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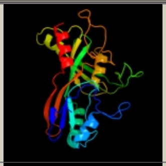
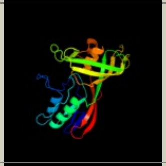
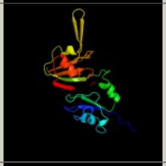
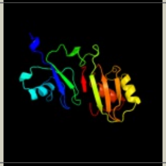
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0AA41 |
| Date | Thu Jan 5 11:11:52 GMT 2012 |
| Unique Job ID | a3bde3b0c6bec88a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1v9fA_ | Alignment |  | 100.0 | 28 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d;<br>**PDBTitle:** crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli |
| 2 | d1v9fa_ | Alignment |  | 100.0 | 28 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase RsuA/RluD |
| 3 | c1qyuA_ | Alignment |  | 100.0 | 27 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d;<br>**PDBTitle:** structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud |
| 4 | d1v9ka_ | Alignment |  | 100.0 | 34 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase RsuA/RluD |
| 5 | c2i82D_ | Alignment |  | 100.0 | 36 | **PDB header:**lyase/rna<br>**Chain:** D: **PDB Molecule:**ribosomal large subunit pseudouridine synthase a;<br>**PDBTitle:** crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure |
| 6 | c1vioA_ | Alignment |  | 100.0 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a;<br>**PDBTitle:** crystal structure of pseudouridylate synthase |
| 7 | c1kskA_ | Alignment |  | 100.0 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a;<br>**PDBTitle:** structure of rsua |
| 8 | c2omlA_ | Alignment |  | 100.0 | 19 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e;<br>**PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue |
| 9 | c2olwB_ | Alignment |  | 100.0 | 19 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e;<br>**PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue |
| 10 | c3dh3C_ | Alignment |  | 100.0 | 20 | **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 |
| 11 | d1kska4 | Alignment |  | 100.0 | 18 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase RsuA/RluD |

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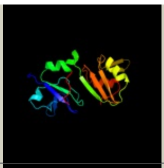
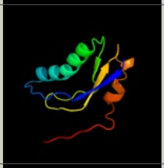
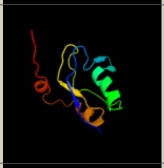
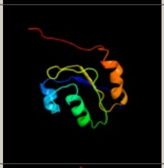
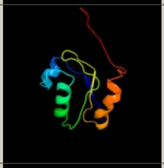
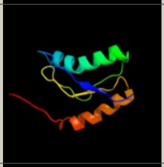
|---|---|---|---|---|---|---|
| 12 | d1vioa1 | Alignment |  | 100.0 | 21 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase RsuA/RluD |
| 13 | c2gmlA_ | Alignment |  | 100.0 | 21 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f;<br>**PDBTitle:** crystal structure of catalytic domain of e.coli rluf |
| 14 | d1k8wa5 | Alignment |  | 97.7 | 20 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 15 | d1sgva2 | Alignment |  | 97.6 | 27 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 16 | d2apoa2 | Alignment |  | 97.5 | 22 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 17 | d2ey4a2 | Alignment |  | 97.5 | 23 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 18 | c2ey4A_ | Alignment |  | 97.4 | 23 | **PDB header:**isomerase/biosynthetic protein<br>**Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b;<br>**PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex |
| 19 | d1r3ea2 | Alignment |  | 97.4 | 20 | **Fold:**Pseudouridine synthase<br>**Superfamily:**Pseudouridine synthase<br>**Family:**Pseudouridine synthase II TruB |
| 20 | c3uaiA_ | Alignment |  | 97.1 | 26 | **PDB header:**isomerase/chaperone<br>**Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4;<br>**PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae |
| 21 | c2apoA_ | Alignment | not modelled | 97.0 | 21 | **PDB header:**isomerase/rna binding protein<br>**Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b;<br>**PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex |
| 22 | c1k8wA_ | Alignment | not modelled | 97.0 | 20 | **PDB header:**lyase/rna<br>**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 |
| 23 | c1sgvA_ | Alignment | not modelled | 96.6 | 27 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**trna pseudouridine synthase b;<br>**PDBTitle:** structure of trna psi55 pseudouridine synthase (trub) |
| 24 | c1ze2B_ | Alignment | not modelled | 95.1 | 28 | **PDB header:**lyase/rna<br>**Chain:** B: **PDB Molecule:**trna pseudouridine synthase b;<br>**PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate |
| 25 | c3n1tE_ | Alignment | not modelled | 24.0 | 42 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**hit-like protein hint;<br>**PDBTitle:** crystal structure of the h101a mutant echint gmp complex |
| 26 | d1rzya_ | Alignment | not modelled | 22.8 | 25 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins |
| 27 | c2zodB_ | Alignment | not modelled | 21.9 | 23 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**selenide, water dikinase;<br>**PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus |
| 28 | c3l7xA_ | Alignment | not modelled | 21.4 | 33 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle<br>**PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159 |

