Phyre$^2$

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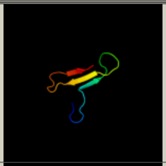
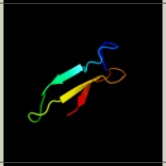
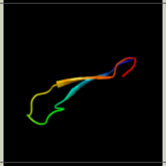
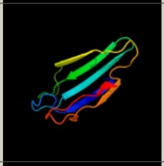
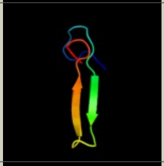
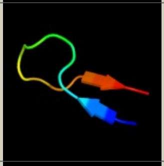
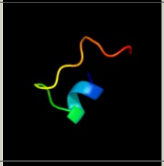
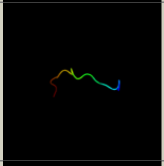
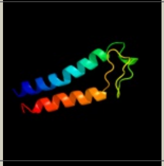
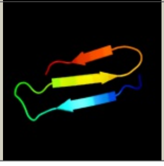
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P45804 |
| Date | Thu Jan 5 12:03:49 GMT 2012 |
| Unique Job ID | 1e3cecdfbfaf4d4f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2zuxA_ | Alignment |  | 84.5 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**yesw protein;<br>**PDBTitle:** crystal structure of rhamnogalacturonan lyase yesw2 complexed with rhamnose |
| 2 | c2zuyA_ | Alignment |  | 81.8 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**yesx protein;<br>**PDBTitle:** crystal structure of exotype rhamnogalacturonan lyase yesx |
| 3 | c2c4dA_ | Alignment |  | 68.2 | 24 | **PDB header:**lectin<br>**Chain:** A: **PDB Molecule:**psathyrella velutina lectin pvl;<br>**PDBTitle:** 2.6a crystal structure of psathyrella velutina lectin in2 complex with n-acetylglucosamine |
| 4 | c3fcsA_ | Alignment |  | 58.4 | 16 | **PDB header:**cell adhesion/blood clotting<br>**Chain:** A: **PDB Molecule:**integrin, alpha 2b;<br>**PDBTitle:** structure of complete ectodomain of integrin aiibb3 |
| 5 | d1k1xa2 | Alignment |  | 53.6 | 24 | **Fold:**Supersandwich<br>**Superfamily:**Galactose mutarotase-like<br>**Family:**4-alpha-glucanotransferase, C-terminal domain |
| 6 | c3od9B_ | Alignment |  | 49.5 | 50 | **PDB header:**hydrolase inhibitor<br>**Chain:** B: **PDB Molecule:**putative exported protein;<br>**PDBTitle:** crystal structure of plii-ah, periplasmic lysozyme inhibitor of i-type2 lysozyme from aeromonas hydrophyla |
| 7 | d1ig4a_ | Alignment |  | 22.4 | 11 | **Fold:**DNA-binding domain<br>**Superfamily:**DNA-binding domain<br>**Family:**Methyl-CpG-binding domain, MBD |
| 8 | c2xq2A_ | Alignment |  | 21.3 | 8 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**sodium/glucose cotransporter;<br>**PDBTitle:** structure of the k294a mutant of vsglt |
| 9 | c2k2dA_ | Alignment |  | 20.9 | 13 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain-<br>**PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c |
| 10 | c2bbjB_ | Alignment |  | 19.1 | 13 | **PDB header:**metal transport/membrane protein<br>**Chain:** B: **PDB Molecule:**divalent cation transport-related protein;<br>**PDBTitle:** crystal structure of the cora mg2+ transporter |
| 11 | c2rrfA_ | Alignment |  | 18.2 | 25 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 21;<br>**PDBTitle:** the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21 |

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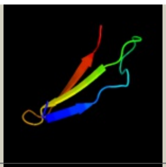
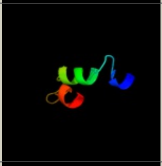
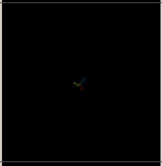
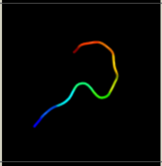
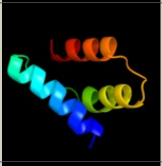
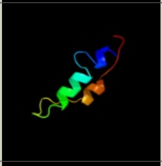
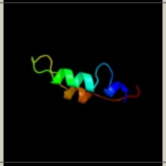
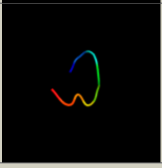
| 12 | d1jv2a4 | Alignment |  | 17.1 | 26 | **Fold:**7-bladed beta-propeller<br>**Superfamily:**Integrin alpha N-terminal domain<br>**Family:**Integrin alpha N-terminal domain |
| 13 | c2q14A_ | Alignment |  | 16.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphohydrolase;<br>**PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution |
| 14 | c1mv3A_ | Alignment |  | 16.4 | 29 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**myc box dependent interacting protein 1;<br>**PDBTitle:** nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc |
| 15 | c3f2eA_ | Alignment |  | 16.0 | 42 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**sirv coat protein;<br>**PDBTitle:** crystal structure of yellowstone sirv coat protein c-2 terminus |
| 16 | d1qusa_ | Alignment |  | 15.7 | 30 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Bacterial muramidase, catalytic domain |
| 17 | c3dd7A_ | Alignment |  | 14.3 | 11 | **PDB header:**ribosome inhibitor<br>**Chain:** A: **PDB Molecule:**death on curing protein;<br>**PDBTitle:** structure of doch66y in complex with the c-terminal domain of phd |
| 18 | c2o6iA_ | Alignment |  | 13.6 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hd domain protein;<br>**PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase |
| 19 | d2o6ia1 | Alignment |  | 13.6 | 17 | **Fold:**HD-domain/PDEase-like<br>**Superfamily:**HD-domain/PDEase-like<br>**Family:**HD domain |
| 20 | c1s8kA_ | Alignment |  | 13.4 | 56 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**toxin bmkk4;<br>**PDBTitle:** solution structure of bmkk4, a novel potassium channel2 blocker from scorpion buthus martensii karsch, 253 structures |
| 21 | d2ppxa1 | Alignment | not modelled | 12.3 | 14 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**SinR domain-like |
| 22 | c2ppxA_ | Alignment | not modelled | 12.3 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu1735;<br>**PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens |
| 23 | c2dk6A_ | Alignment | not modelled | 12.1 | 10 | **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) |
| 24 | c2kq5A_ | Alignment | not modelled | 11.7 | 22 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**avirulence protein;<br>**PDBTitle:** solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha |
| 25 | c1w1nA_ | Alignment | not modelled | 11.6 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase tor1;<br>**PDBTitle:** the solution structure of the fatc domain of the protein2 kinase tor1 from yeast |
| 26 | c1x4rA_ | Alignment | not modelled | 11.5 | 26 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**parp14 protein;<br>**PDBTitle:** solution structure of wwe domain in parp14 protein |
| 27 | c2k0rA_ | Alignment | not modelled | 11.5 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbd;<br>**PDBTitle:** solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis |
| 28 | d1r4ga_ | Alignment | not modelled | 11.4 | 21 | **Fold:**immunoglobulin/albumin-binding domain-like<br>**Superfamily:**Phosphoprotein XD domain<br>**Family:**Phosphoprotein XD domain |
|  |  |  |  |  |  | **PDB header:**transferase |

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|---|---|---|---|---|---|---|
| 29 | c1k1yA_ | Alignment | not modelled | 11.3 | 28 | **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase;<br>**PDBTitle:** crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose |
| 30 | d1nekd_ | Alignment | not modelled | 10.9 | 15 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Fumarate reductase respiratory complex transmembrane subunits<br>**Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD) |
| 31 | c2ky8A_ | Alignment | not modelled | 10.9 | 17 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2;<br>**PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence |
| 32 | c2qf9B_ | Alignment | not modelled | 10.8 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative secreted protein;<br>**PDBTitle:** crystal structure of putative secreted protein duf305 from2 streptomyces coelicolor |
| 33 | d1ujra_ | Alignment | not modelled | 10.7 | 20 | **Fold:**WWE domain<br>**Superfamily:**WWE domain<br>**Family:**WWE domain |
| 34 | c1pzuH_ | Alignment | not modelled | 10.6 | 14 | **PDB header:**transcription/dna<br>**Chain:** H: **PDB Molecule:**nuclear factor of activated t-cells, cytoplasmic<br>**PDBTitle:** an asymmetric nfat1-rhr homodimer on a pseudo-palindromic,2 kappa-b site |
