Alignment | not modelled | 7.2 | 13 | **PDB header:**calcium binding protein<br>**Chain:** C: **PDB Molecule:**calcium-binding protein 1;<br>**PDBTitle:** crystal structure of the calcium sensor calcium-binding protein 12 (cabp1) |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 56 | c1e0fJ_ | Alignment | not modelled | 7.2 | 28 | **PDB header:**coagulation/crystal structure/heparin-b<br>**Chain:** J: **PDB Molecule:**haemadin;<br>**PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor |
| 57 | d1lkja_ | Alignment | not modelled | 7.2 | 10 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 58 | d1zaca_ | Alignment | not modelled | 7.2 | 14 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 59 | d2tpta1 | Alignment | not modelled | 7.1 | 17 | **Fold:**Methionine synthase domain-like<br>**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain<br>**Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain |
| 60 | c3j04E_ | Alignment | not modelled | 7.1 | 13 | **PDB header:**structural protein<br>**Chain:** E: **PDB Molecule:**myosin regulatory light chain 2, smooth muscle major<br>**PDBTitle:** em structure of the heavy meromyosin subfragment of chick smooth2 muscle myosin with regulatory light chain in phosphorylated state |
| 61 | d1sw8a_ | Alignment | not modelled | 7.0 | 13 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 62 | c1e0fK_ | Alignment | not modelled | 6.8 | 28 | **PDB header:**coagulation/crystal structure/heparin-b<br>**Chain:** K: **PDB Molecule:**haemadin;<br>**PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor |
| 63 | c1e0fI_ | Alignment | not modelled | 6.8 | 28 | **PDB header:**coagulation/crystal structure/heparin-b<br>**Chain:** I: **PDB Molecule:**haemadin;<br>**PDBTitle:** crystal structure of the human alpha-thrombin-haemadin2 complex: an exosite ii-binding inhibitor |
| 64 | d1e0fi_ | Alignment | not modelled | 6.8 | 28 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**Leech antihemostatic proteins<br>**Family:**Hirudin-like |
| 65 | d1gv2a2 | Alignment | not modelled | 6.8 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 66 | c3cvgC_ | Alignment | not modelled | 6.7 | 12 | **PDB header:**metal binding protein<br>**Chain:** C: **PDB Molecule:**putative metal binding protein;<br>**PDBTitle:** crystal structure of a periplasmic putative metal binding protein |
| 67 | d1w0ta_ | Alignment | not modelled | 6.7 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**DNA-binding domain of telomeric protein |
| 68 | c1mseC_ | Alignment | not modelled | 6.7 | 25 | **PDB header:**dna binding protein/dna<br>**Chain:** C: **PDB Molecule:**c-myb dna-binding domain;<br>**PDBTitle:** solution structure of a specific dna complex of the myb dna-2 binding domain with cooperative recognition helices |
| 69 | c2xqoA_ | Alignment | not modelled | 6.7 | 60 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cellulosome enzyme, dockerin type i;<br>**PDBTitle:** ctcel124: a cellulase from clostridium thermocellum |
| 70 | c1xuzA_ | Alignment | not modelled | 6.6 | 13 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac;<br>**PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol |
| 71 | c3cerD_ | Alignment | not modelled | 6.6 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein;<br>**PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13 |
| 72 | c3sggA_ | Alignment | not modelled | 6.6 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hypothetical hydrolase;<br>**PDBTitle:** crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution |
| 73 | c2ggmA_ | Alignment | not modelled | 6.5 | 6 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**centrin-2;<br>**PDBTitle:** human centrin 2 xeroderma pigmentosum group c protein2 complex |
| 74 | d1gm5a1 | Alignment | not modelled | 6.5 | 27 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**RecG, N-terminal domain<br>**Family:**RecG, N-terminal domain |
| 75 | c3p45F_ | Alignment | not modelled | 6.4 | 28 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**caspase-6;<br>**PDBTitle:** crystal structure of apo-caspase-6 at physiological ph |
| 76 | d1h4ba_ | Alignment | not modelled | 6.4 | 20 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Polcalcin |
