# Phyre$^2$

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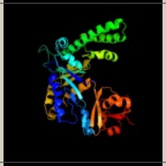
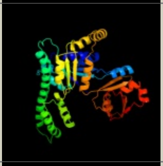
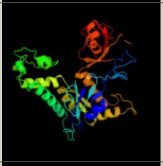
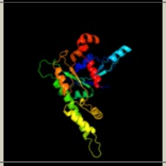
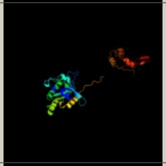
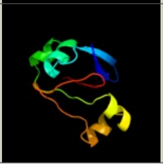
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ABU2 |
| Date | Thu Jan 5 11:16:24 GMT 2012 |
| Unique Job ID | 77810ed7919b2ae8 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1ni3A_ | Alignment |  | 100.0 | 41 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**ychf gtp-binding protein;<br>**PDBTitle:** structure of the schizosaccharomyces pombe ychf gtpase |
| 2 | c1jalA_ | Alignment |  | 100.0 | 82 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ychf protein;<br>**PDBTitle:** ychf protein (hi0393) |
| 3 | c2dwqB_ | Alignment |  | 100.0 | 48 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**gtp-binding protein;<br>**PDBTitle:** thermus thermophilus ychf gtp-binding protein |
| 4 | c2ohfA_ | Alignment |  | 100.0 | 45 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gtp-binding protein 9;<br>**PDBTitle:** crystal structure of human ola1 in complex with amppcp |
| 5 | c1wxqA_ | Alignment |  | 100.0 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**gtp-binding protein;<br>**PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3 |
| 6 | d1jala1 | Alignment |  | 100.0 | 83 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 7 | d1ni3a1 | Alignment |  | 100.0 | 40 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 8 | d1wxqa1 | Alignment |  | 100.0 | 22 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 9 | d1jala2 | Alignment |  | 100.0 | 79 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**TGS-like<br>**Family:**G domain-linked domain |
| 10 | c1udxA_ | Alignment |  | 100.0 | 33 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**the gtp-binding protein obg;<br>**PDBTitle:** crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8 |
| 11 | d1ni3a2 | Alignment |  | 100.0 | 46 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**TGS-like<br>**Family:**G domain-linked domain |

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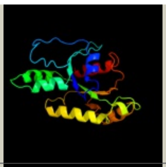
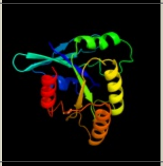
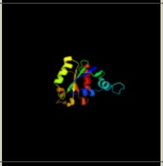
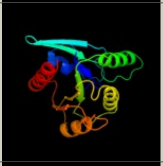
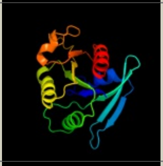
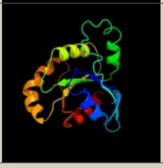
|---|---|---|---|---|---|---|
| 12 | c1lnzA_ | Alignment |  | 100.0 | 38 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**spo0b-associated gtp-binding protein;<br>**PDBTitle:** structure of the obg gtp-binding protein |
| 13 | c2e87A_ | Alignment |  | 99.9 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ph1320;<br>**PDBTitle:** crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp |
| 14 | c1xzqA_ | Alignment |  | 99.9 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable trna modification gtpase trme;<br>**PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf |
| 15 | c3ievA_ | Alignment |  | 99.9 | 27 | **PDB header:**nucleotide binding protein/rna<br>**Chain:** A: **PDB Molecule:**gtp-binding protein era;<br>**PDBTitle:** crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna |
| 16 | c3gehA_ | Alignment |  | 99.9 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**trna modification gtpase mnme;<br>**PDBTitle:** crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn |
| 17 | c1wf3A_ | Alignment |  | 99.9 | 30 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gtp-binding protein;<br>**PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8 |
| 18 | c3k53B_ | Alignment |  | 99.9 | 24 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**ferrous iron transport protein b;<br>**PDBTitle:** crystal structure of nfeob from p. furiosus |
| 19 | c2qthA_ | Alignment |  | 99.8 | 24 | **PDB header:**nucleotide binding protein<br>**Chain:** A: **PDB Molecule:**gtp-binding protein;<br>**PDBTitle:** crystal structure of a gtp-binding protein from the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp |
| 20 | c1mkyA_ | Alignment |  | 99.8 | 33 | **PDB header:**ligand binding protein<br>**Chain:** A: **PDB Molecule:**probable gtp-binding protein enga;<br>**PDBTitle:** structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains |
| 21 | c3lx8A_ | Alignment | not modelled | 99.8 | 25 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**ferrous iron uptake transporter protein b;<br>**PDBTitle:** crystal structure of gdp-bound nfeob from s. thermophilus |
| 22 | c3a1vB_ | Alignment | not modelled | 99.8 | 25 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**iron(ii) transport protein b;<br>**PDBTitle:** crystal structue of the cytosolic domain of t. maritima feob2 iron iransporter in apo form |
| 23 | c3i8sC_ | Alignment | not modelled | 99.8 | 22 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**ferrous iron transport protein b;<br>**PDBTitle:** structure of the cytosolic domain of e. coli feob, nucleotide-free2 form |
| 24 | c1egaB_ | Alignment | not modelled | 99.8 | 28 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protein (gtp-binding protein era);<br>**PDBTitle:** crystal structure of a widely conserved gtpase era |
| 25 | c3ibyA_ | Alignment | not modelled | 99.8 | 32 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**ferrous iron transport protein b;<br>**PDBTitle:** structure of cytosolic domain of l. pneumophila feob |
| 26 | c2hjgA_ | Alignment | not modelled | 99.8 | 26 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gtp-binding protein enga;<br>**PDBTitle:** the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp |
| 27 | d2bv3a2 | Alignment | not modelled | 99.8 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 28 | c2ekiA_ | Alignment | not modelled | 99.8 | 24 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1;<br>**PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1 |

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| 29 | d1h65a_ | Alignment | not modelled | 99.7 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 30 | c2j3eA_ | Alignment | not modelled | 99.7 | 18 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**t7i23.11 protein;<br>**PDBTitle:** dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159 |
| 31 | d2dy1a2 | Alignment | not modelled | 99.7 | 23 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 32 | c2wwwB_ | Alignment | not modelled | 99.7 | 16 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**methylmalonic aciduria type a protein,<br>**PDBTitle:** crystal structure of methylmalonic acidemia type a protein |
| 33 | c1kk3A_ | Alignment | not modelled | 99.7 | 23 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eif2gamma;<br>**PDBTitle:** structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+ |
| 34 | c3qq5A_ | Alignment | not modelled | 99.7 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**small gtp-binding protein;<br>**PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf |
| 35 | c3md0A_ | Alignment | not modelled | 99.7 | 20 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**arginine/ornithine transport system atpase;<br>**PDBTitle:** crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein) |
| 36 | c2xtpA_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**gtpase imap family member 2;<br>**PDBTitle:** crystal structure of nucleotide-free human gimap2, amino2 acid residues 1-260 |
| 37 | d1lnza2 | Alignment | not modelled | 99.7 | 38 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 38 | c3nxsA_ | Alignment | not modelled | 99.6 | 22 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**lao/ao transport system atpase;<br>**PDBTitle:** crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp |
| 39 | d2qm8a1 | Alignment | not modelled | 99.6 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 40 | d1tq4a_ | Alignment | not modelled | 99.6 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 41 | d2p67a1 | Alignment | not modelled | 99.6 | 26 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 42 | c2bvnB_ | Alignment | not modelled | 99.6 | 20 | **PDB header:**elongation factor<br>**Chain:** B: **PDB Molecule:**elongation factor tu;<br>**PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia |
| 43 | c3lxwA_ | Alignment | not modelled | 99.6 | 24 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**gtpase imap family member 1;<br>**PDBTitle:** crystal structure of human gtpase imap family member 1 |
| 44 | d1zunb3 | Alignment | not modelled | 99.6 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 45 | d2cxxa1 | Alignment | not modelled | 99.6 | 20 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 46 | c1wb1C_ | Alignment | not modelled | 99.5 | 18 | **PDB header:**protein synthesis<br>**Chain:** C: **PDB Molecule:**translation elongation factor selb;<br>**PDBTitle:** crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp |
| 47 | c2qptA_ | Alignment | not modelled | 99.5 | 19 | **PDB header:**endocytosis<br>**Chain:** A: **PDB Molecule:**eh domain-containing protein-2;<br>**PDBTitle:** crystal structure of an ehd atpase involved in membrane remodelling |
| 48 | c2xtnA_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**gtpase imap family member 2;<br>**PDBTitle:** crystal structure of gtp-bound human gimap2, amino acid2 residues 1-234 |
| 49 | c2qu8A_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative nucleolar gtp-binding protein 1;<br>**PDBTitle:** crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum |
| 50 | d1udxa2 | Alignment | not modelled | 99.5 | 39 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 51 | d1f60a3 | Alignment | not modelled | 99.5 | 14 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 52 | d2c78a3 | Alignment | not modelled | 99.5 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 53 | c3r7wC_ | Alignment | not modelled | 99.5 | 16 | **PDB header:**protein transport<br>**Chain:** C: **PDB Molecule:**gtp-binding protein gtr1;<br>**PDBTitle:** crystal structure of gtr1p-gtr2p complex |

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| 54 | c2plfA_ | Alignment | not modelled | 99.5 | 25 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit;<br>**PDBTitle:** the structure of aif2gamma subunit from the archaeon2 sulfolobus solfataricus in the nucleotide-free form. |
| 55 | d1wxqa2 | Alignment | not modelled | 99.5 | 27 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**TGS-like<br>**Family:**G domain-linked domain |
| 56 | c2j69D_ | Alignment | not modelled | 99.5 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**bacterial dynamin-like protein;<br>**PDBTitle:** bacterial dynamin-like protein bdlp |
| 57 | c3p1jC_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**gtpase imap family member 2;<br>**PDBTitle:** crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state |
| 58 | c2wsmB_ | Alignment | not modelled | 99.5 | 13 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**hydrogenase expression/formation protein (hypb);<br>**PDBTitle:** crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus |
| 59 | c2wjjB_ | Alignment | not modelled | 99.5 | 29 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**ferrous iron transport protein b homolog;<br>**PDBTitle:** structure and function of the feob g-domain from2 methanococcus jannaschii |
| 60 | d1kk1a3 | Alignment | not modelled | 99.5 | 25 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 61 | c3t1tC_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**gliding protein mgla;<br>**PDBTitle:** mgla bound to gdp in p1 tetrameric arrangement |
| 62 | c2dy1A_ | Alignment | not modelled | 99.4 | 22 | **PDB header:**signaling protein, translation<br>**Chain:** A: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus |
| 63 | d1svia_ | Alignment | not modelled | 99.4 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 64 | c3degC_ | Alignment | not modelled | 99.4 | 16 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**gtp-binding protein lepa;<br>**PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp |
| 65 | d1d2ea3 | Alignment | not modelled | 99.4 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 66 | c3lxxA_ | Alignment | not modelled | 99.4 | 21 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**gtpase imap family member 4;<br>**PDBTitle:** crystal structure of human gtpase imap family member 4 |
| 67 | c3izyP_ | Alignment | not modelled | 99.4 | 20 | **PDB header:**rna, ribosomal protein<br>**Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial;<br>**PDBTitle:** mammalian mitochondrial translation initiation factor 2 |
| 68 | d1wf3a1 | Alignment | not modelled | 99.4 | 29 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 69 | c2ywfA_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**gtp-binding protein lepa;<br>**PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus |
| 70 | d2gj8a1 | Alignment | not modelled | 99.4 | 22 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 71 | c1d2eA_ | Alignment | not modelled | 99.4 | 24 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**elongation factor tu (ef-tu);<br>**PDBTitle:** crystal structure of mitochondrial ef-tu in complex with gdp |
