Phyre2

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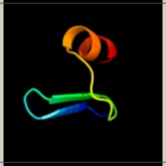
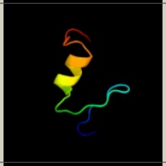
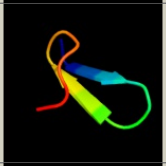
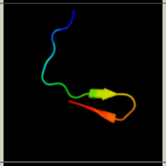
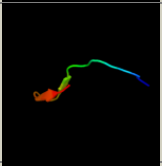
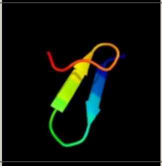
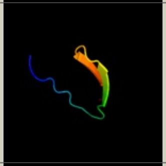
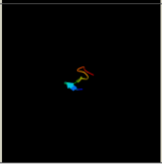
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77804 |
| Date | Thu Jan 5 12:32:59 GMT 2012 |
| Unique Job ID | 932326283466f949 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1j20a2 | Alignment |  | 32.8 | 16 | **Fold:**Argininosuccinate synthetase, C-terminal domain<br>**Superfamily:**Argininosuccinate synthetase, C-terminal domain<br>**Family:**Argininosuccinate synthetase, C-terminal domain |
| 2 | d1k92a2 | Alignment |  | 32.4 | 19 | **Fold:**Argininosuccinate synthetase, C-terminal domain<br>**Superfamily:**Argininosuccinate synthetase, C-terminal domain<br>**Family:**Argininosuccinate synthetase, C-terminal domain |
| 3 | c2pfuA_ | Alignment |  | 29.6 | 6 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**biopolymer transport exbd protein;<br>**PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli |
| 4 | c3obaA_ | Alignment |  | 25.6 | 31 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis |
| 5 | c1bhgB_ | Alignment |  | 23.4 | 19 | **PDB header:**glycosidase<br>**Chain:** B: **PDB Molecule:**beta-glucuronidase;<br>**PDBTitle:** human beta-glucuronidase at 2.6 a resolution |
| 6 | d1d6za4 | Alignment |  | 22.6 | 21 | **Fold:**N domain of copper amine oxidase-like<br>**Superfamily:**Copper amine oxidase, domain N<br>**Family:**Copper amine oxidase, domain N |
| 7 | c1nvpC_ | Alignment |  | 22.5 | 24 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**transcription initiation factor iia beta chain;<br>**PDBTitle:** human tfiia/tbp/dna complex |
| 8 | d1nvpc_ | Alignment |  | 22.5 | 24 | **Fold:**Transcription factor IIA (TFIIA), beta-barrel domain<br>**Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain<br>**Family:**Transcription factor IIA (TFIIA), beta-barrel domain |
| 9 | c3mv14_ | Alignment |  | 22.5 | 31 | **PDB header:**hydrolase<br>**Chain:** 4: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium |
| 10 | c3ipfA_ | Alignment |  | 22.5 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c. |
| 11 | c3lpgA_ | Alignment |  | 22.3 | 19 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** A: **PDB Molecule:**beta-glucuronidase;<br>**PDBTitle:** structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea |

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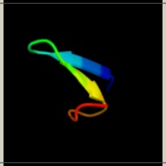
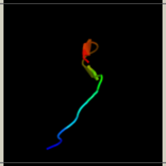
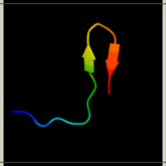
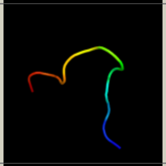
|---|---|---|---|---|---|---|
| 12 | d2g82a1 | Alignment |  | 22.0 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 13 | c1jz6C_ | Alignment |  | 21.9 | 31 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole |
| 14 | c1nh2C_ | Alignment |  | 21.7 | 18 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain;<br>**PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex |
| 15 | d1nh2c_ | Alignment |  | 21.7 | 18 | **Fold:**Transcription factor IIA (TFIIA), beta-barrel domain<br>**Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain<br>**Family:**Transcription factor IIA (TFIIA), beta-barrel domain |
| 16 | d1vc2a1 | Alignment |  | 21.5 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 17 | c1yq2C_ | Alignment |  | 21.4 | 19 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1) |
| 18 | c3bgaB_ | Alignment |  | 20.8 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482 |
| 19 | d6paxa1 | Alignment |  | 20.8 | 23 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 20 | d2b4ro1 | Alignment |  | 18.6 | 22 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 21 | d1yqea1 | Alignment | not modelled | 17.2 | 16 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**AF0625-like<br>**Family:**AF0625-like |
| 22 | d1gado1 | Alignment | not modelled | 16.3 | 22 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 23 | d1ytfc_ | Alignment | not modelled | 16.3 | 19 | **Fold:**Transcription factor IIA (TFIIA), beta-barrel domain<br>**Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain<br>**Family:**Transcription factor IIA (TFIIA), beta-barrel domain |