| 77 | c2l7eA_ | Alignment | not modelled | 6.3 | 80 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription initiation factor tfiid subunit 14;<br>**PDBTitle:** the structure of a domain from yeast |
| 78 | c3mseB_ | Alignment | not modelled | 6.2 | 9 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**calcium-dependent protein kinase, putative;<br>**PDBTitle:** crystal structure of c-terminal domain of pf110239. |
| 79 | d1guua_ | Alignment | not modelled | 6.2 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 80 | c1guuA_ | Alignment | not modelled | 6.2 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**myb proto-oncogene protein;<br>**PDBTitle:** crystal structure of c-myb r1 |
|  |  |  |  |  |  | **PDB header:**rna binding protein |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 81 | c3bmbB_ | Alignment | not modelled | 6.1 | 13 | **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase;<br>**PDBTitle:** crystal structure of a new rna polymerase interacting2 protein |
| 82 | d1kbhb_ | Alignment | not modelled | 6.0 | 22 | **Fold:**Nuclear receptor coactivator interlocking domain<br>**Superfamily:**Nuclear receptor coactivator interlocking domain<br>**Family:**Nuclear receptor coactivator interlocking domain |
| 83 | c2krcA_ | Alignment | not modelled | 6.0 | 6 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta;<br>**PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase |
| 84 | d1pdza2 | Alignment | not modelled | 5.9 | 18 | **Fold:**Enolase N-terminal domain-like<br>**Superfamily:**Enolase N-terminal domain-like<br>**Family:**Enolase N-terminal domain-like |
| 85 | c3osgA_ | Alignment | not modelled | 5.9 | 21 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**myb21;<br>**PDBTitle:** the structure of protozoan parasite trichomonas vaginalis myb2 in2 complex with mre-1-12 dna |
| 86 | d1o20a_ | Alignment | not modelled | 5.9 | 16 | **Fold:**ALDH-like<br>**Superfamily:**ALDH-like<br>**Family:**ALDH-like |
| 87 | d1eh1a_ | Alignment | not modelled | 5.8 | 24 | **Fold:**RRF/tRNA synthetase additional domain-like<br>**Superfamily:**Ribosome recycling factor, RRF<br>**Family:**Ribosome recycling factor, RRF |
| 88 | c2kn2A_ | Alignment | not modelled | 5.7 | 12 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**calmodulin;<br>**PDBTitle:** solution structure of the c-terminal domain of soybean calmodulin2 isoform 4 fused with the calmodulin-binding domain of ntmkp1 |
| 89 | c3mn2B_ | Alignment | not modelled | 5.7 | 16 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**probable arac family transcriptional regulator;<br>**PDBTitle:** the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009 |
| 90 | d1q8ca_ | Alignment | not modelled | 5.7 | 32 | **Fold:**NusB-like<br>**Superfamily:**NusB-like<br>**Family:**Hypothetical protein MG027 |
| 91 | c2amiA_ | Alignment | not modelled | 5.6 | 7 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**caltractin;<br>**PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin |
| 92 | c1eptB_ | Alignment | not modelled | 5.6 | 71 | **PDB header:**hydrolase (serine protease)<br>**Chain:** B: **PDB Molecule:**porcine e-trypsin;<br>**PDBTitle:** refined 1.8 angstroms resolution crystal structure of2 porcine epsilon-trypsin |
| 93 | d2doda1 | Alignment | not modelled | 5.6 | 19 | **Fold:**Another 3-helical bundle<br>**Superfamily:**FF domain<br>**Family:**FF domain |
| 94 | d2pq3a1 | Alignment | not modelled | 5.5 | 15 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 95 | d1a5ja1 | Alignment | not modelled | 5.5 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 96 | c2bsjB_ | Alignment | not modelled | 5.5 | 50 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**chaperone protein syct;<br>**PDBTitle:** native crystal structure of the type iii secretion2 chaperone syct from yersinia enterocolitica |
| 97 | d1dvia_ | Alignment | not modelled | 5.4 | 8 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Penta-EF-hand proteins |
| 98 | d1a5ja2 | Alignment | not modelled | 5.3 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 99 | d1w0ua_ | Alignment | not modelled | 5.3 | 19 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**DNA-binding domain of telomeric protein |