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| 29 | d1emsa1 | Alignment | not modelled | 20.0 | 17 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins |
| 30 | c1mzwB_ | Alignment | not modelled | 18.7 | 31 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**u4/u6 snrnp 60kda protein;<br>**PDBTitle:** crystal structure of a u4/u6 snrnp complex between human2 spliceosomal cyclophilin h and a u4/u6-60k peptide |
| 31 | d1kpfa_ | Alignment | not modelled | 16.6 | 25 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins |
| 32 | d1fita_ | Alignment | not modelled | 15.3 | 18 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins |
| 33 | c3o0mB_ | Alignment | not modelled | 15.0 | 25 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hit family protein;<br>**PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis |
| 34 | c1emsB_ | Alignment | not modelled | 14.7 | 17 | **PDB header:**antitumor protein<br>**Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein;<br>**PDBTitle:** crystal structure of the c. elegans nitfhit protein |
| 35 | c2zauB_ | Alignment | not modelled | 13.0 | 24 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**selenide, water dikinase;<br>**PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus |
| 36 | d1guqa2 | Alignment | not modelled | 12.2 | 25 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**Hexose-1-phosphate uridylyltransferase |
| 37 | c3p0tB_ | Alignment | not modelled | 12.0 | 33 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis |
| 38 | d1qwga_ | Alignment | not modelled | 11.1 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA<br>**Family:**(2r)-phospho-3-sulfolactate synthase ComA |
| 39 | d2oika1 | Alignment | not modelled | 10.2 | 50 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins |
| 40 | c3lb5B_ | Alignment | not modelled | 10.1 | 23 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**hit-like protein involved in cell-cycle regulation;<br>**PDBTitle:** crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand |
| 41 | c2jv2A_ | Alignment | not modelled | 10.0 | 7 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500;<br>**PDBTitle:** solution structure of the n-terminal domain of ph1500 |
| 42 | d2aaaa1 | Alignment | not modelled | 10.0 | 29 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**alpha-Amylases, C-terminal beta-sheet domain |
| 43 | c1xquA_ | Alignment | not modelled | 9.6 | 42 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hit family hydrolase;<br>**PDBTitle:** hit family hydrolase from clostridium thermocellum cth-393 |
| 44 | d1xqua_ | Alignment | not modelled | 9.6 | 42 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins |
| 45 | c3zrhA_ | Alignment | not modelled | 9.4 | 31 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1;<br>**PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd) |
| 46 | d1gr0a1 | Alignment | not modelled | 9.3 | 21 | **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 | c2lf6A_ | Alignment | not modelled | 9.2 | 24 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**effector protein hopab1;<br>**PDBTitle:** solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a |
| 48 | d2zoda2 | Alignment | not modelled | 8.4 | 17 | **Fold:**PurM C-terminal domain-like<br>**Superfamily:**PurM C-terminal domain-like<br>**Family:**PurM C-terminal domain-like |
| 49 | d1vjpa1 | Alignment | not modelled | 7.8 | 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 |
| 50 | c2do5A_ | Alignment | not modelled | 7.8 | 35 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**splicing factor 3b subunit 2;<br>**PDBTitle:** solution structure of the sap domain of human splicing2 factor 3b subunit 2 |
| 51 | c3ksvA_ | Alignment | not modelled | 7.7 | 8 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** hypothetical protein from leishmania major |
| 52 | c2oi2A_ | Alignment | not modelled | 7.5 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mevalonate kinase;<br>**PDBTitle:** streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate |
| 53 | c2eo4A_ | Alignment | not modelled | 7.4 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**150aa long hypothetical histidine triad nucleotide-binding<br>**PDBTitle:** crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7 |

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| 54 | c3oj7A_ | Alignment | not modelled | 6.9 | 33 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**putative histidine triad family protein;<br>**PDBTitle:** crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate |
| 55 | d1k8ga2 | Alignment | not modelled | 6.8 | 27 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 56 | c2lkyA_ | Alignment | not modelled | 6.8 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b |
| 57 | c1u83A_ | Alignment | not modelled | 6.6 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**phosphosulfolactate synthase;<br>**PDBTitle:** psl synthase from bacillus subtilis |
| 58 | d1u83a_ | Alignment | not modelled | 6.6 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA<br>**Family:**(2r)-phospho-3-sulfolactate synthase ComA |
| 59 | c3imiB_ | Alignment | not modelled | 6.4 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hit family protein;<br>**PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor' |
| 60 | c3anoA_ | Alignment | not modelled | 6.4 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ap-4-a phosphorylase;<br>**PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv |
| 61 | c1e0aB_ | Alignment | not modelled | 6.4 | 28 | **PDB header:**signalling protein<br>**Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha;<br>**PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase |
| 62 | c2kvcA_ | Alignment | not modelled | 6.4 | 31 | **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 |
| 63 | d1u2ca2 | Alignment | not modelled | 6.2 | 27 | **Fold:**Dystroglycan, domain 2<br>**Superfamily:**Dystroglycan, domain 2<br>**Family:**Dystroglycan, domain 2 |
| 64 | d1jb7a2 | Alignment | not modelled | 6.1 | 27 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 65 | d1w91a1 | Alignment | not modelled | 6.1 | 36 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51 |
| 66 | d2al1a1 | Alignment | not modelled | 6.1 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Enolase C-terminal domain-like<br>**Family:**Enolase |
| 67 | d2guya1 | Alignment | not modelled | 6.0 | 27 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**alpha-Amylases, C-terminal beta-sheet domain |
| 68 | c2odbB_ | Alignment | not modelled | 6.0 | 31 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6;<br>**PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6) |
| 69 | c1u1iC_ | Alignment | not modelled | 5.7 | 16 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**myo-inositol-1-phosphate synthase;<br>**PDBTitle:** myo-inositol phosphate synthase mips from a. fulgidus |
| 70 | d1z84a2 | Alignment | not modelled | 5.4 | 17 | **Fold:**HIT-like<br>**Superfamily:**HIT-like<br>**Family:**Hexose-1-phosphate uridylyltransferase |
| 71 | d2hx5a1 | Alignment | not modelled | 5.1 | 14 | **Fold:**Thioesterase/thiol ester dehydrase-isomerase<br>**Superfamily:**Thioesterase/thiol ester dehydrase-isomerase<br>**Family:**4HBT-like |