| 24 | c1k97A_ | Alignment | not modelled | 16.2 | 19 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**argininosuccinate synthase;<br>**PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline |
| 25 | d1zud21 | Alignment | not modelled | 15.7 | 38 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |
| 26 | d1j0xo1 | Alignment | not modelled | 14.8 | 18 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 27 | d1obfo1 | Alignment | not modelled | 14.5 | 18 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 28 | c2gfqC_ | Alignment | not modelled | 13.5 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**upf0204 protein ph0006;<br>**PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii |
|  |  |  |  |  |  | **Fold:**NAD(P)-binding Rossmann-fold domains |

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|---|---|---|---|---|---|---|
| 29 | d1hdgo1 | Alignment | not modelled | 13.4 | 12 | **Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 30 | d1k78a1 | Alignment | not modelled | 13.4 | 21 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 31 | c2w7vB_ | Alignment | not modelled | 12.7 | 17 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**general secretion pathway protein l;<br>**PDBTitle:** periplasmic domain of epsl from vibrio parahaemolyticus |
| 32 | c3mhaB_ | Alignment | not modelled | 12.5 | 67 | **PDB header:**lipid binding protein<br>**Chain:** B: **PDB Molecule:**lipoprotein lprg;<br>**PDBTitle:** crystal structure of lprg from mycobacterium tuberculosis bound to pim |
| 33 | c2kl0A_ | Alignment | not modelled | 11.9 | 25 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this;<br>**PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325 |
| 34 | d1x87a_ | Alignment | not modelled | 11.5 | 24 | **Fold:**Urocanase<br>**Superfamily:**Urocanase<br>**Family:**Urocanase |
| 35 | c1rm1C_ | Alignment | not modelled | 10.9 | 19 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain;<br>**PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex |
| 36 | c3cmgA_ | Alignment | not modelled | 10.8 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative beta-galactosidase;<br>**PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis |
| 37 | d1k8ba_ | Alignment | not modelled | 10.6 | 13 | **Fold:**Ribosome binding domain-like<br>**Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain<br>**Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain |
| 38 | d3cmco1 | Alignment | not modelled | 10.5 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 39 | d2caya1 | Alignment | not modelled | 10.4 | 19 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**VPS36 N-terminal domain-like |
| 40 | d2odgc1 | Alignment | not modelled | 10.4 | 50 | **Fold:**LEM/SAP HeH motif<br>**Superfamily:**LEM domain<br>**Family:**LEM domain |
| 41 | c2jv8A_ | Alignment | not modelled | 10.3 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ne1242;<br>**PDBTitle:** solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4 |
| 42 | c2gjhA_ | Alignment | not modelled | 10.3 | 20 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**designed protein;<br>**PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7) |
| 43 | c1ifpA_ | Alignment | not modelled | 10.2 | 29 | **PDB header:**virus<br>**Chain:** A: **PDB Molecule:**major coat protein assembly;<br>**PDBTitle:** inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly |
| 44 | d1dm9a_ | Alignment | not modelled | 10.2 | 31 | **Fold:**Alpha-L RNA-binding motif<br>**Superfamily:**Alpha-L RNA-binding motif<br>**Family:**Heat shock protein 15 kD |
| 45 | c1dm9A_ | Alignment | not modelled | 10.2 | 31 | **PDB header:**structural genomics<br>**Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka<br>**PDBTitle:** heat shock protein 15 kd |
| 46 | d3gpdg1 | Alignment | not modelled | 10.0 | 12 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 47 | c1kskA_ | Alignment | not modelled | 9.5 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a;<br>**PDBTitle:** structure of rsua |
| 48 | d1dssg1 | Alignment | not modelled | 9.4 | 17 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 49 | c1tygG_ | Alignment | not modelled | 9.3 | 25 | **PDB header:**biosynthetic protein<br>**Chain:** G: **PDB Molecule:**yjbs;<br>**PDBTitle:** structure of the thiazole synthase/this complex |
| 50 | d2cu3a1 | Alignment | not modelled | 9.3 | 45 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |
| 51 | c2cqjA_ | Alignment | not modelled | 9.2 | 8 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein<br>**PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog |
| 52 | d1dk7a_ | Alignment | not modelled | 9.0 | 11 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 53 | c1kh2D_ | Alignment | not modelled | 9.0 | 15 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**argininosuccinate synthetase;<br>**PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp |
| 54 | c3iz6I_ | Alignment | not modelled | 8.9 | 36 | **PDB header:**ribosome<br>**Chain:** I: **PDB Molecule:**40s ribosomal protein s16 (s9p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |

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| 55 | d1oela2 | Alignment | not modelled | 8.7 | 11 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 56 | c3c8vA_ | Alignment | not modelled | 8.7 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative acetyltransferase;<br>**PDBTitle:** crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution |
| 57 | d1vioa2 | Alignment | not modelled | 8.6 | 8 | **Fold:**Alpha-L RNA-binding motif<br>**Superfamily:**Alpha-L RNA-binding motif<br>**Family:**Pseudouridine synthase RsuA N-terminal domain |
| 58 | d1srva_ | Alignment | not modelled | 8.6 | 25 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 59 | d1u8fo1 | Alignment | not modelled | 8.5 | 24 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 60 | c1spfA_ | Alignment | not modelled | 8.4 | 46 | **PDB header:**lipoprotein(surface film)<br>**Chain:** A: **PDB Molecule:**pulmonary surfactant-associated polypeptide c;<br>**PDBTitle:** the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix |
| 61 | c1zeqX_ | Alignment | not modelled | 8.4 | 8 | **PDB header:**metal binding protein<br>**Chain:** X: **PDB Molecule:**cation efflux system protein cusf;<br>**PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli |
| 62 | d1tygb_ | Alignment | not modelled | 8.3 | 25 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**MoaD/ThiS<br>**Family:**ThiS |
| 63 | c2zkqi_ | Alignment | not modelled | 8.2 | 45 | **PDB header:**ribosomal protein/rna<br>**Chain:** I: **PDB Molecule:**<br>**PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 64 | d2pila_ | Alignment | not modelled | 8.1 | 11 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**Pilin |
| 65 | d1kh0a_ | Alignment | not modelled | 7.9 | 26 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Immunoglobulin-binding domains<br>**Family:**Immunoglobulin-binding domains |
| 66 | c3m6cA_ | Alignment | not modelled | 7.8 | 22 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**60 kda chaperonin 1;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis groel1 apical domain |
| 67 | c2kd2A_ | Alignment | not modelled | 7.8 | 26 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1;<br>**PDBTitle:** nmr structure of faim-ctd |
| 68 | c3fn9B_ | Alignment | not modelled | 7.8 | 33 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative beta-galactosidase;<br>**PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis |
| 69 | d1gwma_ | Alignment | not modelled | 7.7 | 7 | **Fold:**Galactose-binding domain-like<br>**Superfamily:**Galactose-binding domain-like<br>**Family:**Family 29 carbohydrate binding module, CBM29 |
| 70 | d1v6ga2 | Alignment | not modelled | 7.6 | 27 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 71 | d1sjpa2 | Alignment | not modelled | 7.5 | 25 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 72 | c3dh3C_ | Alignment | not modelled | 7.5 | 29 | **PDB header:**isomerase/rna<br>**Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f;<br>**PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate |
| 73 | c2jwlB_ | Alignment | not modelled | 7.3 | 10 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**protein tolr;<br>**PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data |
| 74 | c3pcqX_ | Alignment | not modelled | 7.1 | 24 | **PDB header:**photosynthesis<br>**Chain:** X: **PDB Molecule:**photosystem i 4.8k protein;<br>**PDBTitle:** femtosecond x-ray protein nanocrystallography |
| 75 | d1b77a2 | Alignment | not modelled | 7.1 | 19 | **Fold:**DNA clamp<br>**Superfamily:**DNA clamp<br>**Family:**DNA polymerase processivity factor |
| 76 | d1z45a1 | Alignment | not modelled | 7.1 | 18 | **Fold:**Supersandwich<br>**Superfamily:**Galactose mutarotase-like<br>**Family:**Aldose 1-epimerase (mutarotase) |
| 77 | c3mk7B_ | Alignment | not modelled | 7.1 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o;<br>**PDBTitle:** the structure of cbb3 cytochrome oxidase |
| 78 | c3em0A_ | Alignment | not modelled | 7.1 | 14 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**ileal bile acid-binding protein;<br>**PDBTitle:** crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b). |
| 79 | c3e8tA_ | Alignment | not modelled | 7.0 | 11 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**takeout-like protein 1;<br>**PDBTitle:** crystal structure of epiphyas postvittana takeout 1 |
|  |  |  |  |  |  | **PDB header:**ribosome<br>**Chain:** I: **PDB Molecule:**40s ribosomal protein s16; |

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|---|---|---|---|---|---|---|
| 80 | c1s1hl_ | Alignment | not modelled | 7.0 | 36 | **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i. |
| 81 | d1we3a2 | Alignment | not modelled | 7.0 | 25 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 82 | d1sjpa3 | Alignment | not modelled | 6.9 | 13 | **Fold:**GroEL-intermediate domain like<br>**Superfamily:**GroEL-intermediate domain like<br>**Family:**GroEL-like chaperone, intermediate domain |
| 83 | d1ffva2 | Alignment | not modelled | 6.9 | 22 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**2Fe-2S ferredoxin-like<br>**Family:**2Fe-2S ferredoxin domains from multidomain proteins |
| 84 | c1vioA_ | Alignment | not modelled | 6.9 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a;<br>**PDBTitle:** crystal structure of pseudouridylate synthase |
| 85 | d2axtj1 | Alignment | not modelled | 6.8 | 26 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction center protein J, PsbJ<br>**Family:**PsbJ-like |
| 86 | d1pdnc_ | Alignment | not modelled | 6.6 | 19 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Paired domain |
| 87 | c2wj7D_ | Alignment | not modelled | 6.6 | 47 | **PDB header:**chaperone<br>**Chain:** D: **PDB Molecule:**alpha-crystallin b chain;<br>**PDBTitle:** human alphab crystallin |
| 88 | c2ci8A_ | Alignment | not modelled | 6.6 | 26 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**cytoplasmic protein nck1;<br>**PDBTitle:** sh2 domain of human nck1 adaptor protein - uncomplexed |
| 89 | d1kida_ | Alignment | not modelled | 6.5 | 38 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**GroEL apical domain-like<br>**Family:**GroEL-like chaperone, apical domain |
| 90 | d2p4pa1 | Alignment | not modelled | 6.5 | 17 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CorC/HlyC domain-like |
| 91 | d2pkqo1 | Alignment | not modelled | 6.5 | 13 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 92 | c3r45C_ | Alignment | not modelled | 6.5 | 18 | **PDB header:**nuclear protein<br>**Chain:** C: **PDB Molecule:**holliday junction recognition protein;<br>**PDBTitle:** structure of a cenp-a-histone h4 heterodimer in complex with chaperone2 hjurp |
| 93 | d1yqga1 | Alignment | not modelled | 6.5 | 18 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**ProC C-terminal domain-like |
| 94 | d1of5b_ | Alignment | not modelled | 6.4 | 24 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**NTF2-like |
| 95 | d1rm6c2 | Alignment | not modelled | 6.3 | 44 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**2Fe-2S ferredoxin-like<br>**Family:**2Fe-2S ferredoxin domains from multidomain proteins |
| 96 | d2ahra1 | Alignment | not modelled | 6.3 | 13 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**ProC C-terminal domain-like |
| 97 | d1czda2 | Alignment | not modelled | 6.3 | 16 | **Fold:**DNA clamp<br>**Superfamily:**DNA clamp<br>**Family:**DNA polymerase processivity factor |
| 98 | c3a1zC_ | Alignment | not modelled | 6.3 | 10 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**hemolymph juvenile hormone binding protein;<br>**PDBTitle:** crystal structure of juvenile hormone binding protein from silkworm |
| 99 | d1dgja2 | Alignment | not modelled | 6.3 | 25 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**2Fe-2S ferredoxin-like<br>**Family:**2Fe-2S ferredoxin domains from multidomain proteins |