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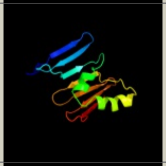
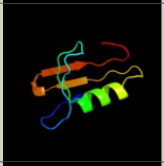
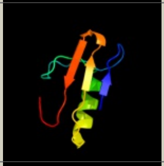
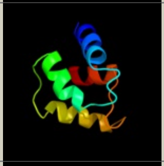
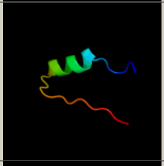
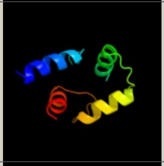
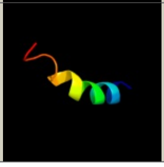
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P75988 |
| Date | Thu Jan 5 12:16:58 GMT 2012 |
| Unique Job ID | de4eb824eb653d95 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2hh8a1 | Alignment |  | 100.0 | 46 | **Fold:**YdfO-like<br>**Superfamily:**YdfO-like<br>**Family:**YdfO-like |
| 2 | d3elga1 | Alignment |  | 89.3 | 8 | **Fold:**BLIP-like<br>**Superfamily:**BT0923-like<br>**Family:**BT0923-like |
| 3 | d3duea1 | Alignment |  | 82.4 | 7 | **Fold:**BLIP-like<br>**Superfamily:**BT0923-like<br>**Family:**BT0923-like |
| 4 | c3ot2B_ | Alignment |  | 24.4 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution |
| 5 | c3ot2A_ | Alignment |  | 24.4 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution |
| 6 | c2k7bA_ | Alignment |  | 24.2 | 11 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**calcium-binding protein 1;<br>**PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain |
| 7 | c1irjG_ | Alignment |  | 23.7 | 19 | **PDB header:**metal binding protein<br>**Chain:** G: **PDB Molecule:**migration inhibitory factor-related protein 14;<br>**PDBTitle:** crystal structure of the mrp14 complexed with chaps |
| 8 | c3l23A_ | Alignment |  | 22.9 | 11 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution |
| 9 | c2ph7B_ | Alignment |  | 22.1 | 25 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein af_2093;<br>**PDBTitle:** crystal structure of af2093 from archaeoglobus fulgidus |
| 10 | d1avsa_ | Alignment |  | 21.7 | 13 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 11 | c1m7lA_ | Alignment |  | 21.2 | 37 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein d;<br>**PDBTitle:** solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d |

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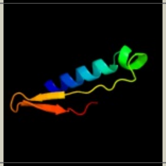
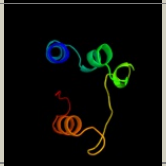
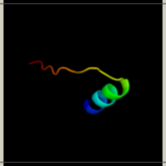
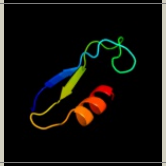
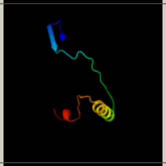
| 12 | d1m39a_ | Alignment |  | 20.0 | 18 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 13 | c2w3nA_ | Alignment |  | 18.4 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans |
| 14 | c1f8aB_ | Alignment |  | 18.2 | 11 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima-<br>**PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains |
| 15 | c3obeB_ | Alignment |  | 18.1 | 11 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution |
| 16 | d1wxaa1 | Alignment |  | 16.5 | 18 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**Ras-binding domain, RBD |
| 17 | d2gaxa1 | Alignment |  | 16.2 | 8 | **Fold:**Peptidyl-tRNA hydrolase II<br>**Superfamily:**Peptidyl-tRNA hydrolase II<br>**Family:**Peptidyl-tRNA hydrolase II |
| 18 | c2rqsA_ | Alignment |  | 16.1 | 17 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase;<br>**PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin) |
| 19 | d1xk4a1 | Alignment |  | 16.0 | 13 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 20 | d1ekja_ | Alignment |  | 15.9 | 7 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 21 | c2qlxA_ | Alignment | not modelled | 15.7 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**l-rhamnose mutarotase;<br>**PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose |
| 22 | c2qlwA_ | Alignment | not modelled | 15.7 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**rhau;<br>**PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum |
| 23 | c2hklB_ | Alignment | not modelled | 15.3 | 15 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**l,d-transpeptidase;<br>**PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant |
| 24 | d1dj0a_ | Alignment | not modelled | 14.3 | 12 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase I TruA |
| 25 | d3buxb3 | Alignment | not modelled | 14.2 | 39 | **Fold:**SH2-like<br>**Superfamily:**SH2 domain<br>**Family:**SH2 domain |
| 26 | c3ec8A_ | Alignment | not modelled | 13.9 | 9 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein flj10324;<br>**PDBTitle:** the crystal structure of the ra domain of flj10324 (radil) |
| 27 | d1i6pa_ | Alignment | not modelled | 13.8 | 20 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 28 | c2b1uA_ | Alignment | not modelled | 13.8 | 13 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**calmodulin-like protein 5;<br>**PDBTitle:** solution structure of calmodulin-like skin protein c2 terminal domain |
| | | | | | | **Fold:**Ferredoxin-like |

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| 29 | d1x8da1 | Alignment | not modelled | 13.7 | 21 | **Superfamily:**Dimeric alpha+beta barrel<br>**Family:**YiiL-like |
| 30 | d1j55a_ | Alignment | not modelled | 12.8 | 15 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 31 | d4icba_ | Alignment | not modelled | 12.7 | 12 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calbindin D9K |
| 32 | d1k8ua_ | Alignment | not modelled | 12.7 | 23 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 33 | c2z4hB_ | Alignment | not modelled | 12.3 | 8 | **PDB header:**signaling protein activator<br>**Chain:** B: **PDB Molecule:**copper homeostasis protein cutf;<br>**PDBTitle:** crystal structure of the cpx pathway activator nlpe from2 escherichia coli |
| 34 | c1vs3B_ | Alignment | not modelled | 12.2 | 12 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**trna pseudouridine synthase a;<br>**PDBTitle:** crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8 |
| 35 | c2k2aA_ | Alignment | not modelled | 12.1 | 25 | **PDB header:**contractile protein<br>**Chain:** A: **PDB Molecule:**troponin c;<br>**PDBTitle:** solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1 |
| 36 | d1urra_ | Alignment | not modelled | 12.1 | 7 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 37 | d1f53a_ | Alignment | not modelled | 11.6 | 20 | **Fold:**gamma-Crystallin-like<br>**Superfamily:**gamma-Crystallin-like<br>**Family:**Killer toxin-like protein SKLP |
| 38 | c2kaxA_ | Alignment | not modelled | 11.5 | 13 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**protein s100-a5;<br>**PDBTitle:** solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states |
| 39 | c2ggmA_ | Alignment | not modelled | 11.1 | 11 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**centrin-2;<br>**PDBTitle:** human centrin 2 xeroderma pigmentosum group c protein2 complex |
| 40 | c3p6lA_ | Alignment | not modelled | 10.9 | 9 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution |
| 41 | d1pvaa_ | Alignment | not modelled | 10.8 | 22 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Parvalbumin |
| 42 | d2p5zx2 | Alignment | not modelled | 10.7 | 12 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| 43 | c2i18A_ | Alignment | not modelled | 10.7 | 18 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**calcium-binding protein;<br>**PDBTitle:** the refined structure of c-terminal domain of an ef-hand2 calcium binding protein from entamoeba histolytica |
| 44 | d1g33a_ | Alignment | not modelled | 10.6 | 19 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Parvalbumin |
| 45 | d1e8aa_ | Alignment | not modelled | 10.5 | 19 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 46 | c2pmyB_ | Alignment | not modelled | 10.5 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**ras and ef-hand domain-containing protein;<br>**PDBTitle:** ef-hand domain of human rasef |
| 47 | d2g0wa1 | Alignment | not modelled | 10.4 | 23 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**IolI-like |
| 48 | d1apsa_ | Alignment | not modelled | 10.3 | 3 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 49 | c2rgiA_ | Alignment | not modelled | 10.3 | 23 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**protein s100-a2;<br>**PDBTitle:** crystal structure of ca2+-free s100a2 at 1.6 a resolution |
| 50 | d1c7va_ | Alignment | not modelled | 10.1 | 11 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 51 | d1xk4c1 | Alignment | not modelled | 9.9 | 19 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 52 | d1j6ya_ | Alignment | not modelled | 9.8 | 18 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 53 | d1g5ca_ | Alignment | not modelled | 9.7 | 13 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 54 | d1eq3a_ | Alignment | not modelled | 9.7 | 10 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 55 | d3d37a1 | Alignment | not modelled | 9.6 | 13 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| | | | | | | **Fold:**EF Hand-like |

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| 56 | d1fw4a_ | Alignment | not modelled | 9.5 | 12 | **Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 57 | c2dk6A_ | Alignment | not modelled | 9.4 | 18 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**parp11 protein;<br>**PDBTitle:** solution structure of wwe domain in poly (adp-ribose)2 polymerase family, member 11 (parp 11) |
| 58 | c2p5zX_ | Alignment | not modelled | 9.4 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** X: **PDB Molecule:**type vi secretion system component;<br>**PDBTitle:** the e. coli c3393 protein is a component of the type vi secretion2 system and exhibits structural similarity to t4 bacteriophage tail3 proteins gp27 and gp5 |
| 59 | d1oqpa_ | Alignment | not modelled | 9.3 | 10 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 60 | c3ucoB_ | Alignment | not modelled | 9.2 | 9 | **PDB header:**lyase/lyase inhibitor<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide |
| 61 | c2a8cE_ | Alignment | not modelled | 9.0 | 16 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** haemophilus influenzae beta-carbonic anhydrase |
| 62 | c2a4jA_ | Alignment | not modelled | 9.0 | 14 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**centrin 2;<br>**PDBTitle:** solution structure of the c-terminal domain (t94-y172) of2 the human centrin 2 in complex with a 17 residues peptide3 (p1-xpc) from xeroderma pigmentosum group c protein |
| 63 | c2l0vB_ | Alignment | not modelled | 8.9 | 23 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**protein s100-a16;<br>**PDBTitle:** solution structure of calcium(ii) bound s100a16 |
| 64 | c2kz2A_ | Alignment | not modelled | 8.7 | 13 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**calmodulin;<br>**PDBTitle:** calmodulin, c-terminal domain, f92e mutant |
| 65 | c3fdqB_ | Alignment | not modelled | 8.6 | 40 | **PDB header:**dna binding protein/dna<br>**Chain:** B: **PDB Molecule:**motility gene repressor mogr;<br>**PDBTitle:** recognition of at-rich dna binding sites by the mogr2 repressor |
| 66 | d1zmba1 | Alignment | not modelled | 8.5 | 24 | **Fold:**Flavodoxin-like<br>**Superfamily:**SGNH hydrolase<br>**Family:**Putative acetylxylan esterase-like |
| 67 | d1a4pa_ | Alignment | not modelled | 8.5 | 26 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 68 | d3cdda2 | Alignment | not modelled | 8.5 | 13 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| 69 | c1q88B_ | Alignment | not modelled | 8.5 | 17 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**39 kda initiator binding protein;<br>**PDBTitle:** crystal structure of the c-domain of the t.vaginalis inr2 binding protein, ibp39 (monoclinic form) |
| 70 | d2acya_ | Alignment | not modelled | 8.4 | 7 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 71 | d1cb1a_ | Alignment | not modelled | 8.4 | 9 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calbindin D9K |
| 72 | c2ktgA_ | Alignment | not modelled | 8.4 | 11 | **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 |
| 73 | c2k7wB_ | Alignment | not modelled | 8.4 | 29 | **PDB header:**apoptosis<br>**Chain:** B: **PDB Molecule:**bcl-2-like protein 11;<br>**PDBTitle:** bax activation is initiated at a novel interaction site |
| 74 | c3ox6C_ | Alignment | not modelled | 8.4 | 19 | **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) |
| 75 | c3h4sE_ | Alignment | not modelled | 8.3 | 13 | **PDB header:**motor protein/calcium binding protein<br>**Chain:** E: **PDB Molecule:**kcbp interacting ca2+-binding protein;<br>**PDBTitle:** structure of the complex of a mitotic kinesin with its2 calcium binding regulator |
| 76 | c3lmzA_ | Alignment | not modelled | 8.3 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative sugar isomerase;<br>**PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution |
| 77 | c3cnyA_ | Alignment | not modelled | 8.2 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**inositol catabolism protein iole;<br>**PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution |
| 78 | c2ciuA_ | Alignment | not modelled | 8.2 | 18 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**import inner membrane translocase subunit tim21<br>**PDBTitle:** structure of the ims domain of the mitochondrial import2 protein tim21 from s. cerevisiae |
| 79 | c1ponB_ | Alignment | not modelled | 8.2 | 30 | **PDB header:**calcium-binding protein<br>**Chain:** B: **PDB Molecule:**troponin c;<br>**PDBTitle:** site iii-site iv troponin c heterodimer, nmr |
| 80 | d1ftpa_ | Alignment | not modelled | 8.1 | 14 | **Fold:**Lipocalins<br>**Superfamily:**Lipocalins<br>**Family:**Fatty acid binding protein-like |
| | | | | | | **PDB header:**insulin-like brain-secretory peptide<br>**Chain:** B: **PDB Molecule:**bombyxin-ii,bombyxin a-6; |

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| 81 | c1bomB_ | Alignment | not modelled | 8.1 | 33 | **PDBTitle:** three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkmoth bombyx3 mori: comparison with insulin and relaxin |
| 82 | c3fs7D_ | Alignment | not modelled | 8.0 | 22 | **PDB header:**metal binding protein<br>**Chain:** D: **PDB Molecule:**parvalbumin, thymic;<br>**PDBTitle:** crystal structure of gallus gallus beta-parvalbumin (avian2 thymic hormone) |
| 83 | d1wrka1 | Alignment | not modelled | 8.0 | 13 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 84 | d1m45a_ | Alignment | not modelled | 8.0 | 6 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 85 | d2pq3a1 | Alignment | not modelled | 8.0 | 16 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 86 | d1ksoa_ | Alignment | not modelled | 7.9 | 23 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 87 | c1x5bA_ | Alignment | not modelled | 7.9 | 15 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2;<br>**PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2 |
| 88 | c2bjeA_ | Alignment | not modelled | 7.9 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acylphosphatase;<br>**PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group |
| 89 | d1sw8a_ | Alignment | not modelled | 7.8 | 20 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 90 | d1wdja_ | Alignment | not modelled | 7.8 | 13 | **Fold:**Restriction endonuclease-like<br>**Superfamily:**Restriction endonuclease-like<br>**Family:**Hypothetical protein TT1808 (TTHA1514) |
| 91 | c3ereD_ | Alignment | not modelled | 7.8 | 15 | **PDB header:**dna binding protein/dna<br>**Chain:** D: **PDB Molecule:**arginine repressor;<br>**PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator |
| 92 | c3ngfA_ | Alignment | not modelled | 7.7 | 27 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ap endonuclease, family 2;<br>**PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis |
| 93 | d1qx2a_ | Alignment | not modelled | 7.6 | 13 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calbindin D9K |
| 94 | c2kdhA_ | Alignment | not modelled | 7.6 | 11 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles;<br>**PDBTitle:** the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate |
| 95 | d2obha1 | Alignment | not modelled | 7.5 | 15 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 96 | c1ozsA_ | Alignment | not modelled | 7.4 | 13 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles;<br>**PDBTitle:** c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i |
| 97 | d1q88a_ | Alignment | not modelled | 7.4 | 17 | **Fold:**39 kda initiator binding protein, IBP39, C-terminal domains<br>**Superfamily:**39 kda initiator binding protein, IBP39, C-terminal domains<br>**Family:**39 kda initiator binding protein, IBP39, C-terminal domains |
| 98 | d1yuta1 | Alignment | not modelled | 7.4 | 10 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**S100 proteins |
| 99 | d1zaca_ | Alignment | not modelled | 7.4 | 19 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |