# Phyre$^2$

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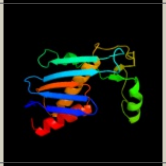
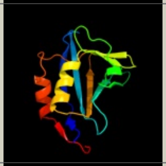
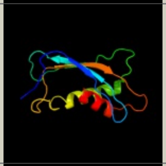
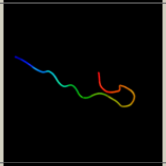
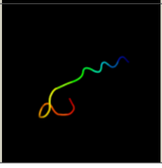
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A725 |
| Date | Thu Jan 5 11:04:35 GMT 2012 |
| Unique Job ID | 5d53229bf91cffc5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3nzkB_ | Alignment |  | 100.0 | 93 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine<br>**PDBTitle:** structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor |
| 2 | c2vesA_ | Alignment |  | 100.0 | 59 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine<br>**PDBTitle:** crystal structure of lpxc from pseudomonas aeruginosa2 complexed with the potent bb-78485 inhibitor |
| 3 | c2go4A_ | Alignment |  | 100.0 | 34 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine<br>**PDBTitle:** crystal structure of aquifex aeolicus lpxc complexed with tu-514 |
| 4 | d1p42a2 | Alignment |  | 100.0 | 33 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC |
| 5 | d1p42a1 | Alignment |  | 100.0 | 33 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC |
| 6 | d2bv3a3 | Alignment |  | 86.3 | 17 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 7 | d1pkpa1 | Alignment |  | 66.7 | 47 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 8 | d2uube1 | Alignment |  | 65.3 | 47 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 9 | c2zkqe_ | Alignment |  | 55.1 | 47 | **PDB header:**ribosomal protein/rna<br>**Chain:** E: **PDB Molecule:**rna expansion segment es6 part ii;<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 |
| 10 | d2qale1 | Alignment |  | 53.5 | 33 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 11 | c1s1hE_ | Alignment |  | 52.7 | 47 | **PDB header:**ribosome<br>**Chain:** E: **PDB Molecule:**40s ribosomal protein s2;<br>**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. |

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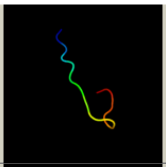
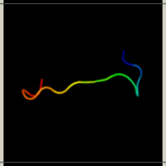
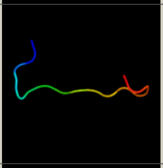
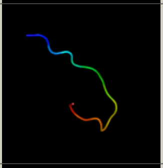
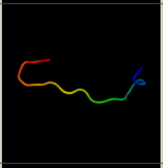
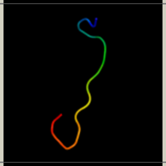
| 12 | c3bbnE_ | Alignment |  | 50.7 | 53 | **PDB header:**ribosome<br>**Chain:** E: **PDB Molecule:**ribosomal protein s5;<br>**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome. |
| 13 | d1u5tb2 | Alignment |  | 45.6 | 50 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Vacuolar sorting protein domain |
| 14 | d2azea1 | Alignment |  | 45.4 | 25 | **Fold:**E2F-DP heterodimerization region<br>**Superfamily:**E2F-DP heterodimerization region<br>**Family:**DP dimerization segment |
| 15 | c2zkru_ | Alignment |  | 43.2 | 31 | **PDB header:**ribosomal protein/rna<br>**Chain:** U: **PDB Molecule:**rna expansion segment es41;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 16 | d1vqou1 | Alignment |  | 41.1 | 19 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**Ribosomal protein L24e |
| 17 | c2xzmE_ | Alignment |  | 41.1 | 47 | **PDB header:**ribosome<br>**Chain:** E: **PDB Molecule:**ribosomal protein s5 containing protein;<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 |
| 18 | c3izcZ_ | Alignment |  | 41.0 | 19 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**60s ribosomal protein rpl24 (l24e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 19 | c4a1eT_ | Alignment |  | 40.8 | 13 | **PDB header:**ribosome<br>**Chain:** T: **PDB Molecule:**rpl24;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1 |
| 20 | c3ccjU_ | Alignment |  | 40.6 | 19 | **PDB header:**ribosome<br>**Chain:** U: **PDB Molecule:**50s ribosomal protein l24e;<br>**PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation c2534u |
| 21 | c1eg0B_ | Alignment | not modelled | 39.4 | 47 | **PDB header:**ribosome<br>**PDB COMPND:** |
| 22 | c3iz5Z_ | Alignment | not modelled | 39.3 | 19 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 23 | c1p6gE_ | Alignment | not modelled | 36.9 | 33 | **PDB header:**ribosome<br>**Chain:** E: **PDB Molecule:**30s ribosomal protein s5;<br>**PDBTitle:** real space refined coordinates of the 30s subunit fitted2 into the low resolution cryo-em map of the ef-g.gtp state3 of e. coli 70s ribosome |
| 24 | d1j6xa_ | Alignment | not modelled | 29.7 | 25 | **Fold:**LuxS/MPP-like metallohydrolase<br>**Superfamily:**LuxS/MPP-like metallohydrolase<br>**Family:**Autoinducer-2 production protein LuxS |
| 25 | d2hi6a1 | Alignment | not modelled | 28.4 | 20 | **Fold:**The "swivelling" beta/beta/alpha domain<br>**Superfamily:**LeuD/IlvD-like<br>**Family:**AF0055-like |
| 26 | d1w07a3 | Alignment | not modelled | 27.8 | 12 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**acyl-CoA oxidase N-terminal domains |
| 27 | d1j98a_ | Alignment | not modelled | 27.1 | 55 | **Fold:**LuxS/MPP-like metallohydrolase<br>**Superfamily:**LuxS/MPP-like metallohydrolase<br>**Family:**Autoinducer-2 production protein LuxS |
| 28 | c1s1iS_ | Alignment | not modelled | 25.9 | 19 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**60s ribosomal protein l24-a;<br>**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, 1s1i,4 |

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|---|---|---|---|---|---|---|
| | | | | | | contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h. |
| 29 | d1l4db_ | Alignment | not modelled | 25.7 | 21 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Staphylokinase/streptokinase<br>**Family:**Staphylokinase/streptokinase |
| 30 | d1vjea_ | Alignment | not modelled | 24.8 | 35 | **Fold:**LuxS/MPP-like metallohydrolase<br>**Superfamily:**LuxS/MPP-like metallohydrolase<br>**Family:**Autoinducer-2 production protein LuxS |
| 31 | d1j6wa_ | Alignment | not modelled | 22.4 | 29 | **Fold:**LuxS/MPP-like metallohydrolase<br>**Superfamily:**LuxS/MPP-like metallohydrolase<br>**Family:**Autoinducer-2 production protein LuxS |
| 32 | d2dy1a3 | Alignment | not modelled | 22.2 | 19 | **Fold:**Ribosomal protein S5 domain 2-like<br>**Superfamily:**Ribosomal protein S5 domain 2-like<br>**Family:**Translational machinery components |
| 33 | c2ddhA_ | Alignment | not modelled | 19.9 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa oxidase;<br>**PDBTitle:** crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate |
| 34 | d1bmlc1 | Alignment | not modelled | 18.2 | 21 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Staphylokinase/streptokinase<br>**Family:**Staphylokinase/streptokinase |
| 35 | c1w07A_ | Alignment | not modelled | 17.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**acyl-coa oxidase;<br>**PDBTitle:** arabidopsis thaliana acyl-coa oxidase 1 |
| 36 | c2ow8f_ | Alignment | not modelled | 16.6 | 47 | **PDB header:**ribosome<br>**Chain:** F: **PDB Molecule:**<br>**PDBTitle:** crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa. |
| 37 | d1gsoa2 | Alignment | not modelled | 15.2 | 22 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 38 | d1l4zb_ | Alignment | not modelled | 14.5 | 21 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Staphylokinase/streptokinase<br>**Family:**Staphylokinase/streptokinase |
| 39 | d2pw9a1 | Alignment | not modelled | 14.2 | 15 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**FdhD/NarQ |
| 40 | d1vh1a_ | Alignment | not modelled | 14.1 | 12 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**Cytidylytransferase |
| 41 | c2fonA_ | Alignment | not modelled | 13.8 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**peroxisomal acyl-coa oxidase 1a;<br>**PDBTitle:** x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato) |
| 42 | d2ddha3 | Alignment | not modelled | 13.4 | 9 | **Fold:**Acyl-CoA dehydrogenase NM domain-like<br>**Superfamily:**Acyl-CoA dehydrogenase NM domain-like<br>**Family:**acyl-CoA oxidase N-terminal domains |
| 43 | c3izbE_ | Alignment | not modelled | 13.2 | 47 | **PDB header:**ribosome<br>**Chain:** E: **PDB Molecule:**40s ribosomal protein rps2 (s5p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 44 | c2kyzA_ | Alignment | not modelled | 13.0 | 15 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**heavy metal binding protein;<br>**PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima |
| 45 | c3iz6E_ | Alignment | not modelled | 13.0 | 40 | **PDB header:**ribosome<br>**Chain:** E: **PDB Molecule:**40s ribosomal protein s2 (s5p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 46 | c3m05A_ | Alignment | not modelled | 12.9 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480;<br>**PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745 |
| 47 | d1pvxa_ | Alignment | not modelled | 12.5 | 23 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Xylanase/endoglucanase 11/12 |
| 48 | d1v54i_ | Alignment | not modelled | 12.4 | 26 | **Fold:**Single transmembrane helix<br>**Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc<br>**Family:**Mitochondrial cytochrome c oxidase subunit VIc |
| 49 | d1vh3a_ | Alignment | not modelled | 12.2 | 12 | **Fold:**Nucleotide-diphospho-sugar transferases<br>**Superfamily:**Nucleotide-diphospho-sugar transferases<br>**Family:**Cytidylytransferase |
| 50 | d1vaea_ | Alignment | not modelled | 11.9 | 19 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 51 | c2yuyA_ | Alignment | not modelled | 11.2 | 22 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**rho gtpase activating protein 21;<br>**PDBTitle:** solution structure of pdz domain of rho gtpase activating2 protein 21 |
| 52 | d1ky9b2 | Alignment | not modelled | 11.0 | 24 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**HtrA-like serine proteases |
| 53 | c3m0dC_ | Alignment | not modelled | 10.6 | 30 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**tnf receptor-associated factor 1;<br>**PDBTitle:** crystal structure of the traf1:traf2:ciap2 complex |
| 54 | d1gpca_ | Alignment | not modelled | 10.5 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Phage ssDNA-binding proteins |

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| 55 | c2vsvB_ | Alignment | not modelled | 10.1 | 15 | **PDB header:**protein-binding<br>**Chain:** B: **PDB Molecule:**rhophilin-2;<br>**PDBTitle:** crystal structure of the pdz domain of human rhophilin-2 |
| 56 | c2lfcA_ | Alignment | not modelled | 10.1 | 33 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit;<br>**PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j |
| 57 | d1u3ba2 | Alignment | not modelled | 10.1 | 22 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 58 | d1y0pa3 | Alignment | not modelled | 9.9 | 42 | **Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 59 | d1s1ma2 | Alignment | not modelled | 9.3 | 20 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 60 | c1n0fF_ | Alignment | not modelled | 9.1 | 11 | **PDB header:**biosynthetic protein<br>**Chain:** F: **PDB Molecule:**protein mraz;<br>**PDBTitle:** crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif |
| 61 | d1v97a2 | Alignment | not modelled | 9.0 | 39 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**2Fe-2S ferredoxin-like<br>**Family:**2Fe-2S ferredoxin domains from multidomain proteins |
| 62 | c2krgA_ | Alignment | not modelled | 8.7 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf1;<br>**PDBTitle:** solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358) |
| 63 | c2qdrA_ | Alignment | not modelled | 8.5 | 22 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution |
| 64 | c2dcoA_ | Alignment | not modelled | 8.4 | 56 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**s1p4 first extracellular loop peptidomimetic;<br>**PDBTitle:** s1p4 first extracellular loop peptidomimetic |
| 65 | d1nz8a_ | Alignment | not modelled | 8.3 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**N-utilization substance G protein NusG, N-terminal domain<br>**Family:**N-utilization substance G protein NusG, N-terminal domain |
| 66 | c2kr7A_ | Alignment | not modelled | 8.2 | 32 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd;<br>**PDBTitle:** solution structure of helicobacter pylori slyd |
| 67 | d1xpma2 | Alignment | not modelled | 8.1 | 18 | **Fold:**Thiolase-like<br>**Superfamily:**Thiolase-like<br>**Family:**Chalcone synthase-like |
| 68 | d1qo8a3 | Alignment | not modelled | 8.0 | 32 | **Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 69 | d1n62a2 | Alignment | not modelled | 8.0 | 27 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**2Fe-2S ferredoxin-like<br>**Family:**2Fe-2S ferredoxin domains from multidomain proteins |
| 70 | d1nfpa_ | Alignment | not modelled | 8.0 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Non-fluorescent flavoprotein (luxF, FP390) |
| 71 | c3smaD_ | Alignment | not modelled | 7.9 | 26 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**frbf;<br>**PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf |
| 72 | c2ad5B_ | Alignment | not modelled | 7.9 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**ctp synthase;<br>**PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution. |
| 73 | d1ynaa_ | Alignment | not modelled | 7.8 | 16 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Xylanase/endoglucanase 11/12 |
| 74 | d1gpma2 | Alignment | not modelled | 7.6 | 23 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 75 | d1jvna1 | Alignment | not modelled | 7.6 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Histidine biosynthesis enzymes |
| 76 | d1d4ca3 | Alignment | not modelled | 7.5 | 32 | **Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain<br>**Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain |
| 77 | c2qktB_ | Alignment | not modelled | 7.4 | 15 | **PDB header:**peptide binding protein<br>**Chain:** B: **PDB Molecule:**inactivation-no-after-potential d protein;<br>**PDBTitle:** crystal structure of the 5th pdz domain of inad |
| 78 | c4a8al_ | Alignment | not modelled | 7.2 | 35 | **PDB header:**hydrolase/hydrolase<br>**Chain:** I: **PDB Molecule:**periplasmic ph-dependent serine endoprotease degq; |

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| | | | | | | **PDBTitle:** asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme |
| 79 | d1vq2a_ | Alignment | not modelled | 7.2 | 22 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Deoxycytidylate deaminase-like |
| 80 | c2hfpB_ | Alignment | not modelled | 7.2 | 80 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**src peptide fragment;<br>**PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands |
| 81 | c3kmgE_ | Alignment | not modelled | 7.1 | 80 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**steroid receptor coactivator-1;<br>**PDBTitle:** the x-ray crystal structure of ppar-gamma in complex with an indole2 derivative modulator, gsk538, and an src-1 peptide |
| 82 | c2x7jA_ | Alignment | not modelled | 7.1 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene<br>**PDBTitle:** structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis |
| 83 | c1fm6E_ | Alignment | not modelled | 7.1 | 80 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**steroid receptor coactivator;<br>**PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides. |
| 84 | c1k74E_ | Alignment | not modelled | 7.1 | 80 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**steroid receptor coactivator;<br>**PDBTitle:** the 2.3 angstrom resolution crystal structure of the2 heterodimer of the human ppargamma and rxralpha ligand3 binding domains respectively bound with gw409544 and 9-cis4 retinoic acid and co-activator peptides. |
| 85 | c1fm9E_ | Alignment | not modelled | 7.1 | 80 | **PDB header:**transcription<br>**Chain:** E: **PDB Molecule:**steroid receptor coactivator;<br>**PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and gi262570 and co-activator peptides. |
| 86 | d1rm6c2 | Alignment | not modelled | 7.0 | 36 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**2Fe-2S ferredoxin-like<br>**Family:**2Fe-2S ferredoxin domains from multidomain proteins |
| 87 | c1p8dC_ | Alignment | not modelled | 7.0 | 80 | **PDB header:**membrane protein/protein binding<br>**Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3;<br>**PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol |
| 88 | d1ukka_ | Alignment | not modelled | 7.0 | 40 | **Fold:**OsmC-like<br>**Superfamily:**OsmC-like<br>**Family:**Ohr/OsmC resistance proteins |
| 89 | c1fm6V_ | Alignment | not modelled | 7.0 | 80 | **PDB header:**transcription<br>**Chain:** V: **PDB Molecule:**steroid receptor coactivator;<br>**PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides. |
| 90 | d1vcoa2 | Alignment | not modelled | 7.0 | 18 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 91 | c3ipqB_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**nuclear receptor coactivator 1;<br>**PDBTitle:** x-ray structure of gw3965 synthetic agonist bound to the lxr-alpha |
| 92 | c3ipuD_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**nuclear receptor coactivator 1;<br>**PDBTitle:** x-ray structure of benzisoxazole urea synthetic agonist bound to the2 lxr-alpha |
| 93 | c1nrlC_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3;<br>**PDBTitle:** crystal structure of the human pxr-lbd in complex with an2 src-1 coactivator peptide and sr12813 |
| 94 | c3ipsD_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**nuclear receptor coactivator 1;<br>**PDBTitle:** x-ray structure of benzisoxazole synthetic agonist bound to the lxr-2 alpha |
| 95 | c3ipuC_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1;<br>**PDBTitle:** x-ray structure of benzisoxazole urea synthetic agonist bound to the2 lxr-alpha |
| 96 | c3ipsC_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1;<br>**PDBTitle:** x-ray structure of benzisoxazole synthetic agonist bound to the lxr-2 alpha |
| 97 | c1nrlD_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3;<br>**PDBTitle:** crystal structure of the human pxr-lbd in complex with an2 src-1 coactivator peptide and sr12813 |
| 98 | c1fm6Y_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** Y: **PDB Molecule:**steroid receptor coactivator;<br>**PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides. |
| 99 | c1k7lB_ | Alignment | not modelled | 6.9 | 80 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**steroid receptor coactivator;<br>**PDBTitle:** the 2.5 angstrom resolution crystal structure of the human2 pparalpha ligand binding domain bound with gw409544 and a3 co-activator peptide. |