| 35 | c1l5gA_ | Alignment | not modelled | 10.5 | 24 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha v;<br>**PDBTitle:** crystal structure of the extracellular segment of integrin avb3 in2 complex with an arg-gly-asp ligand |
| 36 | c2d8jA_ | Alignment | not modelled | 10.5 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fyn-related kinase;<br>**PDBTitle:** solution structure of the sh3 domain of fyn-related kinase |
| 37 | d1a3qa1 | Alignment | not modelled | 10.5 | 18 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain |
| 38 | c2ov2O_ | Alignment | not modelled | 10.3 | 27 | **PDB header:**protein binding/transferase<br>**Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4;<br>**PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4) |
| 39 | c2dbmA_ | Alignment | not modelled | 10.2 | 15 | **PDB header:**transferase, signaling protein<br>**Chain:** A: **PDB Molecule:**sh3-containing grb2-like protein 2;<br>**PDBTitle:** solution structures of the sh3 domain of human sh3-2 containing grb2-like protein 2 |
| 40 | d2r6gf1 | Alignment | not modelled | 10.0 | 11 | **Fold:**MalF N-terminal region-like<br>**Superfamily:**MalF N-terminal region-like<br>**Family:**MalF N-terminal region-like |
| 41 | d1ofcx1 | Alignment | not modelled | 9.7 | 15 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Myb/SANT domain |
| 42 | c2yrvA_ | Alignment | not modelled | 9.7 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a;<br>**PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1 |
| 43 | c1yn8E_ | Alignment | not modelled | 9.7 | 8 | **PDB header:**unknown function<br>**Chain:** E: **PDB Molecule:**nap1-binding protein 2;<br>**PDBTitle:** sh3 domain of yeast nbp2 |
| 44 | c2yunA_ | Alignment | not modelled | 9.5 | 6 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**nostrin;<br>**PDBTitle:** solution structure of the sh3 domain of human nostrin |
| 45 | d1jo8a_ | Alignment | not modelled | 9.4 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 46 | c3v4vA_ | Alignment | not modelled | 9.4 | 24 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-4;<br>**PDBTitle:** crystal structure of a4b7 headpiece complexed with fab act-1 and2 ro0505376 |
| 47 | c2hw4A_ | Alignment | not modelled | 9.4 | 15 | **PDB header:**structural genomics, hydrolase<br>**Chain:** A: **PDB Molecule:**14 kda phosphohistidine phosphatase;<br>**PDBTitle:** crystal structure of human phosphohistidine phosphatase |
| 48 | d1tyea_ | Alignment | not modelled | 9.2 | 23 | **Fold:**7-bladed beta-propeller<br>**Superfamily:**Integrin alpha N-terminal domain<br>**Family:**Integrin alpha N-terminal domain |
| 49 | c2x3wD_ | Alignment | not modelled | 9.1 | 19 | **PDB header:**endocytosis<br>**Chain:** D: **PDB Molecule:**protein kinase c and casein kinase substrate in neurons<br>**PDBTitle:** structure of mouse syndapin i (crystal form 2) |
| 50 | c1jrjA_ | Alignment | not modelled | 9.0 | 17 | **PDB header:**hormone/growth factor<br>**Chain:** A: **PDB Molecule:**exendin-4;<br>**PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol |
| 51 | c2ed1A_ | Alignment | not modelled | 9.0 | 27 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**130 kda phosphatidylinositol 4,5-biphosphate-<br>**PDBTitle:** solution structure of the sh3 domain of 130 kda2 phosphatidylinositol 4,5-biphosphate-dependent arf1 gtpase-3 activating protein |
| 52 | c1z9zA_ | Alignment | not modelled | 8.9 | 19 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1;<br>**PDBTitle:** crystal structure of yeast sla1 sh3 domain 3 |
| 53 | c2j8aA_ | Alignment | not modelled | 8.8 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4<br>**PDBTitle:** x-ray structure of the n-terminus rrm domain of set1 |
| | | | | | | **PDB header:**lyase/rna |

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| 54 | c1k8wA_ | Alignment | not modelled | 8.7 | 18 | **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b;<br>**PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna |
| 55 | c3fmyA_ | Alignment | not modelled | 8.6 | 21 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa<br>**PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021) |
| 56 | d1sjqa_ | Alignment | not modelled | 8.6 | 13 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD<br>**Family:**Canonical RBD |
| 57 | d1shfa_ | Alignment | not modelled | 8.6 | 16 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 58 | c2hlgA_ | Alignment | not modelled | 8.6 | 67 | **PDB header:**plant protein<br>**Chain:** A: **PDB Molecule:**fruit-specific protein;<br>**PDBTitle:** nmr solution structure of a new tomato peptide |
| 59 | c3mmlE_ | Alignment | not modelled | 8.4 | 7 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**allophanate hydrolase subunit 2;<br>**PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436 |
| 60 | c2y3nB_ | Alignment | not modelled | 8.3 | 71 | **PDB header:**structrual protein/hydrolase<br>**Chain:** B: **PDB Molecule:**cellulosomal family-48 processive glycoside hydrolase;<br>**PDBTitle:** type ii cohesin-dockerin domain from bacteroides cellolosolvens |
| 61 | d1ohzb_ | Alignment | not modelled | 8.3 | 57 | **Fold:**Type I dockerin domain<br>**Superfamily:**Type I dockerin domain<br>**Family:**Type I dockerin domain |
| 62 | c2egcA_ | Alignment | not modelled | 8.2 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a;<br>**PDBTitle:** solution structure of the fifth sh3 domain from human2 kiaa0418 protein |
| 63 | d1k4us_ | Alignment | not modelled | 8.2 | 10 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 64 | d1dava_ | Alignment | not modelled | 8.2 | 57 | **Fold:**Type I dockerin domain<br>**Superfamily:**Type I dockerin domain<br>**Family:**Type I dockerin domain |
| 65 | d1vlba4 | Alignment | not modelled | 8.2 | 15 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 66 | d1t0ha_ | Alignment | not modelled | 8.1 | 6 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 67 | c1jqsB_ | Alignment | not modelled | 7.9 | 33 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog |
| 68 | d1k8wa5 | Alignment | not modelled | 7.9 | 18 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 69 | d1ujya_ | Alignment | not modelled | 7.9 | 10 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 70 | d1q90b_ | Alignment | not modelled | 7.8 | 13 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 71 | d1wosa2 | Alignment | not modelled | 7.7 | 15 | **Fold:**Folate-binding domain<br>**Superfamily:**Folate-binding domain<br>**Family:**Aminomethyltransferase folate-binding domain |
| 72 | d1gcqa_ | Alignment | not modelled | 7.7 | 23 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 73 | d1u5ta2 | Alignment | not modelled | 7.7 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Vacuolar sorting protein domain |
| 74 | c1wxpA_ | Alignment | not modelled | 7.7 | 12 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**tho complex subunit 1;<br>**PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84 |
| 75 | d1cska_ | Alignment | not modelled | 7.6 | 8 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 76 | d2hw4a1 | Alignment | not modelled | 7.6 | 15 | **Fold:**PHP14-like<br>**Superfamily:**PHP14-like<br>**Family:**Janus/Ocnus |
| 77 | c2vn5B_ | Alignment | not modelled | 7.6 | 57 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**endoglucanase a;<br>**PDBTitle:** the clostridium cellulolyticum dockerin displays a dual2 binding mode for its cohesin partner |
| 78 | d1r3ea2 | Alignment | not modelled | 7.5 | 20 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 79 | c1griA_ | Alignment | not modelled | 7.4 | 18 | **PDB header:**signal transduction adaptor<br>**Chain:** A: **PDB Molecule:**growth factor bound protein 2;<br>**PDBTitle:** grb2 |
| 80 | d1x4da1 | Alignment | not modelled | 7.4 | 29 | **Fold:**Ferredoxin-like<br>**Superfamily:**RNA-binding domain, RBD |

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|---|---|---|---|---|---|---|
| | | | | | | **Family:**Canonical RBD |
| 81 | c1gm5A_ | Alignment | not modelled | 7.4 | 17 | **PDB header:**helicase<br>**Chain:** A: **PDB Molecule:**recg;<br>**PDBTitle:** structure of recg bound to three-way dna junction |
| 82 | d1uj0a_ | Alignment | not modelled | 7.4 | 26 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 83 | d1rm6a2 | Alignment | not modelled | 7.4 | 20 | **Fold:**Molybdenum cofactor-binding domain<br>**Superfamily:**Molybdenum cofactor-binding domain<br>**Family:**Molybdenum cofactor-binding domain |
| 84 | c2qneA_ | Alignment | not modelled | 7.3 | 8 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative methyltransferase;<br>**PDBTitle:** crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution |
| 85 | d2fc6a1 | Alignment | not modelled | 7.3 | 33 | **Fold:**CCCH zinc finger<br>**Superfamily:**CCCH zinc finger<br>**Family:**CCCH zinc finger |
| 86 | c2dnuA_ | Alignment | not modelled | 7.2 | 11 | **PDB header:**structural genomics, structural protein<br>**Chain:** A: **PDB Molecule:**sh3 multiple domains 1;<br>**PDBTitle:** solution structure of rsgi ruh-061, a sh3 domain from human |
| 87 | d1m3ya1 | Alignment | not modelled | 7.2 | 30 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Group II dsDNA viruses VP<br>**Family:**Major capsid protein vp54 |
| 88 | c3p0dD_ | Alignment | not modelled | 7.2 | 57 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**glycoside hydrolase family 9;<br>**PDBTitle:** crystal structure of a multimodular ternary protein complex from2 clostridium thermocellum |
| 89 | c1a3qA_ | Alignment | not modelled | 7.2 | 18 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**protein (nuclear factor kappa-b p52);<br>**PDBTitle:** human nf-kappa-b p52 bound to dna |
| 90 | c1w70A_ | Alignment | not modelled | 7.1 | 16 | **PDB header:**sh3 domain<br>**Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4;<br>**PDBTitle:** sh3 domain of p40phox complexed with c-terminal polyproline2 region of p47phox |
| 91 | d1efna_ | Alignment | not modelled | 7.1 | 16 | **Fold:**SH3-like barrel<br>**Superfamily:**SH3-domain<br>**Family:**SH3-domain |
| 92 | d2fb1a2 | Alignment | not modelled | 7.1 | 12 | **Fold:**Nudix<br>**Superfamily:**Nudix<br>**Family:**BT0354 N-terminal domain-like |
| 93 | c2fb1A_ | Alignment | not modelled | 7.0 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein;<br>**PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron |
| 94 | c3eamB_ | Alignment | not modelled | 7.0 | 13 | **PDB header:**membrane protein, transport protein<br>**Chain:** B: **PDB Molecule:**glr4197 protein;<br>**PDBTitle:** an open-pore structure of a bacterial pentameric ligand-2 gated ion channel |
| 95 | d2cclb1 | Alignment | not modelled | 7.0 | 57 | **Fold:**Type I dockerin domain<br>**Superfamily:**Type I dockerin domain<br>**Family:**Type I dockerin domain |
| 96 | c2dl4A_ | Alignment | not modelled | 7.0 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein stac;<br>**PDBTitle:** solution structure of the first sh3 domain of stac protein |
| 97 | d2bvca1 | Alignment | not modelled | 7.0 | 29 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Glutamine synthetase, N-terminal domain<br>**Family:**Glutamine synthetase, N-terminal domain |
| 98 | c2k21A_ | Alignment | not modelled | 6.8 | 18 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e<br>**PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c |
| 99 | c2xmfA_ | Alignment | not modelled | 6.8 | 13 | **PDB header:**motor protein<br>**Chain:** A: **PDB Molecule:**myosin 1e sh3;<br>**PDBTitle:** myosin 1e sh3 |