Phyre2

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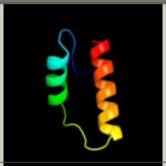
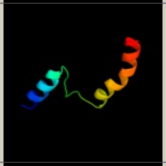
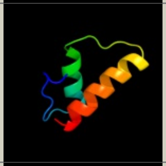
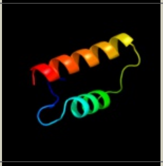
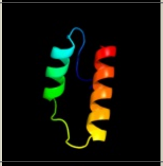
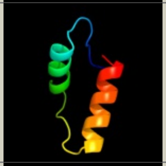
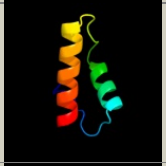
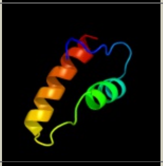
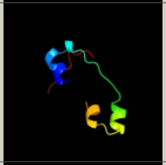
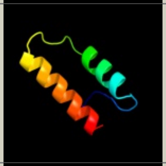
| Email | l.a.kelley@imperial.ac.uk |
| Description | P24082 |
| Date | Thu Jan 5 11:40:43 GMT 2012 |
| Unique Job ID | c4293149cc0b3a3a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2r09A_ | Alignment |  | 70.9 | 11 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**cytohesin-3;<br>**PDBTitle:** crystal structure of autoinhibited form of grp1 arf gtpase exchange2 factor |
| 2 | d1nxha_ | Alignment |  | 69.1 | 23 | **Fold:**Hypothetical protein MTH393<br>**Superfamily:**Hypothetical protein MTH393<br>**Family:**Hypothetical protein MTH393 |
| 3 | d1re0b_ | Alignment |  | 67.6 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 4 | d1xsza1 | Alignment |  | 67.1 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 5 | d1pbva_ | Alignment |  | 66.6 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 6 | d1ku1a_ | Alignment |  | 65.9 | 12 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 7 | d2r09a1 | Alignment |  | 65.3 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 8 | d1r8se_ | Alignment |  | 63.7 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 9 | c2bkxB_ | Alignment |  | 58.3 | 24 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase;<br>**PDBTitle:** structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily |
| 10 | c1xszA_ | Alignment |  | 56.5 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**guanine nucleotide exchange protein;<br>**PDBTitle:** the structure of ralf |
| 11 | d1a8ra_ | Alignment |  | 51.9 | 30 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |

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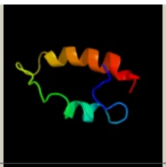
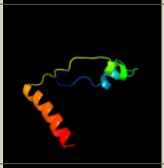
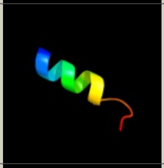
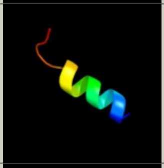
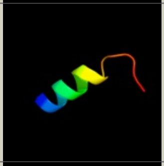
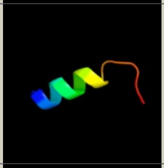
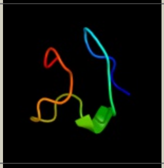
|---|---|---|---|---|---|---|
| 12 | d1bc9a_ | Alignment |  | 43.4 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**Sec7 domain<br>**Family:**Sec7 domain |
| 13 | c2plyB_ | Alignment |  | 43.2 | 19 | **PDB header:**translation/rna<br>**Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor;<br>**PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna. |
| 14 | c1is7F_ | Alignment |  | 43.0 | 50 | **PDB header:**hydrolase/protein binding<br>**Chain:** F: **PDB Molecule:**gtp cyclohydrolase i;<br>**PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex |
| 15 | d1wpla_ | Alignment |  | 43.0 | 50 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |
| 16 | c1wm9D_ | Alignment |  | 42.4 | 44 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**gtp cyclohydrolase i;<br>**PDBTitle:** structure of gtp cyclohydrolase i from thermus thermophilus hb8 |
| 17 | d1wura1 | Alignment |  | 42.4 | 44 | **Fold:**T-fold<br>**Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like<br>**Family:**GTP cyclohydrolase I |
| 18 | c2kriB_ | Alignment |  | 35.8 | 32 | **PDB header:**protein binding/endocytosis<br>**Chain:** B: **PDB Molecule:**low-density lipoprotein receptor;<br>**PDBTitle:** structure of a complex between domain v of beta2-2 glycoprotein i and the fourth ligand-binding module from3 ldlr determined with haddock |
| 19 | d2fcwb2 | Alignment |  | 35.7 | 32 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 20 | d2fcwb1 | Alignment |  | 33.0 | 32 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 21 | c3a7qB_ | Alignment | not modelled | 32.9 | 28 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**low-density lipoprotein receptor-related protein 8;<br>**PDBTitle:** structural basis for specific recognition of reelin by its receptors |
| 22 | c1wloA_ | Alignment | not modelled | 30.6 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**sufe protein;<br>**PDBTitle:** solution structure of the hypothetical protein from thermus2 thermophilus hb8 |
| 23 | d1ni7a_ | Alignment | not modelled | 30.3 | 20 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**SufE-like |
| 24 | c1f8zA_ | Alignment | not modelled | 29.7 | 16 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**low-density lipoprotein receptor;<br>**PDBTitle:** nmr structure of the sixth ligand-binding module of the ldl2 receptor |
| 25 | d1f8za_ | Alignment | not modelled | 29.7 | 16 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 26 | c1d2jA_ | Alignment | not modelled | 28.9 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**low-density lipoprotein receptor;<br>**PDBTitle:** ldl receptor ligand-binding module 6 |
| 27 | d1ajja_ | Alignment | not modelled | 28.3 | 24 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 28 | d1n7da7 | Alignment | not modelled | 28.1 | 32 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| | | | | | | **PDB header:**hydrolase |

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| 29 | c3a23A_ | Alignment | not modelled | 23.2 | 13 | **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase;<br>**PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose |
| 30 | c2ekwC_ | Alignment | not modelled | 23.1 | 21 | **PDB header:**contractile protein<br>**Chain:** C: **PDB Molecule:**myosin catalytic light chain lc-1, mantle muscle;<br>**PDBTitle:** the crystal structure of squid myosin s1 in the presence of2 so4 2- |
| 31 | d1j8ea_ | Alignment | not modelled | 23.1 | 28 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 32 | c4a18U_ | Alignment | not modelled | 22.8 | 33 | **PDB header:**ribosome<br>**Chain:** U: **PDB Molecule:**rpl13;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1 |
| 33 | c3u5eL_ | Alignment | not modelled | 22.2 | 27 | **PDB header:**ribosome<br>**Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a;<br>**PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution |
| 34 | d2enda_ | Alignment | not modelled | 22.1 | 13 | **Fold:**T4 endonuclease V<br>**Superfamily:**T4 endonuclease V<br>**Family:**T4 endonuclease V |
| 35 | c2eboB_ | Alignment | not modelled | 21.6 | 14 | **PDB header:**envelope glycoprotein<br>**Chain:** B: **PDB Molecule:**ebola virus envelope glycoprotein;<br>**PDBTitle:** core structure of gp2 from ebola virus |
| 36 | d1e7la1 | Alignment | not modelled | 21.4 | 12 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**Recombination endonuclease VII, C-terminal and dimerization domains<br>**Family:**Recombination endonuclease VII, C-terminal and dimerization domains |
| 37 | d2gtln2 | Alignment | not modelled | 21.0 | 24 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 38 | c1tpgA_ | Alignment | not modelled | 20.1 | 12 | **PDB header:**plasminogen activation<br>**Chain:** A: **PDB Molecule:**t-plasminogen activator f1-g;<br>**PDBTitle:** f1-g module pair residues 1-91 (c83s) of tissue-type2 plasminogen activator (t-pa) (nmr, 298k, ph2.95,3 representative structure) |
| 39 | d2gtlm2 | Alignment | not modelled | 18.9 | 24 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 40 | c3fwcO_ | Alignment | not modelled | 18.6 | 18 | **PDB header:**cell cycle, transcription<br>**Chain:** O: **PDB Molecule:**protein sus1;<br>**PDBTitle:** sac3:sus1:cdc31 complex |
| 41 | c1ponB_ | Alignment | not modelled | 16.1 | 33 | **PDB header:**calcium-binding protein<br>**Chain:** B: **PDB Molecule:**troponin c;<br>**PDBTitle:** site iii-site iv troponin c heterodimer, nmr |
| 42 | c3qfwB_ | Alignment | not modelled | 16.0 | 27 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase/oxygenase large<br>**PDBTitle:** crystal structure of rubisco-like protein from rhodopseudomonas2 palustris |
| 43 | d1qwoa_ | Alignment | not modelled | 16.0 | 23 | **Fold:**Phosphoglycerate mutase-like<br>**Superfamily:**Phosphoglycerate mutase-like<br>**Family:**Histidine acid phosphatase |
| 44 | d1bjfa_ | Alignment | not modelled | 15.9 | 18 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 45 | d2gtlo2 | Alignment | not modelled | 15.7 | 32 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 46 | c1mgpA_ | Alignment | not modelled | 15.6 | 12 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**hypothetical protein tm841;<br>**PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function |
| 47 | d1mgpa_ | Alignment | not modelled | 15.6 | 12 | **Fold:**DAK1/DegV-like<br>**Superfamily:**DAK1/DegV-like<br>**Family:**DegV-like |
| 48 | d1f7ea_ | Alignment | not modelled | 15.4 | 13 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**EGF/Laminin<br>**Family:**EGF-type module |
| 49 | c1tt3A_ | Alignment | not modelled | 15.2 | 39 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**omega-conotoxin mviia;<br>**PDBTitle:** nmr soulution structure of omega-conotoxin [k10]mviia |
| 50 | d1g8ia_ | Alignment | not modelled | 15.1 | 23 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 51 | d1mzga_ | Alignment | not modelled | 14.8 | 8 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**SufE-like |
| 52 | c3h5cB_ | Alignment | not modelled | 14.8 | 28 | **PDB header:**hydrolase inhibitor/blood clotting<br>**Chain:** B: **PDB Molecule:**vitamin k-dependent protein z;<br>**PDBTitle:** x-ray structure of protein z-protein z inhibitor complex |
| 53 | c2xzmS_ | Alignment | not modelled | 14.6 | 17 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**rps15e;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 54 | d1wdcc_ | Alignment | not modelled | 14.5 | 12 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |

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| 55 | c2xgvA_ | Alignment | not modelled | 13.9 | 11 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**psiv capsid n-terminal domain;<br>**PDBTitle:** structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik) |
| 56 | c2lgpA_ | Alignment | not modelled | 13.4 | 33 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**low-density lipoprotein receptor;<br>**PDBTitle:** solution structure of la45 from ldlr |
| 57 | c3gmxB_ | Alignment | not modelled | 13.3 | 35 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**blp;<br>**PDBTitle:** crystal structure of beta-lactamse inhibitory protein-like2 protein (blp) at 1.05 angstrom resolution |
| 58 | d2bbga_ | Alignment | not modelled | 13.2 | 27 | **Fold:**Amb V allergen<br>**Superfamily:**Amb V allergen<br>**Family:**Amb V allergen |
| 59 | d1cixa_ | Alignment | not modelled | 12.6 | 46 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**omega toxin-like<br>**Family:**Spider toxins |
| 60 | c1g6uB_ | Alignment | not modelled | 12.3 | 27 | **PDB header:**de novo protein<br>**Chain:** B: **PDB Molecule:**domain swapped dimer;<br>**PDBTitle:** crystal structure of a domain swapped dimer |
| 61 | c3gmvX_ | Alignment | not modelled | 12.3 | 26 | **PDB header:**protein binding<br>**Chain:** X: **PDB Molecule:**beta-lactamase inhibitory protein blip-i;<br>**PDBTitle:** crystal structure of beta-lactamse inhibitory protein-i2 (blip-i) in apo form |
| 62 | c2i1pA_ | Alignment | not modelled | 12.2 | 21 | **PDB header:**ligand binding protein<br>**Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein<br>**PDBTitle:** solution structure of the twelfth cysteine-rich ligand-2 binding repeat in rat megalin |
| 63 | c2jm4A_ | Alignment | not modelled | 12.1 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**relaxin receptor 1;<br>**PDBTitle:** the solution nmr structure of the relaxin (rxfp1) receptor2 ldla module. |
| 64 | c3pbiA_ | Alignment | not modelled | 12.1 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**invasion protein;<br>**PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution |
| 65 | d2o8ra1 | Alignment | not modelled | 12.0 | 13 | **Fold:**Spectrin repeat-like<br>**Superfamily:**PPK N-terminal domain-like<br>**Family:**PPK N-terminal domain-like |
| 66 | d1whra_ | Alignment | not modelled | 11.9 | 15 | **Fold:**IF3-like<br>**Superfamily:**R3H domain<br>**Family:**R3H domain |
| 67 | c2k1gA_ | Alignment | not modelled | 11.8 | 27 | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**lipoprotein spr;<br>**PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162 |
| 68 | c2on3A_ | Alignment | not modelled | 11.6 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ornithine decarboxylase;<br>**PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane |
| 69 | c2fcdA_ | Alignment | not modelled | 11.5 | 22 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**myosin light chain 1;<br>**PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae |
| 70 | c2xivA_ | Alignment | not modelled | 11.3 | 21 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**hypothetical invasion protein;<br>**PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis |
| 71 | c2knyA_ | Alignment | not modelled | 11.1 | 32 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**lrp-1, linker, apo-e;<br>**PDBTitle:** fusion construct of cr17 from lrp-1 and apoe residues 130-149 |
| 72 | d1bpoa1 | Alignment | not modelled | 10.9 | 29 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**ARM repeat<br>**Family:**Clathrin heavy-chain linker domain |
| 73 | c2fylB_ | Alignment | not modelled | 10.9 | 23 | **PDB header:**surface active protein<br>**Chain:** B: **PDB Molecule:**low-density lipoprotein receptor-related protein<br>**PDBTitle:** haddock model of the complex between double module of lrp,2 cr56, and first domain of receptor associated protein, rap-3 d1. |
| 74 | c2fcwB_ | Alignment | not modelled | 10.1 | 32 | **PDB header:**lipid transport/endocytosis/chaperone<br>**Chain:** B: **PDB Molecule:**low-density lipoprotein receptor;<br>**PDBTitle:** structure of a complex between the pair of the ldl receptor2 ligand-binding modules 3-4 and the receptor associated3 protein (rap). |
| 75 | d1o66a_ | Alignment | not modelled | 9.7 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Phosphoenolpyruvate/pyruvate domain<br>**Family:**Ketopantoate hydroxymethyltransferase PanB |
| 76 | d1odha_ | Alignment | not modelled | 9.6 | 37 | **Fold:**GCM domain<br>**Superfamily:**GCM domain<br>**Family:**GCM domain |
| 77 | c2iswB_ | Alignment | not modelled | 9.5 | 9 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase;<br>**PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate |
| 78 | d1dval1 | Alignment | not modelled | 9.5 | 19 | **Fold:**Knottins (small inhibitors, toxins, lectins)<br>**Superfamily:**EGF/Laminin<br>**Family:**EGF-type module |
| 79 | d1r75a_ | Alignment | not modelled | 9.4 | 26 | **Fold:**Smp-1-like<br>**Superfamily:**Smp-1-like<br>**Family:**Smp-1-like |

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|---|---|---|---|---|---|---|
| 80 | c2kvcA_ | Alignment | not modelled | 9.2 | 23 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a |
| 81 | d1k7ba_ | Alignment | not modelled | 9.1 | 24 | **Fold:**LDL receptor-like module<br>**Superfamily:**LDL receptor-like module<br>**Family:**LDL receptor-like module |
| 82 | c3gt2A_ | Alignment | not modelled | 9.1 | 13 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c |
| 83 | c3i86A_ | Alignment | not modelled | 9.1 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204 |
| 84 | d1k4ta3 | Alignment | not modelled | 9.0 | 17 | **Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment<br>**Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment<br>**Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment |
| 85 | c2rpbA_ | Alignment | not modelled | 8.9 | 6 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**hypothetical membrane protein;<br>**PDBTitle:** the solution structure of membrane protein |
| 86 | d3by5a1 | Alignment | not modelled | 8.8 | 12 | **Fold:**CobE/GbiG C-terminal domain-like<br>**Superfamily:**CobE/GbiG C-terminal domain-like<br>**Family:**CobE/GbiG C-terminal domain-like |
| 87 | c3by5A_ | Alignment | not modelled | 8.8 | 12 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein;<br>**PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58 |
| 88 | c3si5X_ | Alignment | not modelled | 8.8 | 38 | **PDB header:**cell cycle<br>**Chain:** X: **PDB Molecule:**protein casc5;<br>**PDBTitle:** kinetochore-bubr1 kinase complex |
| 89 | d1ay7b_ | Alignment | not modelled | 8.7 | 13 | **Fold:**Barstar-like<br>**Superfamily:**Barstar-related<br>**Family:**Barstar-related |
| 90 | c2knxA_ | Alignment | not modelled | 8.2 | 32 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**prolow-density lipoprotein receptor-related protein 1;<br>**PDBTitle:** solution structure of complement repeat cr17 from lrp-1 |
| 91 | c2ojlB_ | Alignment | not modelled | 8.2 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68. |
| 92 | c3n2bD_ | Alignment | not modelled | 7.5 | 17 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae. |
| 93 | c2ri0B_ | Alignment | not modelled | 7.5 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase;<br>**PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans |
| 94 | c2xr9A_ | Alignment | not modelled | 7.4 | 31 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family<br>**PDBTitle:** crystal structure of autotaxin (enpp2) |
| 95 | d2v9va1 | Alignment | not modelled | 7.4 | 71 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**C-terminal fragment of elongation factor SelB |
| 96 | c2npbA_ | Alignment | not modelled | 7.3 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**selenoprotein w;<br>**PDBTitle:** nmr solution structure of mouse selw |
| 97 | d2j8ba1 | Alignment | not modelled | 7.2 | 18 | **Fold:**Snake toxin-like<br>**Superfamily:**Snake toxin-like<br>**Family:**Extracellular domain of cell surface receptors |
| 98 | c1y89B_ | Alignment | not modelled | 7.1 | 38 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**devb protein;<br>**PDBTitle:** crystal structure of devb protein |
| 99 | c2p0gB_ | Alignment | not modelled | 7.1 | 30 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**selenoprotein w-related protein;<br>**PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75 |