| 72 | c2qagC_ | Alignment | not modelled | 99.4 | 14 | **PDB header:**cell cycle, structural protein<br>**Chain:** C: **PDB Molecule:**septin-7;<br>**PDBTitle:** crystal structure of human septin trimer 2/6/7 |
| 73 | c1mj1A_ | Alignment | not modelled | 99.4 | 23 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**elongation factor tu;<br>**PDBTitle:** fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome |
| 74 | c3p1jB_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**gtpase imap family member 2;<br>**PDBTitle:** crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state |
| 75 | d1egaa1 | Alignment | not modelled | 99.4 | 23 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 76 | c3o47A_ | Alignment | not modelled | 99.4 | 25 | **PDB header:**hydrolase, hydrolase activator<br>**Chain:** A: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1, adp-<br>**PDBTitle:** crystal structure of arfgap1-arf1 fusion protein |
| 77 | c2qa5A_ | Alignment | not modelled | 99.4 | 24 | **PDB header:**cell cycle, structural protein<br>**Chain:** A: **PDB Molecule:**septin-2;<br>**PDBTitle:** crystal structure of sept2 g-domain |
| 78 | c1s0uA_ | Alignment | not modelled | 99.4 | 28 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit;<br>**PDBTitle:** eif2gamma apo |
| 79 | c3pqcA_ | Alignment | not modelled | 99.4 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable gtp-binding protein engb;<br>**PDBTitle:** crystal structure of thermotoga maritima ribosome |

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| | | | | | | biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp |
| 80 | c2elfA_ | Alignment | not modelled | 99.4 | 14 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**protein translation elongation factor 1a;<br>**PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei |
| 81 | c1zunB_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**sulfate adenylate transferase, subunit<br>**PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae |
| 82 | d1wb1a4 | Alignment | not modelled | 99.3 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 83 | c1zo1I_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**translation/rna<br>**Chain:** I: **PDB Molecule:**translation initiation factor 2;<br>**PDBTitle:** if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex |
| 84 | c3ftqA_ | Alignment | not modelled | 99.3 | 20 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**septin-2;<br>**PDBTitle:** crystal structure of septin 2 in complex with gppnhp and2 mg2+ |
| 85 | c1skqB_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**elongation factor 1-alpha;<br>**PDBTitle:** the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp |
| 86 | d1n0ua2 | Alignment | not modelled | 99.3 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 87 | c2dykB_ | Alignment | not modelled | 99.3 | 35 | **PDB header:**ribosome<br>**Chain:** B: **PDB Molecule:**gtp-binding protein;<br>**PDBTitle:** crystal structure of n-terminal gtp-binding domain of enga from2 thermus thermophilus hb8 |
| 88 | d1puia_ | Alignment | not modelled | 99.3 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 89 | c3lvrE_ | Alignment | not modelled | 99.3 | 21 | **PDB header:**protein transport<br>**Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain-<br>**PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium |
| 90 | d1jnya3 | Alignment | not modelled | 99.3 | 15 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 91 | c2q3fB_ | Alignment | not modelled | 99.3 | 17 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**ras-related gtp-binding protein d;<br>**PDBTitle:** x-ray crystal structure of putative human ras-related gtp2 binding d in complex with gmppnp |
| 92 | c3t5dC_ | Alignment | not modelled | 99.3 | 21 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**septin-7;<br>**PDBTitle:** crystal structure of septin 7 in complex with gdp |
| 93 | c1g7tA_ | Alignment | not modelled | 99.3 | 22 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor if2/eif5b;<br>**PDBTitle:** x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp |
| 94 | c3a1wA_ | Alignment | not modelled | 99.3 | 26 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**iron(ii) transport protein b;<br>**PDBTitle:** crystal structue of the g domain of t. maritima feob iron2 iransporter |
| 95 | d2qn6a3 | Alignment | not modelled | 99.3 | 22 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 96 | c3p27A_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein;<br>**PDBTitle:** crystal structure of a translational gtpase (gdp form) |
| 97 | c3ec1A_ | Alignment | not modelled | 99.3 | 30 | **PDB header:**hydrolase, signaling protein<br>**Chain:** A: **PDB Molecule:**yqeh gtpase;<br>**PDBTitle:** structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog) |
| 98 | c2hf9A_ | Alignment | not modelled | 99.3 | 13 | **PDB header:**hydrolase, metal binding protein<br>**Chain:** A: **PDB Molecule:**probable hydrogenase nickel incorporation<br>**PDBTitle:** crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form |
| 99 | c2bm0A_ | Alignment | not modelled | 99.3 | 18 | **PDB header:**elongation factor<br>**Chain:** A: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a |
| 100 | c2qagA_ | Alignment | not modelled | 99.2 | 17 | **PDB header:**cell cycle, structural protein<br>**Chain:** A: **PDB Molecule:**septin-2;<br>**PDBTitle:** crystal structure of human septin trimer 2/6/7 |
| 101 | d1jwyb_ | Alignment | not modelled | 99.2 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 102 | c3geiB_ | Alignment | not modelled | 99.2 | 26 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**trna modification gtpase mnme;<br>**PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp |
| 103 | d1zcaa2 | Alignment | not modelled | 99.2 | 21 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 104 | c2gedB_ | Alignment | not modelled | 99.2 | 26 | **PDB header:**protein transport, signaling protein<br>**Chain:** B: **PDB Molecule:**signal recognition particle receptor beta<br>**PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form |

| | | | | | | |
|---|---|---|---|---|---|---|
| 105 | c2wkqA_ | <br>Alignment | not modelled | 99.2 | 19 | **PDB header:**transferase, cell adhesion<br>**Chain:** A: **PDB Molecule:**nph1-1, ras-related c3 botulinum toxin substrate<br>**PDBTitle:** structure of a photoactivatable rac1 containing the lov22 c450a mutant |
| 106 | d1mkya2 | <br>Alignment | not modelled | 99.2 | 27 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 107 | d1yrba1 | <br>Alignment | not modelled | 99.2 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nitrogenase iron protein-like |
| 108 | d1s0ua3 | <br>Alignment | not modelled | 99.2 | 16 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 109 | d1efca3 | <br>Alignment | not modelled | 99.2 | 19 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 110 | c3hvzB_ | <br>Alignment | not modelled | 99.2 | 34 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a |
| 111 | c2qagB_ | <br>Alignment | not modelled | 99.2 | 17 | **PDB header:**cell cycle, structural protein<br>**Chain:** B: **PDB Molecule:**septin-6;<br>**PDBTitle:** crystal structure of human septin trimer 2/6/7 |
| 112 | c2kmmA_ | <br>Alignment | not modelled | 99.2 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'-<br>**PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481) |
| 113 | c2h5eB_ | <br>Alignment | not modelled | 99.2 | 18 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**peptide chain release factor rf-3;<br>**PDBTitle:** crystal structure of e.coli polypeptide release factor rf3 |
| 114 | c2rdo7_ | <br>Alignment | not modelled | 99.2 | 22 | **PDB header:**ribosome<br>**Chain:** 7: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound |
| 115 | d1r5ba3 | <br>Alignment | not modelled | 99.2 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 116 | c1g7cA_ | <br>Alignment | not modelled | 99.2 | 13 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**elongation factor 1-alpha;<br>**PDBTitle:** yeast eef1a:eef1ba in complex with gdpnp |
| 117 | c2x2fD_ | <br>Alignment | not modelled | 99.2 | 15 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**dynamin-1;<br>**PDBTitle:** dynamin 1 gtpase dimer, short axis form |
| 118 | c2xexA_ | <br>Alignment | not modelled | 99.2 | 16 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g |
| 119 | d2fh5b1 | <br>Alignment | not modelled | 99.2 | 22 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 120 | c3h2yA_ | <br>Alignment | not modelled | 99.1 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**gtpase family protein;<br>**PDBTitle:** crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound |